

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 15:59:55 ; Search time 104 Seconds
(without alignments)
1342.370 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 541
Sequence: 1 MGWVGVQLVLVADCTIFA.....FAEENIODEGTHVVEGDY 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_todent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	5	015681 toxoplasma
2	9	1.7	280	13	073716 grus americana
3	9	1.7	387	16	09K675 bacillus ha
4	9	1.7	401	16	09A9P5 caulobacter
5	9	1.7	923	16	08X7V7 escherichia
6	8	1.5	121	4	09BWR5
7	8	1.5	126	4	09B8T4
8	8	1.5	130	13	090230
9	8	1.5	133	5	09VNS5
10	8	1.5	143	5	08M221
11	8	1.5	145	4	08NCV9
12	8	1.5	199	2	08X04
13	8	1.5	210	2	08GC96
14	8	1.5	256	4	09B336
15	8	1.5	256	4	096NG2
16	8	1.5	256	4	096IK7

17	8	1.5	257	11	09D1F4	09d1f4 mus musculus
18	8	1.5	284	16	09EWP8	09ewp8 streptococ
19	8	1.5	346	7	P79458	P79458 ambystoma m
20	8	1.5	383	16	08YB66	08yeb66 bruceella me
21	8	1.5	383	16	08FX9	08fx900 bruceella su
22	8	1.5	396	16	08YXS0	08yxs00 anabaena sp
23	8	1.5	437	4	096OH1	096oh1 homo sapien
24	8	1.5	437	4	08N6Q3	08n6q3 homo sapien
25	8	1.5	437	4	09HDA5	09hda5 homo sapien
26	8	1.5	463	16	08ZFW8	08zfw8 yersinia pe
27	8	1.5	468	16	08G7P9	08g7p9 bifidobacte
28	8	1.5	476	12	08U736	08u736 west nile v
29	8	1.5	501	12	09W184	09w184 west nile v
30	8	1.5	501	12	091MB8	091mb8 west nile v
31	8	1.5	501	12	091MC1	091mc1 west nile v
32	8	1.5	501	12	091MB6	091mb6 west nile v
33	8	1.5	501	12	091MB5	091mb5 west nile v
34	8	1.5	501	12	091MB2	091mb2 west nile v
35	8	1.5	501	12	091MC2	091mc2 west nile v
36	8	1.5	501	12	08UT35	08ut35 west nile v
37	8	1.5	501	12	091MB7	091mb7 west nile v
38	8	1.5	501	12	091MB4	091mb4 west nile v
39	8	1.5	501	12	091MB3	091mb3 west nile v
40	8	1.5	501	12	091MC0	091mc0 west nile v
41	8	1.5	501	12	091MB9	091mb9 west nile v
42	8	1.5	502	12	08U740	08u740 west nile v
43	8	1.5	515	10	094C03	094cq3 oryza sativ
44	8	1.5	521	10	094C06	094cq6 oryza sativ
45	8	1.5	532	10	094C05	094cq5 oryza sativ
46	8	1.5	535	11	063314	063314 rattus norv
47	8	1.5	556	10	094C02	094cq2 oryza sativ
48	8	1.5	558	4	096D88	096d88 homo sapien
49	8	1.5	585	4	09BWN1	09bwn1 homo sapien
50	8	1.5	585	4	08WYX2	08wxy2 homo-sapien
51	8	1.5	608	11	08K153	08k153 mus musculus
52	8	1.5	637	10	094C04	094cq4 oryza sativ
53	8	1.5	640	10	08S6R0	08s6r0 oryza sativ
54	8	1.5	773	12	09WHD2	09whd2 west nile v
55	8	1.5	773	12	09WHD1	09whd1 west nile v
56	8	1.5	813	12	09J5R9	09j5r9 west nile v
57	8	1.5	1126	10	064605	064605 arabidopsis
58	8	1.5	1266	4	081WK6	081wk6 homo sapien
59	8	1.5	1314	12	08U2J7	08u2j7 cercopithec
60	8	1.5	2189	5	09B105	09b105 elmeria ten
61	8	1.5	3433	12	09EWM6	09ewm6 west nile v
62	8	1.5	3433	12	09EX21	09ex21 west nile v
63	8	1.5	3433	12	08QRN6	08qrn6 west nile v
64	8	1.5	3433	12	08JU45	08ju45 west nile v
65	8	1.5	3433	12	09Q519	09q519 west nile v
66	8	1.5	3433	12	09PD37	09pd37 west nile v
67	8	1.5	3433	12	08JU44	08ju44 west nile v
68	8	1.5	3433	12	08JU43	08ju43 west nile v
69	8	1.5	3433	12	08JU42	08ju42 west nile v
70	8	1.5	3433	12	09Q6P4	09q6p4 west nile v
71	8	1.5	3433	12	09EWM5	09ewm5 west nile v
72	8	1.5	3433	12	09Q3G9	09q3g9 west nile v
73	8	1.5	3433	12	08A273	08a273 west nile v
74	8	1.5	3434	10	09Q9F7	09q9f7 muray val
75	8	1.5	3658	12	09M7K6	09m7k6 arabidopsis
76	7	1.3	25	4	09UL44	09ul44 homo sapien
77	7	1.3	53	16	08E102	08e102 streptococ
78	7	1.3	68	17	08RYJ4	08ryj4 oryza sativ
79	7	1.3	79	17	08RYJ3	08ryj3 mechanopyru
80	7	1.3	80	11	09EON2	09eon2 mus musculu
81	7	1.3	94	2	09S6G6	09s6g6 streptococ
82	7	1.3	111	16	08XNA3	08xna3 clostridium
83	7	1.3	115	16	09L210	09l210 streptococ
84	7	1.3	120	8	035710	035710 rhyalus cyl
85	7	1.3	120	10	08LJ10	08lj10 oryza sativ
86	7	1.3	120	17	08ZUY6	08zuy6 pyrobaculum
87	7	1.3	122	3	09P3K5	09p3k5 neurospora
88	7	1.3	133	16	08XDM8	08xdm8 escherichia
89	7	1.3	133	16	08CW47	08cw47 escherichia

90	1.3	137	11	Q9EON1	Q9eqn1 mus musculu	163	7	1.3	255	16	Q8Y6E0	Q8y6e0 listeria mo
91	1.3	137	11	Q8K160	Q8k160 mus musculu	164	7	1.3	256	16	Q8NMW3	Q8nmw3 corynebacte
92	1.3	140	17	Q8TWR8	Q8twr8 methanopyru	165	7	1.3	256	16	Q9HUY6	Q9huy6 pseudomonas
93	1.3	141	16	Q8FTY7	Q8fty7 corynebacte	166	7	1.3	260	16	Q8DHM4	Q8dhm4 synchococc
94	1.3	151	2	Q8RQ98	Q8rq98 uncultured	167	7	1.3	264	16	Q8B693	Q8b693 streptomyce
95	1.3	151	2	Q9F096	Q9f096 nitrosomona	168	7	1.3	267	10	Q80989	Q80989 arabidopsis
96	1.3	151	2	Q8RO85	Q8r85 uncultured	169	7	1.3	269	10	Q94A83	Q94a83 arabidopsis
97	1.3	151	2	Q9E2S1	Q9e2s1 unidentified	170	7	1.3	269	16	Q34406	Q34406 bacillus su
98	1.3	151	2	Q9F046	Q9f046 unidentified	171	7	1.3	271	16	Q9ZFP8	Q9zfp8 bacillus me
99	1.3	151	2	Q9E2T5	Q9e2t5 unidentified	172	7	1.3	271	16	Q98MC0	Q98mc0 rhizobium l
100	1.3	151	2	Q9E2S2	Q9e2s2 unidentified	173	7	1.3	272	4	Q8N750	Q8n750 homo sapien
101	1.3	151	16	Q8YX85	Q8yx85 anabaena sp	174	7	1.3	276	16	Q8X6Z6	Q8x6z6 escherichia
102	1.3	154	16	Q8D8C8	Q8d8c8 vibrio vuln	175	7	1.3	276	16	Q8FCSS	Q8fcss escherichia
103	1.3	156	16	Q8DXH2	Q8dxh2 streptococc	176	7	1.3	277	16	Q97J80	Q97j80 clostridium
104	1.3	159	8	Q8SIL6	Q8sil6 scaphidura	177	7	1.3	277	16	Q8GSL3	Q8gsl3 bifidobacte
105	1.3	159	8	Q8SIL8	Q8sil8 scaphidura	178	7	1.3	277	16	Q8E3R7	Q8e3r7 streptococc
106	1.3	160	16	Q3J2S5	Q3j2s5 mycobacteri	179	7	1.3	277	16	Q8DYS1	Q8dys1 streptococc
107	1.3	161	16	Q9KUS6	Q9kus6 vibrio chol	180	7	1.3	278	11	Q61350	Q61350 mus musculu
108	1.3	169	16	Q9AAR2	Q9aar2 caulobacter	181	7	1.3	278	11	Q99232	Q99232 mus musculu
109	1.3	171	16	P87069	P87069 laccaria bi	182	7	1.3	280	2	Q9KIB5	Q9kib5 azotobacter
110	1.3	171	16	Q8VUP9	Q8vup9 mycobacteri	183	7	1.3	282	4	Q8WY42	Q8wy42 homo sapien
111	1.3	173	16	Q8HMI4	Q8hmi4 catapus ber	184	7	1.3	282	13	Q90YV9	Q90yv9 elaphe clim
112	1.3	175	16	Q9I2W8	Q9i2w8 pseudomonas	185	7	1.3	286	10	Q94KS6	Q94ks6 zea mays (m
113	1.3	178	2	Q9J3W6	Q9j3w6 anabaena va	186	7	1.3	291	16	Q92DQ2	Q92dq2 listeria in
114	1.3	178	16	Q9J3W8	Q9j3w8 anabaena sp	187	7	1.3	291	16	Q8Y6X5	Q8y6x5 listeria mo
115	1.3	179	16	Q8D7C7	Q8d7c7 vibrio vuln	188	7	1.3	291	17	Q8TL00	Q8tl00 methanocarc
116	1.3	182	5	Q20866	Q20866 caenorhabdi	189	7	1.3	292	3	Q96WP1	Q96wp1 agarcus bi
117	1.3	185	16	Q9S2A7	Q9s2a7 streptomyce	190	7	1.3	293	16	Q9HY65	Q9hy65 pseudomonas
118	1.3	188	16	Q9K1E1	Q9k1e1 neisseria m	191	7	1.3	295	4	Q9H746	Q9h746 homo sapien
119	1.3	190	11	Q89083	Q89083 mus musculu	192	7	1.3	298	8	Q9G811	Q9g811 emberiza sc
120	1.3	193	10	Q8W492	Q8w492 arabidopsis	193	7	1.3	300	5	Q9N8B3	Q9n8b3 trypanosoma
121	1.3	194	10	Q8GZ29	Q8gz29 arabidopsis	194	7	1.3	305	4	Q75308	Q75308 homo sapien
122	1.3	195	16	Q9RKD9	Q9rkd9 streptomyce	195	7	1.3	305	4	Q15287	Q15287 homo sapien
123	1.3	201	11	Q9EON0	Q9eqn0 mus musculu	196	7	1.3	305	11	Q99WZ8	Q99wz8 mus musculu
124	1.3	204	16	Q9I0Z8	Q9i0z8 pseudomonas	197	7	1.3	307	2	Q9ZAV8	Q9zav8 yersinia en
125	1.3	205	11	Q9APC1	Q9apc1 synchococc	198	7	1.3	308	16	Q91E24	Q91e24 pseudomonas
126	1.3	206	16	Q93679	Q93679 mus musculu	199	7	1.3	314	16	Q9CEFM1	Q9cfem1 lactococcus
127	1.3	206	16	Q9HTL7	Q9htl7 pseudomonas	200	7	1.3	315	16	Q8PIT6	Q8pit6 xanthomonas
128	1.3	207	10	P78939	P78939 schizosach	201	7	1.3	317	10	Q9LRS4	Q9lrs4 arabidopsis
129	1.3	207	10	Q9ZPX0	Q9zpx0 arabidopsis	202	7	1.3	324	2	Q05581	Q05581 streptomyce
130	1.3	215	16	Q9WX74	Q9wx74 acetobacter	203	7	1.3	327	2	Q34480	Q34480 bacillus su
131	1.3	216	16	Q8P1B7	Q8p1b7 streptococc	204	7	1.3	330	16	Q9ACY1	Q9acy1 streptomyce
132	1.3	216	16	Q8K7V0	Q8k7v0 streptococc	205	7	1.3	331	2	Q9PDD3	Q9pdd3 brucella ab
133	1.3	218	16	Q8XBC6	Q8xbc6 escherichia	206	7	1.3	332	2	Q8KIM3	Q8kim3 rhizobium e
134	1.3	220	5	Q20008	Q20008 caenorhabdi	207	7	1.3	333	5	Q8TIL4	Q8til4 dictyosteli
135	1.3	220	16	Q9RZ00	Q9rz00 deinococcus	208	7	1.3	336	5	Q8IR84	Q8ir84 anopheles g
136	1.3	221	4	Q8NSH1	Q8nsh1 homo sapien	209	7	1.3	338	5	Q8SRM1	Q8srw1 encephalito
137	1.3	222	16	Q8PD41	Q8pd41 xanthomonas	210	7	1.3	338	16	Q9RRAS	Q9rras yersinia en
138	1.3	226	10	Q9EGU7	Q9egu7 arabidopsis	211	7	1.3	339	3	Q96V05	Q96v05 magnaporthe
139	1.3	227	2	Q9JRA1	Q9jral hydrogenoba	212	7	1.3	341	11	Q61354	Q61354 mus musculu
140	1.3	228	10	Q8H6L6	Q8h6l6 capsicum an	213	7	1.3	344	12	Q89563	Q89563 variola vir
141	1.3	228	10	Q8H6L5	Q8h6l5 capsicum an	214	7	1.3	344	13	Q98T08	Q98t08 gallus gall
142	1.3	228	10	Q8GSF9	Q8gsf9 capsicum an	215	7	1.3	347	8	Q98I39	Q98i39 morus basaa
143	1.3	229	4	Q8NA43	Q8na43 homo sapien	216	7	1.3	349	5	Q9BIJ3	Q9bij3 sarcocystis
144	1.3	231	10	Q9M4R8	Q9m4r8 lycopersico	217	7	1.3	350	5	Q96501	Q96501 supella jon
145	1.3	232	16	Q8EPD0	Q8epd0 corynebacte	218	7	1.3	351	12	Q9DM14	Q9dm14 plurella xy
146	1.3	234	16	Q8U7M2	Q8u7m2 agrobacteri	219	7	1.3	355	10	Q9SBG7	Q9sbg7 arabidopsis
147	1.3	235	16	Q9XQ09	Q9xq09 vibrio chol	220	7	1.3	355	10	Q81242	Q81242 arabidopsis
148	1.3	237	16	Q8RB91	Q8rb91 thermomane	221	7	1.3	355	12	Q00906	Q00906 hepatitis c
149	1.3	244	16	Q8P6B3	Q8p6b3 xanthomonas	222	7	1.3	360	11	Q8R4S8	Q8r4s8 ratus norv
150	1.3	246	16	Q8ZB86	Q8zb86 yersinia pe	223	7	1.3	368	8	Q8WBE1	Q8wbe1 emberiza sc
151	1.3	247	11	Q8BXP1	Q8bxp1 mus musculu	224	7	1.3	372	2	Q9XCVO	Q9xcvo coxiella bu
152	1.3	247	16	Q97MD5	Q97md5 clostridium	225	7	1.3	372	17	Q9YAM9	Q9yam9 aeropyrum p
153	1.3	247	16	Q929V8	Q929v8 listeria in	226	7	1.3	373	16	Q8PEM1	Q8pem1 xanthomonas
154	1.3	247	16	Q8Y5K1	Q8y5k1 listeria mo	227	7	1.3	377	7	Q9GIW6	Q9giw6 ictalurus p
155	1.3	248	10	Q81858	Q81858 arabidopsis	228	7	1.3	379	5	Q45528	Q45528 caenorhabdi
156	1.3	249	16	Q8P8E7	Q8p8e7 leptospira	229	7	1.3	381	16	Q8CV92	Q8cv92 oceanobacil
157	1.3	251	12	Q84603	Q84603 paramesicium	230	7	1.3	381	15	Q8CV92	Q8cv92 oceanobacil
158	1.3	253	4	Q8N6N0	Q8n6n0 homo sapien	231	7	1.3	384	2	Q8KZ77	Q8kz77 uncultured
159	1.3	253	11	Q9CWE5	Q9cwe5 mus musculu	232	7	1.3	386	16	Q8D175	Q8d175 yersinia pe
160	1.3	254	16	Q8BXV2	Q8bxv2 mus musculu	233	7	1.3	387	16	Q8EJL3	Q8ejl3 shewanella
161	1.3	254	16	Q8PB90	Q8pb90 xanthomonas	234	7	1.3	387	17	Q9YAB0	Q9yab0 aeropyrum p
162	1.3	255	16	Q92AR1	Q92arl listeria in	235	7	1.3	390	5	Q9VID2	Q9vid2 drosophila

236	7	1.3	392	5	Q9B110	Q9b110 anopheles g	309	7	1.3	518	16	Q9RW8	Q9rvw8 delnoccocus
237	7	1.3	392	16	Q9KQ6	Q9kmq6 vibrio chol	310	7	1.3	518	16	Q9U69	Q9u69 agrobacteri
238	7	1.3	392	16	Q8EM5	Q8em5 oceanobacil	311	7	1.3	521	11	Q61352	Q61352 mus musculu
239	7	1.3	394	10	Q24091	Q24091 medicago tr	312	7	1.3	521	11	Q925P3	Q925P3 mus musculu
240	7	1.3	395	16	Q8PFI3	Q8pfj3 xanthomonas	313	7	1.3	521	16	Q8P3U4	Q8p3u4 xanthomonas
241	7	1.3	395	16	Q8P403	Q8p403 xanthomonas	314	7	1.3	525	4	Q8IX15	Q8ix15 homo sapien
242	7	1.3	399	16	Q8XMD0	Q8xmd0 clostridium	315	7	1.3	530	16	Q9AC16	Q9ac16 caulobacter
243	7	1.3	401	16	Q32891	Q32891 mycobacteri	316	7	1.3	539	11	Q8ROD9	Q8rod9 mus musculu
244	7	1.3	401	16	Q9XAK0	Q9xak0 streptomyc	317	7	1.3	541	16	Q9K404	Q9k404 vibrio chol
245	7	1.3	403	17	Q29358	Q29358 archaeoglob	318	7	1.3	541	16	Q8FWE7	Q8fwe7 bruceella su
246	7	1.3	405	16	Q69546	Q69546 mycobacteri	319	7	1.3	542	3	Q05379	Q05379 saccharomyc
247	7	1.3	409	16	Q8UBD7	Q8ubd7 agrobacteri	320	7	1.3	550	10	Q65335	Q65335 pisum sativ
248	7	1.3	409	16	Q8P873	Q8p873 xanthomonas	321	7	1.3	554	5	Q9VPX9	Q9vp9 xanthomonia
249	7	1.3	412	16	Q92Y26	Q92y26 rhizobium m	322	7	1.3	554	16	Q8Z0B3	Q8z0b3 bradyrhizob
250	7	1.3	415	16	Q8DIC6	Q8dic6 synecchococ	323	7	1.3	555	2	Q9JMW8	Q9jmw8 dirosophila
251	7	1.3	417	16	Q911G1	Q911g1 pseudomonas	324	7	1.3	557	5	Q8MSB5	Q8mbs dirosophila
252	7	1.3	423	5	Q61532	Q61532 dirosophila	325	7	1.3	563	10	Q04553	Q04553 arabidopsis
253	7	1.3	424	16	Q915K2	Q915k2 pseudomonas	326	7	1.3	566	17	Q976Q3	Q976q3 bulfolobus
254	7	1.3	426	16	Q9A6K4	Q9a6k4 caulobacter	327	7	1.3	567	10	Q8VYE4	Q8vye4 arabidopsis
255	7	1.3	427	17	Q8UIG8	Q8uig8 pyrococcus	328	7	1.3	570	4	Q9H6M6	Q9h6m6 homo sapien
256	7	1.3	429	2	Q8RNM2	Q8rnm2 legionella	329	7	1.3	570	4	Q8I222	Q8i222 homo sapien
257	7	1.3	442	13	Q9W622	Q9w622 xenopus lae	330	7	1.3	572	11	Q8CAL5	Q8cal5 mus musculu
258	7	1.3	444	17	Q28453	Q28453 archaeoglob	331	7	1.3	573	4	Q9P2A5	Q9p2a5 homo sapien
259	7	1.3	449	10	Q9LXQ3	Q9lxq3 arabidopsis	332	7	1.3	578	16	Q8YBX4	Q8ybx4 bruceella me
260	7	1.3	449	16	Q8ZJU4	Q8zju4 salmonella	333	7	1.3	579	10	Q8W0V5	Q8w0v5 lolium pere
261	7	1.3	449	16	Q8ZOT0	Q8zot0 salmonella	334	7	1.3	581	16	Q8DTZ7	Q8dtz7 streptococ
262	7	1.3	454	11	Q91W54	Q91w54 mus musculu	335	7	1.3	583	5	Q21007	Q21007 caenorhadi
263	7	1.3	454	11	Q91W54	Q91w54 mus musculu	336	7	1.3	585	10	Q81393	Q81393 arabidopsis
264	7	1.3	457	2	Q5E076	Q5e076 sphingomona	337	7	1.3	585	10	Q8W4N9	Q8w4n9 arabidopsis
265	7	1.3	458	10	Q9XE15	Q9xel15 zea mays (m	338	7	1.3	585	10	Q8H157	Q8h157 arabidopsis
266	7	1.3	459	16	Q9S4U0	Q9s4u0 mus musculu	339	7	1.3	589	3	Q9URE1	Q9ure1 saccharomyc
267	7	1.3	466	10	Q8T0P5	Q8t0p5 streptococ	340	7	1.3	589	5	Q8SY18	Q8sy18 dirosophila
268	7	1.3	466	10	Q8T0P5	Q8t0p5 streptococ	341	7	1.3	592	16	Q67937	Q67937 aquifex aeo
269	7	1.3	466	10	Q8T0P5	Q8t0p5 streptococ	342	7	1.3	593	5	Q9TX05	Q9tx05 dirosophila
270	7	1.3	466	10	Q8T0P5	Q8t0p5 streptococ	343	7	1.3	600	5	Q8T2G2	Q8t2g2 dictyosteli
271	7	1.3	466	10	Q8T0P5	Q8t0p5 streptococ	344	7	1.3	600	10	Q9CAR8	Q9car8 arabidopsis
272	7	1.3	466	10	Q8T0P5	Q8t0p5 streptococ	345	7	1.3	602	16	Q8CJP2	Q8cjp2 streptomyc
273	7	1.3	466	10	Q8T0P5	Q8t0p5 streptococ	346	7	1.3	605	10	Q8H9F2	Q8h9f2 oryza sativ
274	7	1.3	469	16	Q9JRK0	Q9jrk0 neisseria m	347	7	1.3	606	16	Q9WKN8	Q9wkn8 thermotoga
275	7	1.3	470	2	Q9KJVL	Q9kjl1 lactobacill	348	7	1.3	610	16	Q9KXG9	Q9kxg9 bacillus ha
276	7	1.3	474	10	Q9JLM8	Q9jlm8 arabidopsis	349	7	1.3	611	16	Q8DKF5	Q8dkf5 synecchococ
277	7	1.3	474	16	Q9X929	Q9x929 streptomyc	350	7	1.3	612	16	Q8FQU0	Q8fqu0 corynebacte
278	7	1.3	476	10	Q9SXR2	Q9sxt2 scutellaria	351	7	1.3	631	10	Q9XED8	Q9xed8 arabidopsis
279	7	1.3	477	16	Q9AAR2	Q9aar2 caulobacter	352	7	1.3	648	10	Q94GM3	Q94gm3 oryza sativ
280	7	1.3	480	2	Q9JF90	Q9jfe90 streptomyc	353	7	1.3	645	10	Q9FWZ8	Q9fwz8 arabidopsis
281	7	1.3	480	16	Q9JF90	Q9jfe90 streptomyc	354	7	1.3	645	5	Q21573	Q21573 caenorhadi
282	7	1.3	482	2	Q9APV8	Q9apv8 pseudomonas	355	7	1.3	651	4	Q9NXT9	Q9nxt9 homo sapien
283	7	1.3	482	10	Q8LB19	Q8lb19 arabidopsis	356	7	1.3	651	4	Q9NXT9	Q9nxt9 homo sapien
284	7	1.3	482	10	Q8LB19	Q8lb19 arabidopsis	357	7	1.3	651	10	Q8VXS1	Q8vxs1 solanum tub
285	7	1.3	484	16	Q8VJUS	Q8vj15 raietonia s	358	7	1.3	656	16	Q8DAW4	Q8daw4 vibrio vuln
286	7	1.3	484	16	Q8EMC2	Q8emc2 oceanobacil	359	7	1.3	658	2	Q8GPT3	Q8gpt3 citrobacter
287	7	1.3	487	2	P72269	P72269 rhodococcus	360	7	1.3	658	16	Q9KMG2	Q9kmg2 vibrio chol
288	7	1.3	488	3	Q96U74	Q96u74 neurospora	361	7	1.3	660	16	Q8FL17	Q8fl17 escherichia
289	7	1.3	492	4	Q9H784	Q9h784 homo sapien	362	7	1.3	669	5	Q8SXS8	Q8sxs8 dirosophila
290	7	1.3	492	11	Q8R3T2	Q8r3tc mus musculu	363	7	1.3	669	5	Q9VYE6	Q9vye6 dirosophila
291	7	1.3	492	11	Q8R3T2	Q8r3tc mus musculu	364	7	1.3	671	16	Q9BDY9	Q9bdy9 rhizobium 1
292	7	1.3	493	5	Q8N0N7	Q8n0n7 apis mellif	365	7	1.3	676	10	Q8VXS2	Q8vxs2 solanum tub
293	7	1.3	493	5	Q8N0N7	Q8n0n7 apis mellif	366	7	1.3	676	10	Q8VXS2	Q8vxs2 solanum tub
294	7	1.3	495	2	Q46252	Q46252 clostridium	367	7	1.3	685	16	Q8P7R3	Q8p7r3 xanthomonas
295	7	1.3	495	16	Q8XPO2	Q8xpo2 xanthomonas	368	7	1.3	705	10	Q9LKB0	Q9lkb0 arabidopsis
296	7	1.3	496	13	Q8JFQ5	Q8jfc5 oncorhynch	369	7	1.3	706	3	Q12039	Q12039 saccharomyc
297	7	1.3	497	10	Q22991	Q22991 arabidopsis	370	7	1.3	708	4	Q9UGU9	Q9ugu9 homo sapien
298	7	1.3	498	11	Q8BNB0	Q8bnb0 mus musculu	371	7	1.3	714	4	Q96G17	Q96g17 homo sapien
299	7	1.3	498	11	Q8BNB0	Q8bnb0 mus musculu	372	7	1.3	721	10	Q22208	Q22208 arabidopsis
300	7	1.3	498	11	Q8BNB0	Q8bnb0 mus musculu	373	7	1.3	721	10	Q8L7E7	Q8l7e7 arabidopsis
301	7	1.3	501	2	Q9LAL1	Q9lal1 pseudomonas	374	7	1.3	723	2	Q9EWC1	Q9ewc1 streptomyc
302	7	1.3	503	17	Q8WQW9	Q8wqm9 anophelis g	375	7	1.3	733	16	Q91664	Q91664 pseudomonas
303	7	1.3	503	17	Q8WQW9	Q8wqm9 anophelis g	376	7	1.3	741	16	Q9RWS7	Q9rvw7 delnoccocus
304	7	1.3	505	10	Q8W032	Q8w032 arabidopsis	377	7	1.3	744	2	Q8KTP4	Q8ktp4 listeria mo
305	7	1.3	510	16	Q8EZX5	Q8ezx5 leptospira	378	7	1.3	745	3	Q94464	Q94464 echizosacch
306	7	1.3	512	16	Q9HVA7	Q9hva7 pseudomonas	379	7	1.3	755	3	Q8NIU6	Q8niu6 neurospora
307	7	1.3	517	2	Q9ZGB6	Q9zgb6 streptomyc	380	7	1.3	755	16	Q9RTB1	Q9rtb1 delnoccocus
308	7	1.3	518	5	Q9V6K8	Q9v6k8 dirosophila	381	7	1.3	766	10	Q8H6B0	Q8h6b0 zea mays (m

382	1.3	773	16	08YVD2	08Yvd2 anabaeana sp	455	7	1.3	2064	5	09VP19	09vp19 drosophila
383	1.3	774	4	09SE941	09SE941 homo sapien	456	7	1.3	2138	5	09XZE3	09xez3 ameba prot
384	1.3	778	5	09SX07	09SX07 peraneus mon	457	7	1.3	2492	12	08JTW9	08jtw9 sweet potat
385	1.3	782	10	09L2A0	09L2A0 atribidopsis	458	7	1.3	3177	5	09NA13	09na13 dictyosteli
386	1.3	794	16	09X212	09X212 thermotoga	459	7	1.3	3257	5	09V736	09v736 drosophila
387	1.3	802	4	08TDA0	08tda0 homo sapien	460	6	1.1	22	6	09TRC4	09trc4 canis famli
388	1.3	802	10	08L4U4	08l4u4 oryza sativ	461	6	1.1	24	2	005421	005421 mycobacteri
389	1.3	816	11	08BR55	08br55 mus musculu	462	6	1.1	27	2	056139	056139 streptococc
390	1.3	830	16	09H2Y6	09h2y6 pseudomonas	463	6	1.1	31	2	053411	053411 bacillus mu
391	1.3	839	9	064076	064076 bacteriophia	464	6	1.1	34	6	0951A4	0951a4 macaca mula
392	1.3	839	16	09RX57	09rx57 deinococcus	465	6	1.1	34	6	0951A6	0951a6 sus scrofa
393	1.3	839	16	031945	031945 bacillus su	466	6	1.1	34	11	0912X2	0912x2 cavia porce
394	1.3	845	4	09HAU3	09haug homo sapien	467	6	1.1	38	2	09REY8	09rey8 carnobacter
395	1.3	845	4	09HBB8	09hbb8 homo sapien	468	6	1.1	42	2	09ZPA2	09zfa2 rhodobacter
396	1.3	845	4	09HBB5	09hbb5 homo sapien	469	6	1.1	43	16	09X131	09x131 thermotoga
397	1.3	884	11	08BN06	08bn06 mus musculu	470	6	1.1	46	12	092581	092581 hepatitis c
398	1.3	894	4	08NSL2	08ns12 homo sapien	471	6	1.1	46	16	034568	034568 bacillus su
399	1.3	911	4	09H330	09h330 homo sapien	472	6	1.1	47	11	09OWS6	09ow6 mus musculu
400	1.3	942	5	018298	018298 caenorhabdi	473	6	1.1	47	16	09PJR2	09pj2 chlamydia m
401	1.3	944	12	09DM96	09dm96 rat cytomeg	474	6	1.1	48	5	09V942	09v942 drosophila
402	1.3	962	5	08IGQ1	08igq1 drosophila	475	6	1.1	48	5	09V942	09ifp9 chilo iride
403	1.3	968	3	09Y7J9	09y7j9 schizosacch	476	6	1.1	48	12	091FP9	09k10 vibrio chol
404	1.3	971	4	060337	060337 homo sapien	477	6	1.1	48	16	09KLD0	09wan0 hepatitis c
405	1.3	1010	3	09USN1	09usen1 schizosacch	478	6	1.1	49	12	09WANO	09w9e1 hepatitis c
406	1.3	1013	3	09HFE4	09hfe4 ashyba goos	479	6	1.1	49	12	09W9E1	09wan6 hepatitis c
407	1.3	1014	5	018016	018016 caenorhabdi	480	6	1.1	50	12	09NAM6	09n6e5 human echov
408	1.3	1043	5	08SSW7	08ssw7 dictyosteli	481	6	1.1	53	16	09K6C3	09k6c3 bacillus ha
409	1.3	1050	16	08FN18	08fn18 corynebacte	482	6	1.1	53	16	08U5A8	08u5a8 agrobacteri
410	1.3	1052	3	09PE63	09pe63 schizosacch	483	6	1.1	54	16	08GAJ3	08ga3 escherichia
411	1.3	1061	5	08WRF4	08wrf4 monosiga br	484	6	1.1	56	6	029276	029276 sus scrofa
412	1.3	1068	10	09AXF7	09axf7 chlamydomon	485	6	1.1	56	11	091Z85	091z85 mus musculu
413	1.3	1078	5	09V460	09v460 drosophila	486	6	1.1	56	11	091Z85	09cf17 lactococcus
414	1.3	1081	2	068831	068831 bacterioides	487	6	1.1	58	16	09CFU7	08er9 oceanobacil
415	1.3	1091	16	0928J2	0928j2 listeria in	488	6	1.1	58	16	08ERU9	08e630 bacteriophia
416	1.3	1091	16	08Y4J2	08y4j2 listeria mo	489	6	1.1	60	9	08M630	097974 equus cabal
417	1.3	1092	5	0964R2	0964r2 thelleria t	490	6	1.1	61	6	097974	09tup2 equus cabal
418	1.3	1151	5	096593	096593 heterodera	491	6	1.1	61	6	09TUP2	08e9e5 oryza sativ
419	1.3	1174	16	08ZP89	08zp89 salmoneila	492	6	1.1	61	10	08S9E5	072203 hepatitis c
420	1.3	1174	16	08Z781	08z781 salmoneila	493	6	1.1	62	2	050163	050163 mycobacteri
421	1.3	1174	16	08X9Q3	08x9q3 escherichia	494	6	1.1	62	2	09C5L9	09c6319 mus musculu
422	1.3	1174	16	08FHP2	08fhp2 escherichia	495	6	1.1	62	11	09CSL9	09hs33 halobacteri
423	1.3	1177	16	08ZES0	08zes0 yersinia pe	496	6	1.1	62	17	09HSJ9	09hs33 oryza sativ
424	1.3	1185	16	08KCO2	08kco2 chlorobium	497	6	1.1	63	10	09SPN4	09tpw4 deinococcus
425	1.3	1187	16	08YVR3	08yvr3 anabaena sp	498	6	1.1	63	16	09RTW3	09rps5 rhizobium l
426	1.3	1201	4	08N3V0	08n3v0 homo sapien	499	6	1.1	63	16	09RPE9	09v10 drosophila
427	1.3	1204	4	08NDG4	08ndg4 homo sapien	500	6	1.1	64	5	08U2N1	08uzn1 garlic late
428	1.3	1208	5	018023	018023 caenorhabdi	501	6	1.1	64	12	08U2N1	091jw7 hepatitis c
429	1.3	1234	4	094983	094983 homo sapien	502	6	1.1	64	12	091JW7	08e755 oryza sativ
430	1.3	1241	5	09U144	09u144 leishmania	503	6	1.1	65	10	08S755	09ue5 staphylococ
431	1.3	1250	4	09COJ4	09coj4 homo sapien	504	6	1.1	65	16	099UF9	081lv5 hordeum vul
432	1.3	1251	4	09UBZ9	09ubz9 homo sapien	505	6	1.1	66	10	081LV5	084d2 staphylococ
433	1.3	1253	11	061810	061810 mus musculu	506	6	1.1	67	2	08S4D2	084d2 european el
434	1.3	1256	13	09OMJ3	09omj3 xenopus lae	507	6	1.1	67	12	0842E4	08xw13 ralsconia s
435	1.3	1271	5	09V8K6	09v8k6 drosophila	508	6	1.1	67	16	08XW13	09n626 mytilus edu
436	1.3	1276	13	09OX22	09ox22 brachydantio	509	6	1.1	68	5	09N626	09na66 mytilus edu
437	1.3	1298	5	09XZ32	09xz32 drosophila	510	6	1.1	68	15	011634	011634 human immun
438	1.3	1346	2	04S956	04s956 clostridium	511	6	1.1	68	15	09WMD5	09uad6 glomus moss
439	1.3	1611	2	033957	033957 streptomyce	512	6	1.1	71	3	09WMD5	09uad6 glomus moss
440	1.3	1646	2	093HMO	093hmo streptococc	513	6	1.1	71	3	09WMD5	09uad6 glomus moss
441	1.3	1659	16	097S90	097s90 streptococc	514	6	1.1	72	8	09NAT8	09nat8 mycobacteri
442	1.3	1659	16	08C252	08c252 streptococc	515	6	1.1	73	12	091FP8	09ifp8 chilo iride
443	1.3	1661	6	09GKPI	09gkpi sus scrofa	516	6	1.1	73	12	091FP8	095046 mycobacteri
444	1.3	1730	13	08UVY7	08uvy7 xenopus lae	517	6	1.1	73	16	095046	099qr4 streptomyce
445	1.3	1734	4	09Y6Y1	09y6y1 homo sapien	518	6	1.1	74	16	093QR4	094661 streptococc
446	1.3	1742	16	08P377	08p377 xanthomonas	519	6	1.1	75	2	054661	09pb10 xyella fas
447	1.3	1792	10	08LSR5	08lsr5 oryza sativ	520	6	1.1	75	16	08CSP3	08csp3 archaeoglob
448	1.3	1795	5	076894	076894 drosophila	521	6	1.1	75	17	034839	034839 archaeoglob
449	1.3	1868	3	078615	078615 emericella	522	6	1.1	76	3	09Y8F5	09y8f5 glomus moss
450	1.3	1910	16	08Z8Y3	08z8y3 yersinia pe	523	6	1.1	76	3	09Y8F5	09y8f5 glomus moss
451	1.3	1916	5	09VKG8	09vkg8 drosophila	524	6	1.1	77	2	054671	054671 streptococc
452	1.3	1980	5	09VHD1	09vhd1 drosophila	525	6	1.1	77	2	054671	027725 methanobac
453	1.3	2051	4	09P2F2	09p2f2 homo sapien	526	6	1.1	77	17	027725	
454	1.3	2062	4	09H231	09h231 homo sapien	527	6	1.1	78	6	09N241	09n241 saimiri bol

528	6	1.1	79	5	09W312	09W312 drosophila	601	6	1.1	95	6	097520	097520 pongo pygma
529	6	1.1	79	16	08ZIR4	08ZIR4 yersinia pe	602	6	1.1	95	6	097519	097519 pongo pygma
530	6	1.1	80	3	08JW3	08JW3 colleptic	603	6	1.1	95	16	08ZLS4	08ZLS4 salmonella
531	6	1.1	80	11	08CF36	08CF36 mus musculu	604	6	1.1	95	16	08Z3G9	08Z3G9 salmonella
532	6	1.1	81	2	044114	044114 bynechococ	605	6	1.1	96	5	08Z3G9	08Z3G9 salmonella
533	6	1.1	81	8	08MA07	08MA07 chaetosphae	606	6	1.1	96	5	08Z3G9	08Z3G9 salmonella
534	6	1.1	81	10	08RU61	08RU61 atropa bell	607	6	1.1	96	5	08Z3G9	08Z3G9 salmonella
535	6	1.1	81	10	09LHB8	09LHB8 arabidopsis	608	6	1.1	96	12	09QU12	09QU12 tt virus. o
536	6	1.1	82	8	09TL14	09TL14 nephroselm	609	6	1.1	96	12	09QU18	09QU18 tt virus. o
537	6	1.1	83	2	08LIC4	08LIC4 pasteurella	610	6	1.1	96	12	09QU09	09QU09 tt virus. o
538	6	1.1	84	4	09P183	09P183 homo sapien	611	6	1.1	96	12	09QU24	09QU24 tt virus. o
539	6	1.1	84	10	094AQ4	094AQ4 arabidopsis	612	6	1.1	96	12	09QU28	09QU28 tt virus. o
540	6	1.1	84	10	08HEM9	08HEM9 gosyplum h	613	6	1.1	96	13	08AVT7	08AVT7 xenopus lae
541	6	1.1	84	16	09K8W7	09K8W7 bacillus ha	614	6	1.1	96	15	08JAV5	08JAV5 human immun
542	6	1.1	85	4	08TES9	08TES9 homo sapien	615	6	1.1	96	16	08URE2	08URE2 agrobacteri
543	6	1.1	85	10	08WMB2	08WMB2 capsicum an	616	6	1.1	97	16	08PE65	08PE65 xanthomonas
544	6	1.1	85	10	08LAF8	08LAF8 oryza sativ	617	6	1.1	98	4	016303	016303 homo sapien
545	6	1.1	86	4	09BYL6	09BYL6 homo sapien	618	6	1.1	98	4	016303	016303 homo sapien
546	6	1.1	86	8	020482	020482 andropadu	619	6	1.1	98	5	09BK59	09BK59 caenorhadi
547	6	1.1	86	10	09MLK8	09MLK8 arabidopsis	620	6	1.1	98	8	094X19	094X19 neoceratodu
548	6	1.1	86	10	09CAJ1	09CAJ1 arabidopsis	621	6	1.1	98	10	09FH20	09FH20 arabidopsis
549	6	1.1	87	5	08IC09	08IC09 plasmodium	622	6	1.1	98	10	093347	093347 nicotiana t
550	6	1.1	87	6	09W242	09W242 atelea sp.	623	6	1.1	99	2	08VLJ0	08VLJ0 escherichia
551	6	1.1	87	10	040441	040441 nicotiana g	624	6	1.1	99	2	08GER3	08GER3 erwinia pyr
552	6	1.1	87	11	035365	035365 mus musculu	625	6	1.1	99	4	08N6X9	08N6X9 homo sapien
553	6	1.1	87	11	035365	035365 mus musculu	626	6	1.1	99	4	09UG68	09UG68 homo sapien
554	6	1.1	87	12	08V2T4	08V2T4 camelopx vi	627	6	1.1	99	6	097518	097518 pongo pygma
555	6	1.1	87	16	08XH57	08XH57 clostridium	628	6	1.1	99	8	08SKR4	08SKR4 orthomyx te
556	6	1.1	87	16	08E795	08E795 streptococ	629	6	1.1	99	10	08W537	08W537 retama taet
557	6	1.1	87	16	08E1T1	08E1T1 streptococ	630	6	1.1	99	10	08GYN2	08GYN2 arabidopsis
558	6	1.1	87	17	08ZXY17	08ZXY17 pyrobaculum	631	6	1.1	99	16	097R38	097R38 streptococ
559	6	1.1	88	4	099587	099587 homo sapien	632	6	1.1	99	16	08ZKN6	08ZKN6 salmonella
560	6	1.1	88	8	020506	020506 andropadu	633	6	1.1	99	16	08CLH2	08CLH2 yersinia pe
561	6	1.1	88	13	09PSY9	09PSY9 sparus aura	634	6	1.1	100	2	09X625	09X625 coxiella bu
562	6	1.1	89	16	09K8S2	09K8S2 bacillus ha	635	6	1.1	100	8	08HHT2	08HHT2 poecille atr
563	6	1.1	89	16	08P1V3	08P1V3 xanthomonas	636	6	1.1	100	12	08ORH3	08ORH3 hepatitis c
564	6	1.1	90	4	096GH6	096GH6 homo sapien	637	6	1.1	100	12	08ORG7	08ORG7 hepatitis c
565	6	1.1	90	10	09MW2	09MW2 arabidopsis	638	6	1.1	100	12	08OR12	08OR12 hepatitis c
566	6	1.1	90	11	08CSJ6	08CSJ6 mus musculu	639	6	1.1	100	12	08ORG8	08ORG8 hepatitis c
567	6	1.1	90	13	09DD49	09DD49 cryzias lat	640	6	1.1	100	12	08QRH8	08QRH8 hepatitis c
568	6	1.1	90	13	08UT03	08UT03 cryzias lat	641	6	1.1	100	12	08QRH4	08QRH4 hepatitis c
569	6	1.1	90	13	08AMP6	08AMP6 oreochromis	642	6	1.1	100	15	040277	040277 human immun
570	6	1.1	90	16	097MR2	097MR2 clostridium	643	6	1.1	100	15	091132	091132 human immun
571	6	1.1	91	6	09N244	09N244 naealis lar	644	6	1.1	100	16	08DFK7	08DFK7 vibrio vuln
572	6	1.1	91	6	09N245	09N245 macaca mla	645	6	1.1	101	4	09BX24	09BX24 homo sapien
573	6	1.1	91	6	097517	097517 gotilla gor	646	6	1.1	101	16	09XZ29	09XZ29 thermotoga
574	6	1.1	91	6	097515	097515 pan paniscu	647	6	1.1	102	2	09AFR3	09AFR3 shigella fl
575	6	1.1	91	6	097521	097521 pongo pygma	648	6	1.1	102	8	08WCI6	08WCI6 parus atric
576	6	1.1	91	6	09N243	09N243 presbytis c	649	6	1.1	102	8	08WCI7	08WCI7 parus carol
577	6	1.1	91	6	09N246	09N246 papio hamad	650	6	1.1	102	11	08GCR7	08GCR7 mus musculu
578	6	1.1	91	12	09MN23	09MN23 hepatitis c	651	6	1.1	102	11	08BRD6	08BRD6 mus musculu
579	6	1.1	91	12	09W9K2	09W9K2 hepatitis c	652	6	1.1	102	16	09CFR3	09CFR3 lactococcus
580	6	1.1	91	13	098TB2	098TB2 ambloplites	653	6	1.1	102	17	09UWX1	09UWX1 sulfolobus
581	6	1.1	91	16	08YG26	08YG26 bruceia me	654	6	1.1	103	2	049825	049825 mycobacteri
582	6	1.1	91	16	09CHV2	09CHV2 lactococcus	655	6	1.1	103	11	08VDP22	08VDP22 pseudomonas
583	6	1.1	91	16	08GOW3	08GOW3 bruceia su	656	6	1.1	103	11	08VDP22	08VDP22 mus musculu
584	6	1.1	91	16	08DID7	08DID7 yersinia pe	657	6	1.1	103	13	09PSE1	09PSE1 torpedo cal
585	6	1.1	92	4	08NHM4	08NHM4 homo sapien	658	6	1.1	103	15	040324	040324 human immun
586	6	1.1	92	12	08ULZ1	08ULZ1 mamestra co	659	6	1.1	103	15	0992T8	0992T8 human immun
587	6	1.1	92	12	08V501	08V501 monkeypox v	660	6	1.1	104	8	08SLR8	08SLR8 dunaliella
588	6	1.1	92	12	08OL70	08OL70 mamestra co	661	6	1.1	104	16	08B9P1	08B9P1 shewanella
589	6	1.1	92	16	08XPB6	08XPB6 clostridium	662	6	1.1	105	5	09V941	09V941 drosophila
590	6	1.1	93	6	09N247	09N247 hylobates s	663	6	1.1	105	10	094FC5	094FC5 gosyplum a
591	6	1.1	94	2	09P1P0	09P1P0 shewanella	664	6	1.1	105	10	094FC4	094FC4 gosyplum s
592	6	1.1	94	2	054670	054670 streptococ	665	6	1.1	105	10	094FC3	094FC3 gosyplum l
593	6	1.1	94	6	097950	097950 equus cabal	666	6	1.1	105	10	094FC1	094FC1 oryza sativ
594	6	1.1	94	6	08HYN2	08HYN2 macaca mla	667	6	1.1	105	10	094FC1	094FC1 kokia ditya
595	6	1.1	94	16	08P908	08P908 xanthomonas	668	6	1.1	105	10	094FC2	094FC2 gosyplum b
596	6	1.1	95	4	099586	099586 homo sapien	669	6	1.1	105	15	09M695	09M695 gosyplode
597	6	1.1	95	6	097514	097514 pan troglod	670	6	1.1	105	15	088188	088188 human immun
598	6	1.1	95	6	09N249	09N249 hylobates x	671	6	1.1	105	16	092079	092079 rhizobium m
599	6	1.1	95	6	09N248	09N248 hylobates l	672	6	1.1	106	2	09F6W6	09F6W6 chloroflexu
600	6	1.1	95	6	097516	097516 gotilla gor	673	6	1.1	106	2	08GM40	08GM40 legioneila

674	6	1.1	106	5	08SRV8	08SRV8 encephalico	747	6	1.1	114	6	097534	097534 aotus vocif
675	6	1.1	106	6	08HXF5	08HXF5 macaca fasc	748	6	1.1	114	10	08LJ57	08LJ57 oryza sativ
676	6	1.1	106	11	08CG35	08CG35 ratuca norv	749	6	1.1	114	15	08G517	08G517 human immun
677	6	1.1	106	16	08Z018	08Z018 anabena sp	750	6	1.1	114	15	09WNK4	09WNK4 human immun
678	6	1.1	106	16	08EE21	08EE21 shewanelia	751	6	1.1	114	15	08Q6L8	08Q6L8 human immun
679	6	1.1	106	16	08E803	08E803 shewanelia	752	6	1.1	114	15	08Q6E1	08Q6E1 human immun
680	6	1.1	107	10	080374	080374 aater tripo	753	6	1.1	114	15	08Q6D7	08Q6D7 human immun
681	6	1.1	107	10	080371	080371 aater tripo	754	6	1.1	114	15	08Q6S1	08Q6S1 human immun
682	6	1.1	107	10	080375	080375 aater tripo	755	6	1.1	114	15	08Q6E3	08Q6E3 human immun
683	6	1.1	107	11	08CCU5	08CCU5 mus musculu	756	6	1.1	114	15	09Q452	09Q452 human immun
684	6	1.1	107	16	09PAR7	09PAR7 xyella fas	757	6	1.1	114	15	08Q6L9	08Q6L9 human immun
685	6	1.1	107	16	09KEC3	09KEC3 bacillus ha	758	6	1.1	114	15	08Q6R5	08Q6R5 human immun
686	6	1.1	107	16	092TK9	092TK9 rhizobium h	759	6	1.1	114	15	09WNQ0	09WNQ0 human immun
687	6	1.1	108	16	08YGR7	08YGR7 bruceella me	760	6	1.1	114	15	07Q164	07Q164 human immun
688	6	1.1	108	16	08G147	08G147 bruceella su	761	6	1.1	114	15	09WNR0	09WNR0 human immun
689	6	1.1	108	16	08CKC1	08CKC1 yersinia pe	762	6	1.1	114	15	08Q6O5	08Q6O5 human immun
690	6	1.1	109	2	09XDM3	09XDM3 rhodopseudo	763	6	1.1	114	16	09BLU0	09BLU0 human immun
691	6	1.1	109	2	03O535	03O535 pseudomonas	764	6	1.1	114	16	09K9N3	09K9N3 human immun
692	6	1.1	109	2	09R7F9	09R7F9 unidentified	765	6	1.1	114	16	08PC77	08PC77 human immun
693	6	1.1	109	3	093910	093910 neurospora	766	6	1.1	114	16	08NNE0	08NNE0 human immun
694	6	1.1	109	3	08T785	08T785 cryptospori	767	6	1.1	115	10	043762	043762 hordium vul
695	6	1.1	109	5	09JOM9	09JOM9 human immun	768	6	1.1	115	11	08CS47	08CS47 mus musculu
696	6	1.1	109	15	025421	025421 helicobacte	769	6	1.1	115	15	09QDL3	09QDL3 human immun
697	6	1.1	109	16	091328	091328 pseudomonas	770	6	1.1	115	15	09Q429	09Q429 human immun
698	6	1.1	109	16	08Z4U7	08Z4U7 salmonella	771	6	1.1	115	15	09Q469	09Q469 human immun
699	6	1.1	109	17	08TVZ7	08TVZ7 methanopyru	772	6	1.1	115	16	09RVA4	09RVA4 human immun
700	6	1.1	110	2	08KKB9	08KKB9 helicobacte	773	6	1.1	115	16	08E835	08E835 shewanelia
701	6	1.1	110	2	093EB6	093EB6 rhizobium l	774	6	1.1	116	2	09F817	09F817 carboxydoth
702	6	1.1	110	2	087801	087801 pseudomonas	775	6	1.1	116	2	08KKA0	08KKA0 proteus vul
703	6	1.1	110	2	08G1Q7	08G1Q7 streptomyce	776	6	1.1	116	5	09BNF4	09BNF4 cithonius t
704	6	1.1	110	10	041975	041975 arabidopsis	777	6	1.1	116	8	09ME13	09ME13 lama guanac
705	6	1.1	110	11	091X13	091X13 spermophilu	778	6	1.1	116	8	08HKU3	08HKU3 petrosicire
706	6	1.1	110	16	08PIE7	08PIE7 xanthomonas	779	6	1.1	116	9	08SC58	08SC58 stx2 conver
707	6	1.1	110	16	08P733	08P733 xanthomonas	780	6	1.1	116	10	094DK4	094DK4 oryza sativ
708	6	1.1	111	3	012243	012243 saccharomyc	781	6	1.1	116	11	09CY65	09CY65 mus musculu
709	6	1.1	111	4	09H2B5	09H2B5 homo sapien	782	6	1.1	116	15	08Q6N8	08Q6N8 human immun
710	6	1.1	111	10	041951	041951 arabidopsis	783	6	1.1	116	16	0915Q6	0915Q6 pseudomonas
711	6	1.1	111	10	09SCA7	09SCA7 arabidopsis	784	6	1.1	117	2	P71212	P71212 escherichia
712	6	1.1	111	11	09EBQ7	09EBQ7 ratuca norv	785	6	1.1	117	2	08VMT3	08VMT3 pseudomonas
713	6	1.1	111	11	08ATH0	08ATH0 human immun	786	6	1.1	117	4	09UFL7	09UFL7 homo sapien
714	6	1.1	111	15	08YCT4	08YCT4 bruceella me	787	6	1.1	117	4	09POQ4	09POQ4 homo sapien
715	6	1.1	111	16	08PDT5	08PDT5 xanthomonas	788	6	1.1	117	5	09XXE7	09XXE7 caenorhabdi
716	6	1.1	111	16	09X8N1	09X8N1 streptomyce	789	6	1.1	117	10	094DK6	094DK6 oryza sativ
717	6	1.1	111	16	09EXK3	09EXK3 streptomyce	790	6	1.1	118	5	09NCS1	09NCS1 cryptospori
718	6	1.1	111	16	08UZX1	08UZX1 mus musculu	791	6	1.1	118	9	09G081	09G081 bacterioph
719	6	1.1	112	11	08R1E9	08R1E9 mus musculu	792	6	1.1	118	16	09ISEK3	09ISEK3 pseudomonas
720	6	1.1	112	11	08R1E9	08R1E9 mus musculu	793	6	1.1	119	4	09NSK7	09NSK7 homo sapien
721	6	1.1	112	15	031376	031376 human immun	794	6	1.1	119	16	08ZKL5	08ZKL5 salmonella
722	6	1.1	112	15	08ATH5	08ATH5 human immun	795	6	1.1	119	16	08Z312	08Z312 salmonella
723	6	1.1	112	15	08ATH5	08ATH5 human immun	796	6	1.1	119	16	09SS57	09SS57 pseudomonas
724	6	1.1	112	15	08ATH4	08ATH4 human immun	797	6	1.1	120	2	093HP8	093HP8 streptomyce
725	6	1.1	112	15	08ATH3	08ATH3 human immun	798	6	1.1	120	2	09KWK3	09KWK3 pseudomonas
726	6	1.1	112	15	08ATH2	08ATH2 human immun	799	6	1.1	120	2	09NSB0	09NSB0 caenorhabdi
727	6	1.1	112	15	08ATH1	08ATH1 human immun	800	6	1.1	120	5	042049	042049 arabidopsis
728	6	1.1	112	15	08ATH8	08ATH8 human immun	801	6	1.1	120	10	09SS65	09SS65 pseudomonas
729	6	1.1	112	15	08ATH5	08ATH5 human immun	802	6	1.1	120	16	08FRP4	08FRP4 corynebacte
730	6	1.1	112	15	08ATH3	08ATH3 human immun	803	6	1.1	120	17	08TKG0	08TKG0 methanosarc
731	6	1.1	112	15	08ATH2	08ATH2 human immun	804	6	1.1	121	8	09SEB7	09SEB7 rana sylvat
732	6	1.1	112	15	08ATH1	08ATH1 human immun	805	6	1.1	121	8	09SEB0	09SEB0 rana catesb
733	6	1.1	112	15	08ATHG1	08ATHG1 human immun	806	6	1.1	121	10	08GZV1	08GZV1 oryza sativ
734	6	1.1	113	5	09VZ24	09VZ24 drosophila	807	6	1.1	121	12	072199	072199 hepatitis c
735	6	1.1	113	10	09AS11	09AS11 oryza sativ	808	6	1.1	121	12	072197	072197 hepatitis c
736	6	1.1	113	10	08UAV6	08UAV6 human immun	809	6	1.1	121	12	072200	072200 hepatitis c
737	6	1.1	113	15	08ATH6	08ATH6 human immun	810	6	1.1	121	12	072201	072201 hepatitis c
738	6	1.1	113	15	08ATH7	08ATH7 human immun	811	6	1.1	121	12	072203	072203 hepatitis c
739	6	1.1	113	15	08ATH6	08ATH6 human immun	812	6	1.1	121	12	072198	072198 hepatitis c
740	6	1.1	113	15	08ATH4	08ATH4 human immun	813	6	1.1	121	16	08UWU7	08UWU7 agrobacteri
741	6	1.1	113	17	09HQV3	09HQV3 halobacteri	814	6	1.1	121	16	08FW52	08FW52 bruceella su
742	6	1.1	113	17	08TWG8	08TWG8 methanopyru	815	6	1.1	122	5	046063	046063 drosophila
743	6	1.1	114	4	09UPB9	09UPB9 homo sapien	816	6	1.1	122	16	08ZNB5	08ZNB5 salmonella
744	6	1.1	114	4	09PTH5	09PTH5 aotus lemur	817	6	1.1	122	16	08Z426	08Z426 salmonella
745	6	1.1	114	6	09TTH6	09TTH6 aotus nigri	818	6	1.1	122	16	08VJK5	08VJK5 mycobacteri
746	6	1.1	114	6	097539	097539 aotus nancy	819	6	1.1	123	12	08UKA9	08UKA9 hepatitis c

820	6	1.1	123	16	Q926M4	Q926M4 listeria in	893	6	1.1	138	11	Q99091	Q99191 marmota mon
821	6	1.1	123	16	Q8D359	Q8D359 wigleswort	894	6	1.1	138	12	Q83421	Q83421 pseudorabie
822	6	1.1	123	17	Q9Y9H3	Q9Y9H3 aeropyrum p	895	6	1.1	138	16	Q9PW49	Q9PW49 campylobac
823	6	1.1	124	10	Q9SXX4	Q9SXX4 oryza sativ	896	6	1.1	138	16	Q9PR48	Q9PR48 xylella fas
824	6	1.1	124	17	Q9YEM1	Q9YEM1 aeropyrum p	897	6	1.1	139	5	Q18272	Q18272 caenorhabdi
825	6	1.1	125	2	Q93DY1	Q93DY1 magnetospir	898	6	1.1	139	15	Q8AKW4	Q8AKW4 human immun
826	6	1.1	125	5	Q962D8	Q962D8 drosophila	899	6	1.1	139	15	Q8AKU3	Q8AKU3 human immun
827	6	1.1	125	16	Q8FQE9	Q8FQE9 corynebacte	900	6	1.1	139	15	Q8AKT5	Q8AKT5 human immun
828	6	1.1	125	17	Q974A1	Q974A1 sulfolobus	901	6	1.1	139	16	Q8PJ76	Q8PJ76 xanthomonas
829	6	1.1	125	17	Q8TOYO	Q8TOYO methanocarc	902	6	1.1	139	16	Q8EJ79	Q8EJ79 leprospira
830	6	1.1	126	4	Q81VT3	Q81VT3 homo sapien	903	6	1.1	139	16	Q8BAK5	Q8BAK5 shewanella
831	6	1.1	126	11	Q9D288	Q9D288 mus musculu	904	6	1.1	140	1	Q9Y8U9	Q9Y8U9 halobacteri
832	6	1.1	126	16	Q9J2U4	Q9J2U4 neiseeria m	905	6	1.1	140	2	Q9JNE0	Q9JNE0 myxococcus
833	6	1.1	126	16	Q97T41	Q97T41 streptococc	906	6	1.1	140	5	Q9W569	Q9W569 drosophila
834	6	1.1	126	16	Q8YE28	Q8YE28 brucella me	907	6	1.1	140	8	Q9XKW1	Q9XKW1 paragonimus
835	6	1.1	126	16	Q8FY14	Q8FY14 brucella su	908	6	1.1	140	10	Q8S7D5	Q8S7D5 oryza sativ
836	6	1.1	126	16	Q8CXB2	Q8CXB2 streptococc	909	6	1.1	140	12	Q9D1W9	Q9D1W9 hepatitis c
837	6	1.1	127	16	Q9RSB5	Q9RSB5 delnoccocus	910	6	1.1	140	12	Q99A23	Q99A23 bovine vira
838	6	1.1	128	11	Q9DA35	Q9DA35 mus musculu	911	6	1.1	140	15	Q75101	Q75101 human immun
839	6	1.1	128	11	Q8CD36	Q8CD36 mus musculu	912	6	1.1	140	16	Q8YX23	Q8YX23 anabaena sp
840	6	1.1	128	11	Q8CC20	Q8CC20 mus musculu	913	6	1.1	140	16	Q8XOD4	Q8XOD4 ralatonia s
841	6	1.1	128	12	Q99CY9	Q99CY9 bovine herp	914	6	1.1	140	16	Q9ZLC3	Q9ZLC3 helicobacte
842	6	1.1	128	16	Q9JZZ9	Q9JZZ9 neiseeria m	915	6	1.1	140	16	Q8ZJ23	Q8ZJ23 yerbinta pe
843	6	1.1	128	16	Q8YJ61	Q8YJ61 anabaena sp	916	6	1.1	140	16	Q8ECY0	Q8ECY0 shewanella
844	6	1.1	129	16	Q8XGMO	Q8XGMO salmonella	917	6	1.1	141	2	Q06689	Q06689 treponema p
845	6	1.1	129	16	Q8RIL0	Q8RIL0 fusobacteri	918	6	1.1	141	4	Q9WFK5	Q9WFK5 synechococc
846	6	1.1	129	16	Q8PEJ2	Q8PEJ2 xanthomonas	919	6	1.1	141	4	Q8N2E8	Q8N2E8 homo sapien
847	6	1.1	130	2	Q8KM22	Q8KM22 paracoccus	920	6	1.1	141	9	Q38066	Q38066 bacterioph
848	6	1.1	130	4	Q8N827	Q8N827 homo sapien	921	6	1.1	141	11	Q9QY70	Q9QY70 mus musculu
849	6	1.1	130	10	Q8S3P7	Q8S3P7 oryza sativ	922	6	1.1	141	11	Q61692	Q61692 mus musculu
850	6	1.1	130	16	Q8E2X5	Q8E2X5 streptococc	923	6	1.1	141	16	Q911S8	Q911S8 pseudomonas
851	6	1.1	130	16	Q8DX28	Q8DX28 streptococc	924	6	1.1	141	16	Q911S6	Q911S6 pseudomonas
852	6	1.1	131	16	P73579	P73579 synechocyst	925	6	1.1	141	16	Q8NSE7	Q8NSE7 corynebacte
853	6	1.1	131	16	Q8XW33	Q8XW33 ralatonia s	926	6	1.1	142	4	Q8NE67	Q8NE67 homo sapien
854	6	1.1	131	17	Q9Y9G2	Q9Y9G2 aeropyrum p	927	6	1.1	143	6	Q9N0S6	Q9N0S6 bos taurus
855	6	1.1	132	3	Q9P6S6	Q9P6S6 schizosacch	928	6	1.1	143	10	Q8S363	Q8S363 anticarpus
856	6	1.1	132	3	P78948	P78948 schizosacch	929	6	1.1	143	10	Q8W024	Q8W024 antirrhinum
857	6	1.1	132	5	Q81079	Q81079 drosophila	930	6	1.1	143	17	Q9HMT1	Q9HMT1 halobacteri
858	6	1.1	132	10	Q8S070	Q8S070 oryza sativ	931	6	1.1	144	2	Q9ZNP5	Q9ZNP5 wolbachia s
859	6	1.1	132	16	Q97H58	Q97H58 clostridium	932	6	1.1	144	2	P78000	P78000 kingella de
860	6	1.1	132	16	Q8PR58	Q8PR58 xanthomonas	933	6	1.1	144	6	Q9GL44	Q9GL44 macaca mula
861	6	1.1	132	16	Q8PEA0	Q8PEA0 xanthomonas	934	6	1.1	144	10	Q8VXT0	Q8VXT0 beta vulgar
862	6	1.1	133	2	Q9R489	Q9R489 agrobacteri	935	6	1.1	144	11	Q8BMJ3	Q8BMJ3 mus musculu
863	6	1.1	133	2	Q66170	Q66170 agrobacteri	936	6	1.1	144	11	Q8BMJ8	Q8BMJ8 mus musculu
864	6	1.1	133	5	Q9VCZ4	Q9VCZ4 drosophila	937	6	1.1	144	11	Q8BJZ2	Q8BJZ2 mus musculu
865	6	1.1	133	15	Q8AEP1	Q8AEP1 human immun	938	6	1.1	144	16	Q9RTS8	Q9RTS8 delnoccocus
866	6	1.1	133	16	Q9RU77	Q9RU77 delnoccocus	939	6	1.1	144	17	P95921	P95921 sulfolobus
867	6	1.1	133	16	Q8YML1	Q8YML1 anabaena sp	940	6	1.1	145	8	P92685	P92685 parus ater
868	6	1.1	134	2	Q55063	Q55063 synechocyst	941	6	1.1	145	8	P92684	P92684 parus ater
869	6	1.1	134	2	Q9LAV0	Q9LAV0 caulobacter	942	6	1.1	145	10	Q9FKI2	Q9FKI2 arabidopsis
870	6	1.1	134	2	Q8BTR9	Q8BTR9 uncultured	943	6	1.1	145	10	Q8W027	Q8W027 antirrhinum
871	6	1.1	134	2	Q9A1S6	Q9A1S6 chlamydomphi	944	6	1.1	145	10	Q9S0B9	Q9S0B9 arabidopsis
872	6	1.1	134	16	Q8CYU8	Q8CYU8 streptococc	945	6	1.1	145	10	Q9JVF1	Q9JVF1 arabidopsis
873	6	1.1	135	11	Q63J17	Q63J17 ractus norv	946	6	1.1	145	10	Q8WVK5	Q8WVK5 antirrhinum
874	6	1.1	135	16	Q9A6E3	Q9A6E3 caulobacter	947	6	1.1	145	14	Q991U2	Q991U2 uncultured
875	6	1.1	136	10	Q8LK17	Q8LK17 vicia faba	948	6	1.1	145	16	Q9RTJ9	Q9RTJ9 delnoccocus
876	6	1.1	137	5	Q96335	Q96335 brugia mala	949	6	1.1	146	2	Q9RE93	Q9RE93 enterococcu
877	6	1.1	137	8	Q8HIG1	Q8HIG1 schistosoma	950	6	1.1	146	6	Q8MJ96	Q8MJ96 equus caball
878	6	1.1	137	11	Q8C442	Q8C442 mus musculu	951	6	1.1	146	8	P92702	P92702 parus carol
879	6	1.1	137	11	Q8BN67	Q8BN67 mus musculu	952	6	1.1	146	8	P92686	P92686 parus attic
880	6	1.1	137	16	Q9HYV4	Q9HYV4 pseudomonas	953	6	1.1	146	10	Q8LSN4	Q8LSN4 triticum ae
881	6	1.1	137	16	Q988H6	Q988H6 rhizobium 1	954	6	1.1	146	12	Q8JSM1	Q8JSM1 bovine papl
882	6	1.1	137	16	Q8U693	Q8U693 agrobacteri	955	6	1.1	146	13	Q8OG90	Q8OG90 bovine papl
883	6	1.1	137	16	Q8PIW8	Q8PIW8 xanthomonas	956	6	1.1	147	4	Q9BRU5	Q9BRU5 homo sapien
884	6	1.1	138	2	Q8RK71	Q8RK71 nitrosomona	957	6	1.1	147	6	Q8MIT3	Q8MIT3 bos taurus
885	6	1.1	138	2	Q8RK79	Q8RK79 nitrosomona	958	6	1.1	147	10	Q9JN60	Q9JN60 arabidopsis
886	6	1.1	138	2	Q8RK75	Q8RK75 nitrosomona	959	6	1.1	147	11	Q8VHG9	Q8VHG9 notomys ale
887	6	1.1	138	2	Q8KMP4	Q8KMP4 lactococcus	960	6	1.1	147	12	Q8UJ44	Q8UJ44 virus phich
888	6	1.1	138	2	Q8RK63	Q8RK63 nitrosomona	961	6	1.1	147	12	Q98S06	Q98S06 parametium
889	6	1.1	138	2	Q8RK61	Q8RK61 nitrosomona	962	6	1.1	148	2	Q9ERT0	Q9ERT0 envitroment
890	6	1.1	138	2	Q8GC85	Q8GC85 enterobacte	963	6	1.1	148	2	Q9LAK5	Q9LAK5 uncultured
891	6	1.1	138	5	Q8T957	Q8T957 drosophila	964	6	1.1	148	2	Q9F9A3	Q9F9A3 uncultured
892	6	1.1	138	5	Q8MLE1	Q8MLE1 drosophila	965	6	1.1	148	2	Q9F9A6	Q9F9A6 uncultured

966	6	1.1	148	2	Q8RMP3	Q8RMP3 uncultured
967	6	1.1	148	2	Q9ETL8	Q9ETL8 environment
968	6	1.1	148	2	Q9F9A5	Q9F9A5 uncultured
969	6	1.1	148	2	Q9EUA3	Q9EUA3 environment
970	6	1.1	148	2	Q9ETR1	Q9ETR1 environment
971	6	1.1	148	2	Q9F9A1	Q9F9A1 uncultured
972	6	1.1	148	2	Q9F9A8	Q9F9A8 uncultured
973	6	1.1	148	2	Q9F9A4	Q9F9A4 uncultured
974	6	1.1	148	2	Q9EUD8	Q9EUD8 environment
975	6	1.1	148	5	Q9VEA1	Q9VEA1 drosophila
976	6	1.1	148	5	Q9NJB4	Q9NJB4 drosophila
977	6	1.1	148	5	Q9U9L3	Q9U9L3 anophelis 9
978	6	1.1	148	15	Q8J544	Q8J544 human immun
979	6	1.1	149	2	Q9K4P6	Q9K4P6 unidentifite
980	6	1.1	149	2	Q9K4Q0	Q9K4Q0 unidentifite
981	6	1.1	149	2	Q9K4P7	Q9K4P7 unidentifite
982	6	1.1	149	2	Q9K4N5	Q9K4N5 nitrosomona
983	6	1.1	149	2	Q9K4P2	Q9K4P2 unidentifite
984	6	1.1	149	2	Q9K4P8	Q9K4P8 unidentifite
985	6	1.1	149	2	Q9K2W9	Q9K2W9 unidentifite
986	6	1.1	149	2	Q9K4Q1	Q9K4Q1 unidentifite
987	6	1.1	149	2	Q9K4P9	Q9K4P9 unidentifite
988	6	1.1	149	2	Q9K4P3	Q9K4P3 unidentifite
989	6	1.1	149	2	Q9K4N6	Q9K4N6 nitrosomona
990	6	1.1	149	2	Q9K4N3	Q9K4N3 nitrosomona
991	6	1.1	149	2	Q9K4P5	Q9K4P5 unidentifite
992	6	1.1	149	2	Q9K4N4	Q9K4N4 nitrosomona
993	6	1.1	149	2	Q9K4Q2	Q9K4Q2 unidentifite
994	6	1.1	149	5	Q02582	Q02582 inciliaria f
995	6	1.1	149	8	Q9MD22	Q9MD22 schistosoma
996	6	1.1	149	9	Q80313	Q80313 bacteriophia
997	6	1.1	149	12	Q9IHK7	Q9IHK7 human polio
998	6	1.1	149	12	Q9IHK6	Q9IHK6 human polio
999	6	1.1	149	12	Q9IHK5	Q9IHK5 human polio
1000	6	1.1	149	12	Q9IHL0	Q9IHL0 human polio

ALIGNMENTS

RESULT 1
015681 PRELIMINARY; PRT; 541 AA.
AC 015681;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apical membrane antigen 1 homolog.
GN AMLING.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCB1_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ME49; PubMed=11083833;
RC MEDLINE=20536458; PubMed=11083833;
RA Hehl A.B., Leksula C., Grigg M.E., Bradley P.J., Dubremetz J.F.,
RA Ortega-Barria E., Boothroyd J.C.;
RT "Toxoplasma gondii Homologue of Plasmodium Apical Membrane Antigen 1
RT Is Involved in Invasion of Host Cells.";
RL Infect. Immun. 68:7078-7086(2000).
DR EMBL; AF010264; AAB65410.1;
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MEROZOITESA.
SQ SEQUENCE 541 AA; 59978 MW; DD38EF3A0F258E27 CRC64;

Query Match 100.0%; Score 541; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVLGVQLLVLVADCTIFASGLSSSTRRESQTLASLSTSGNFQANVEKTMERFNL 60

Db |||
1 MGVLGVQLLVLVADCTIFASGLSSSTRRESQTLASLSTSGNFQANVEKTMERFNL 60
QY 61 HHHOSGIYVDIGQDEVDGLTYREPAQLCPWKGHILOQPDRLPYNNFLBVDPTKEY 120
Db 61 HHHOSGIYVDIGQDEVDGLTYREPAQLCPWKGHILOQPDRLPYNNFLBVDPTKEY 120
QY 121 KQSGNPLRGGNLNFVTPSGORTSPFMELEKSNIKASDGLGRCAEPAFTVAMDKN 180
Db 121 KQSGNPLRGGNLNFVTPSGORTSPFMELEKSNIKASDGLGRCAEPAFTVAMDKN 180
QY 181 KATKRYPFVYDSKKRLCHILYVSMQMEGKCYCVXGEPDLTWYCFKPKSVTENHL 240
Db 181 KATKRYPFVYDSKKRLCHILYVSMQMEGKCYCVXGEPDLTWYCFKPKSVTENHL 240
QY 241 IYSAVYGENPDATISKCPNOLAGYFVWKKRCLDYLTLPTTVIERVSKAQCVKT 300
Db 241 IYSAVYGENPDATISKCPNOLAGYFVWKKRCLDYLTLPTTVIERVSKAQCVKT 300
QY 301 FENGVASDOPHTYPLTQASWMDWPLHOSDOPHSGVGRNRYVYVDTTGEGKCALSD 360
Db 301 FENGVASDOPHTYPLTQASWMDWPLHOSDOPHSGVGRNRYVYVDTTGEGKCALSD 360
QY 361 QVPDLVSDSAVSYTAGSLSEETPNFIIPSNBSVTPPETALQCTADYFDPSPGACD 420
Db 361 QVPDLVSDSAVSYTAGSLSEETPNFIIPSNBSVTPPETALQCTADYFDPSPGACD 420
QY 421 VOACKROKTCVGGIOGSTVDTCTADNONGEGSTTALAGLVGVLLALLGGGCVFAK 480
Db 421 VOACKROKTCVGGIOGSTVDTCTADNONGEGSTTALAGLVGVLLALLGGGCVFAK 480
QY 481 RLDRNKGVAHHEHFEQSDRGARKRPSDLMQEAEPFMEAEENIEQDETHVMVGD 540
Db 481 RLDRNKGVAHHEHFEQSDRGARKRPSDLMQEAEPFMEAEENIEQDETHVMVGD 540
QY 541 Y 541
Db 541 Y 541

RESULT 2
073716 PRELIMINARY; PRT; 280 AA.
AC 073716;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-G-like protein.
GN BG2.
OS Grua americana (whooping crane).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Gru.
OX NCB1_TaxID=9117;
RN [1]
RP SEQUENCE FROM N.A.
RC Javari S.I., Goto R.M., Gee G.F., Briles W.E., Miller M.M.;
RT "Identification, inheritance and linkage of B-G-like and MHC class I
RT genes in cranes.";
RL J. Hered. 0:0-0(1998).
DR EMBL; AF031107; AAC23712.1;
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 280 AA; 31411 MW; C379DB8A61C52DD0 CRC64;

Query Match 1.7%; Score 9; DB 13; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VGVQVLVLV 12

Db 249 VGVGVLLVL 257

RESULT 3

ID 09KG75 PRELIMINARY; PRT; 387 AA.

AC 09KG75.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Multidrug-efflux transporter.
GN BH0237.

OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C-125 / JCM 9153;

RA MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.

RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; AP001507; BAB03956.1; -

DR InterPro; IPR007114; MFS.

DR InterPro; IPR005828; Sub_transporter.

DR InterPro; IPR008829; Sug_transporter.

DR InterPro; IPR001958; TCR_Teta.

DR Pfam; PF00083; Sugar_cr.1.

DR PRINTS; PR01035; TCRTETA.

DR PROSITE; PS00850; MFS; 1.

DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.

KM Complete proteome.

SO SEQUENCE 387 AA; 41096 MW; 611247A4EA854BC8 CRC64;

Query Match 1.7%; Score 9; DB 16; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 461 LAVGVLL 469
Db 73 LAVGVLL 81

RESULT 4

ID 09A9P5 PRELIMINARY; PRT; 401 AA.

AC 09A9P5.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein CC0931.

GN CC0931.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.

OX NCBI_TaxID=155892;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;
RC MEDLINE=21173698; PubMed=11259647;

RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A.S., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Koonen J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Ueterbach T., Tran K., Wolf A., Vamathavan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro H., Fraser C.M.,
RA "Complete genome sequence of Caulobacter crescentus";
RA Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

DR EMBL; AE005770; AAK22915.1; -
DR TIGR; CC0931; -
DR InterPro; IPR003838; DUF214.
DR Pfam; PF02687; DUF214; 1.
KW Hypothetical protein; Complete proteome.
SO SEQUENCE 401 AA; 42438 MW; 13A404D0ACBCE8CA CRC64;

Query Match 1.7%; Score 9; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 455 TALVGLAV 463
Db 36 TALVGLAV 44

RESULT 5

ID 08X7V7 PRELIMINARY; PRT; 923 AA.

AC 08X7V7.
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Putative protease (putative ATP-dependent Clp proteinase ATP-binding
DE chain).
GN 20254 OR ECS0223.

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83334;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RC MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., DiMantano E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;

RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RA Nature 409:529-533(2001).

RT [12]
RL SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0509952;
RC MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RA "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).

DR EMBL; AE005198; AAG54523.1; -

DR EMBL; AP002550; BAB33646.1; -

DR InterPro; IPR003593; AAA_ATPase.

DR InterPro; IPR001959; AAA_ATPase_cent.

DR InterPro; IPR001270; Chaprinin_cIPa/B.

DR Pfam; PF00004; AAA; 1.

DR PRINTS; PR00300; CLPPTERSEA.

DR SMART; SM00382; AAA; 2.

DR PROSITE; PS00870; CLPAB_1; 1.

KW Protease; Complete proteome.

SO SEQUENCE 923 AA; 101229 MW; 0D1465A573031035 CRC64;

Query Match 1.7%; Score 9; DB 16; Length 923;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 464 GCVLLALL 472
Db 114 GCVLLALL 122


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RESULT 6
Q9BWR5 PRELIMINARY; PRT; 121 AA.
ID Q9BWR5;
AC Q9BWR5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC000031; AA00031.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 121 AA; 13233 MW; 8BD9FB4B56E478D8 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEETP 386
DB 19 GSLSEETP 26

RESULT 7
Q96BI4 PRELIMINARY; PRT; 126 AA.
ID Q96BI4;
AC Q96BI4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Similar to hypothetical protein MG2865.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015562; AA015562.1; -.
KW Hypothetical protein.
SQ SEQUENCE 126 AA; 13807 MW; 2E34744BBEFC1E9 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEETP 386
DB 24 GSLSEETP 31

RESULT 8
Q90230 PRELIMINARY; PRT; 130 AA.
ID Q90230;
AC Q90230;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ASK1 transcription factor (Fragment).
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;

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OC Ambystoma.
OX NCBI_TaxID=82296;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=95092782; PubMed=7999783;
RA Ludolph D.C., Neff A.W., Parker M.A., Mescher A.L., Smith R.C.,
RA Malachuk G.M.;
RT "Cloning and expression of the axolotl proto-oncogene sk1.";
RL Biochim. Biophys. Acta 1260:102-104(1995).
DR EMBL: D28907; BA018908.1; -.
DR EMBL: X77994; CA54956.1; -.
DR InterPro: IPR003380; Transform_Ski.
DR Pfam: PF02437; Ski_Sno; 1.
KW DNA-binding.
FT NON_TER
FT NON_TER
SQ SEQUENCE 130 AA; 14107 MW; DEB17C02D4C0CF46 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 130;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 ALLGGGCV 477
DB 36 ALLGGGCV 43

RESULT 9
Q9VNS5 PRELIMINARY; PRT; 133 AA.
ID Q9VNS5;
AC Q9VNS5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE CG14453 protein.
GN CG14453.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Fleannkooch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokettier P., Broctier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman J.O., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeswam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mewklow G., Milshina N.V., Modaray C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003598; AAF51845.1;
 DR FlyBase; FBgn0037179; CG14453.
 SQ SEQUENCE 133 AA; 14796 MW; 07BA825ABCD5AEF CRC64;

Query Match 1.5%; Score 8; DB 5; Length 133;
 Best Local Similarity 100.0%; Pred. No. 9.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLLG 473
 Db 6 VLLALLLG 13

RESULT 10
 Q8M221 PRELIMINARY; PRT; 133 AA.
 AC Q8M221-01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE RE13473P.
 GN BCDNA;RE13473.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Archipoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RA Stapleton M., Brokesein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorset V., Dresnak D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guartin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pachet J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celisner S.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY113408; AAM29413.1;
 DR FlyBase; FBgn0063060; BCDNA;RE13473.
 SQ SEQUENCE 133 AA; 14822 MW; 2530B376B8666957 CRC64;

Query Match 1.5%; Score 8; DB 5; Length 133;
 Best Local Similarity 100.0%; Pred. No. 9.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLLG 473
 Db 6 VLLALLLG 13

RESULT 11
 Q8NCV9 PRELIMINARY; PRT; 145 AA.
 AC Q8NCV9-01-OCT-2002 (Tremblrel. 22, Created).
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Glycoprotein NBI precursor.
 GN NBI.
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22006006; Pubmed=12010833;
 RA Kissel K., Scheffler S., Kerowgan M., Bux J.;
 RT "Molecular basis of NBI (HNA-2a, CDI177) deficiency.";
 RL Blood 99:4231-4233(2002).
 DR EMBL; AJ305326; CAC83758.1;
 KW Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 145 GLYCOPROTEIN NBI.
 SQ SEQUENCE 145 AA; 15709 MW; EF7FB498AB39053 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 145;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLLG 473
 Db 4 VLLALLLG 11

RESULT 12
 Q8KX04 PRELIMINARY; PRT; 199 AA.
 AC Q8KX04-01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Hypothetical protein.
 GN SL11486.
 OS *Synechococcus* sp. (strain PCC 7002) (Agmenellum quadruplicatum).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=32049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nomura C.T., Persson S., Zhao J., Bryant D.A.;
 RT "An Analysis of Forty Genes Encoding Electron Transport Proteins from
 RT *Synechococcus* sp. PCC 7002: A Comparative Study of Electron Transport
 RT Proteins from Cyanobacteria and Chloroplasts.";
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF381049; AAN03589.1;
 KW Hypothetical protein.
 SQ SEQUENCE 199 AA; 22445 MW; 454000D4949067P4 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 464 GGVLALLL 471
 Db 119 GGVLALLL 126

RESULT 13
 Q8GC96 PRELIMINARY; PRT; 210 AA.
 AC Q8GC96-01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Putative regulatory protein.
 GN F1MZ GENE.
 OS *Citrobacter freundii*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3009;
 RA Oelschlaeger T.A.;
 RT "Cloning, sequencing and expression of an invasion determinant from
 RT *Citrobacter freundii* strain 3009.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AJ508060; CAD56976.1; --
 SQ SEQUENCE 210 AA; 23624 MW; CDDDE380BF594F57 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 LLEKXSN1 157
 |||||
 DB 22 LLEKXSN1 29

RESULT 14

O96B36 PRELIMINARY; PRT; 256 AA.
 AC O96B36;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC016043; AAH16043.1; --
 DR InterPro; IPR002965; P_Rich_extensn.
 DR PRINTS; PR01217; PRICHEXTENSN.
 DR Hypothetical protein.
 SQ SEQUENCE 256 AA; 27383 MW; F6CB195CBB54326C CRC64;

Query Match 1.5%; Score 8; DB 4; Length 256;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEETP 386
 |||||
 DB 154 GSLSEETP 161

RESULT 15

O96NG2 PRELIMINARY; PRT; 256 AA.
 AC O96NG2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein FLJ30949.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Isthbaehi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
 RA Houtura T., Hirooka S., Murakawa K., Takiguchi S., Kusano J.,
 RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
 RA Sugiyama T., Ise Y., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Magatsuna M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahari K., Masuo Y., Negai K., Isogai T.;
 RT "NEO human cDNA sequencing project."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AK055511; BAB70937.1; --
 DR InterPro; IPR002965; P_Rich_extensn.
 DR PRINTS; PR01217; PRICHEXTENSN.
 DR Hypothetical protein.

SQ SEQUENCE 256 AA; 27298 MW; 312E1A6C8F0F931C CRC64;

Query Match 1.5%; Score 8; DB 4; Length 256;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEETP 386
 |||||
 DB 154 GSLSEETP 161

RESULT 16

O96IK7 PRELIMINARY; PRT; 256 AA.
 AC O96IK7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to RIKEN cDNA 1110012J22 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC007416; AAH07416.1; --
 DR InterPro; IPR002965; P_Rich_extensn.
 DR PRINTS; PR01217; PRICHEXTENSN.
 SQ SEQUENCE 256 AA; 27409 MW; A7D6794DA6385271 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 256;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEETP 386
 |||||
 DB 154 GSLSEETP 161

RESULT 17

O9DIF4 PRELIMINARY; PRT; 257 AA.
 AC O9DIF4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE 1110012J22RIK protein.
 GN 1110012J22RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kaikawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Baturov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein W.D., Bult C., Fletcher C., Fujita K., Gariboldi M.,
 RA Gwuscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshak-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohlschütter S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL: AK003638; BAB22905.1; -.
 DR MGI: 1914855; 1110012J22R1k.
 DR InterPro: IPR002965; P rich exten.
 DR PRINTS: PR01217; PRICHECKTENS.
 SO SEQUENCE 257 AA; 27483 MW; 4BFCC630DBA5EC CRC64;

Query Match 1.5%; Score 8; DB 11; Length 257;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSETP 386
 Db 155 GSLSETP 162

RESULT 18

O9EMP8 PRELIMINARY; PRT; 284 AA.
 AC O9EMP8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative transport system integral membrane protein.
 GN SC07679 OR SC4C2.14.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 CX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=2196410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleeer T., Larke L., Murphree L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL939132; CAC17496.1; -.
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp; 1.
 KW Complete proteome.
 SO SEQUENCE 284 AA; 28595 MW; AAC5F8E795E6F3 CRC64;

Query Match 1.5%; Score 8; DB 16; Length 284;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 LLLALLG 473
 Db 34 LLLALLG 41

RESULT 19

ID P79458 PRELIMINARY; PRT; 346 AA.
 AC P79458;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE MHC class IA alpha chain.

OS Ambystoma mexicanum (Axolotl).
 OC Euryarchaea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Ambystoma; Batrachia; Caudata; Salamandridae; Ambystomatidae;
 OC Ambystoma.
 CX NCBI_TaxID=8296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97190244; PubMed=9038100;
 RA Sammut B., Laurens V., Tounier A.;
 RT "Isolation of Mhc class I cDNAs from the axolotl Ambystoma
 mexicanum";
 RL Immunogenetics 45:285-294(1997).
 CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 CC IMMUNE SYSTEM (BY SIMILARITY).
 CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN) (BY SIMILARITY).
 DR EMBL: U83137; AAC60108.1; -.
 DR HSSP: P01887; ICD1.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; IG; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SMO0407; IGCL; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Glycoprotein; Transmembrane.
 SO SEQUENCE 346 AA; 39057 MW; B659876CEA15954 CRC64;

Query Match 1.5%; Score 8; DB 7; Length 346;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 467 LLLALLG 474
 Db 6 LLLALLG 13

RESULT 20

O8YE66 PRELIMINARY; PRT; 383 AA.
 AC O8YE66;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Benzoyl membrane transport protein.
 GN BME12012.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 CX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Muij C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykide A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldman E.,
 RA Selkov E., Elizer P.H., Hagius S., O'Callaghan D., Leeseon J.-J.,
 RA Haselkorn R., Kyriades N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 Brucella melitensis";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL: AE009634; AAL53193.1; -.
 DR InterPro: IPR004711; BENE.
 DR Pfam: PF03594; BENE; 1.
 DR TIGRFAMs: TIGR00843; BENE; 1.
 KW Complete proteome.
 SO SEQUENCE 383 AA; 39296 MW; 7920480702F49F3E CRC64;

Query Match 1.5%; Score 8; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 ALIAGLAV 463
 |||||
 Db 364 ALIAGLAV 371

RESULT 21

Q8FXX9 PRELIMINARY; PRT; 383 AA.

DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Benzocate transport protein, putative.
 GN BR2115.

OS Brucella suis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.

OX NCBI_TaxID=29461;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1330 / Biovar 1;

RA MEDLINE=22247741; PubMed=12271122;

RA Paulsen I.T., Seeshadt R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 Read T.D., Dodson R.J., Umeyam L., Brinkac L.M., Beanan M.J.,
 Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 Riedmuller S., Tetteil H., Gill S.R., White O., Salzberg S.L.,
 Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
 "The Brucella suis genome reveals fundamental similarities between
 animal and plant pathogens and symbionts.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).

RL EMBL; AE014498; AAN31005.1; -.

DR TIGR; BR2115; -.

KW Complete proteome.

SO SEQUENCE 383 AA; 39371 MW; F7A9D502B71ED2F7 CRC64;

Query Match 1.5%; Score 8; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 ALIAGLAV 463
 |||||
 Db 364 ALIAGLAV 371

RESULT 22

Q8YYS0 PRELIMINARY; PRT; 396 AA.

AC Q8YYS0; 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Hypothetical protein Al10776.

GN ALR0776.

OS Anabaena sp. (strain PCC 7120).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI_TaxID=103690;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21595285; PubMed=11759840; Kuritz T., Sasamoto S.,
 Kaneko T., Nakamura Y., Wolk C.P., Kawashima K., Kimura T.,
 Watanabe A., Iriyuchi M., Ishikawa A., Matsuno A., Muraki A.,
 Kishida Y., Kohara M., Matsumoto M., Takazawa M., Yamada M.,
 Nakazaki N., Shimo S., Sugimoto M.,
 Yasuda M., Tabata S.;
 "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RT DNA Res. 8:205-213(2001).
 RL EMBL; AP003583; BAB72733.1; -.

DR InterPro; IPR001173; Glyco trans 2.
 DR Pfam; PF00535; Glycos transf 2; 1.
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 396 AA; 44424 MW; BEB3E0B541D39CA CRC64;

Query Match 1.5%; Score 8; DB 16; Length 396;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GLSSTRS 29
 |||||
 Db 266 GLSSTRS 273

RESULT 23

Q96QH1 PRELIMINARY; PRT; 437 AA.

AC Q96QH1; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE NBI glycoprotein precursor.

GN NBI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21357611; PubMed=11465086;

RA Kiesel K., Santoso S., Hofmann C., Stroncek D., Bux J.,
 "Molecular basis of the neutrophil glycoprotein NBI (CD177) involved
 in the pathogenesis of immunoneutropenia and transfusion reactions.";
 RT Eur. J. Immunol. 31:1301-1309(2001).

RL EMBL; AJ290452; CAC44459.1; -.

DR EMBL; AJ290452; CAC44459.1; -.

KW SIGNAL.

FT CHAIN.

SO SEQUENCE 437 AA; 46335 MW; 823DAF784986A42F CRC64;

Query Match 1.5%; Score 8; DB 4; Length 437;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALIG 473
 |||||
 Db 4 VLLALIG 11

RESULT 24

Q8N6Q3 PRELIMINARY; PRT; 437 AA.

AC Q8N6Q3; 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)

DE Polychemia rubra vera 1, cell surface receptor.

GN Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP TISSUE=Colon, and Kidney;

RC Strussberg R.;

RA Submitted (May-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC029167; AAH29167.1; -.

KW Receptor.

SO SEQUENCE 437 AA; 46419 MW; CC4DAEC1E7CFC4B CRC64;

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Oy      466 VLLALLG 473
      |||||
Db      4 VLLALLG 11

RESULT 25
Q9HDA5 PRELIMINARY; PRT; 437 AA.
ID 09HDA5;
AC 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
GN Cell surface receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Temerinac S., Kippel S., Roeder S., Luebbert M., Lange W., Azemar M.,
RT "Cloning of PRV-1, a novel member of the UPAR receptor superfamily.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF146747; AAC00895.1; -.
KW Receptor.
SQ SEQUENCE 437 AA; 46363 MW; 3D40648723E43B65 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      466 VLLALLG 473
      |||||
Db      4 VLLALLG 11

RESULT 26
Q8ZFW8 PRELIMINARY; PRT; 463 AA.
ID 08ZFW8;
AC 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TReMBLrel. 23, Last annotation update)
GN Amino acid permease (Putative symporter).
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CO-92 / Biovar Orientalis;
RC MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagsis K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RC MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Zhou S., Schwartz D.C.,
RA Feherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Niles W.L., Mason J.S., Blattner F.R.,
RA Perry R.D.;

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RT      "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AJ414149; CAC90379.1; -.
DR EMBL; AB013863; AAM66167.1; -.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 463 AA; 50183 MW; D0BD3747147F9226 CRC64;

Query Match 1.5%; Score 8; DB 16; Length 463;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      380 SLSETPN 387
      |||||
Db      230 SLSETPN 237

RESULT 27
Q8G7P9 PRELIMINARY; PRT; 468 AA.
ID 08G7P9;
AC 08G7P9;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DE 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
GN Hypothetical membrane protein with unknown function.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RC MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Peesi G., Zwielen M.-C., Desiere F., Bork P., Delley M.,
RA Primore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 468 AA; 49486 MW; 24D405F0F6530A91 CRC64;

Query Match 1.5%; Score 8; DB 16; Length 468;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      462 AVGGVLL 469
      |||||
Db      328 AVGGVLL 335

RESULT 28
Q8JZ36 PRELIMINARY; PRT; 476 AA.
ID 08JZ36;
AC 08JZ36;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DE 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
GN West Nile virus (WNV).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B956;
RC MEDLINE=21992730; PubMed=11996693;
RA Briese T., Ramsaut A., Pothmayr M., Bishara J., Weinberger M.,
RA Pletlik S., Lipkin W.I.;

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RT "Phylogenetic analysis of a human isolate from the 2000 Israel West
RT Nile virus epidemic.";
RL Emerg. Infect. Dis. 8:528-531(2002).
DR EMBL; AF394221; AAM21944.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR001157; Flavi_NSI.
DR Pfam; PF00869; Flavi_glycoprote; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Pfam; PF00948; Flavi_NSI; 1.
DR Prodom; PD001556; Flavi_glycoprote; 1.
DR Prodom; PD001496; Flavi_NSI; 1.
FT NON_TER 1 1
FT CHAIN 1 >414 ENVELOPE GLYCOPROTEIN E.
FT NON_TER 415 >476 NONSTRUCTURAL PROTEIN 1.
FT 476 476
SQ SEQUENCE 476 AA; 51129 MW; D27018C7E6FE15F CRC64;
Query Match 1.5%; Score 8; DB 12; Length 476;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 461 LAVGVLL 468
DB 399 LAVGVLL 406
RESULT 29
Q9WI84 PRELIMINARY; PRT; 501 AA.
ID Q9WI84;
AC Q9WI84;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN E.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCB1_TaxID=11082;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=KN3829;
RA Miller B.R., Nasri R.S., Godsey M.S., Savage H.M., Lucwama J.J.,
RA Lanciotti R.S., Peters C.J., Gubler D.J.;
RT "First field evidence for natural vertical transmission of West Nile
RT virus in Culex univittatus mosquitoes from Rift Valley Province,
RT Kenya".
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF146082; AAD31720.1; -
DR HSPF; P14336; 1SVB.
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprote; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Prodom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1 1
FT NON_TER 501 501
SQ SEQUENCE 501 AA; 53622 MW; D2A9C827F711C00D5 CRC64;
Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 461 LAVGVLL 468
DB 486 LAVGVLL 493
RESULT 30
Q9IMB8 PRELIMINARY; PRT; 501 AA.
ID Q9IMB8;
AC Q9IMB8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCB1_TaxID=11082;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=3000622;
RA Ebel G.D., Dupuis A.P., II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000".
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346313; AAK62760.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprote; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Prodom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1 1
FT NON_TER 501 501
SQ SEQUENCE 501 AA; 53620 MW; FFAF78F09DCD089B CRC64;
Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 461 LAVGVLL 468
DB 486 LAVGVLL 493
RESULT 31
Q9IMC1 PRELIMINARY; PRT; 501 AA.
ID Q9IMC1;
AC Q9IMC1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCB1_TaxID=11082;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=3000365;
RA Ebel G.D., Dupuis A.P., II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000".
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346310; AAK62757.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprote; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Prodom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1 1
FT NON_TER 501 501
SQ SEQUENCE 501 AA; 53620 MW; FFAF78F09DCD089B CRC64;
Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 461 LAVGVLL 468
DB 486 LAVGVLL 493
RESULT 32

091MB6
ID 091MB6 PRELIMINARY; PRT; 501 AA.
AC 091MB6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00-2741;
RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000.";
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346315; AAK62762.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 461 LAVGVLL 468
Db 486 LAVGVLL 493

RESULT 33
091MB5
ID 091MB5 PRELIMINARY; PRT; 501 AA.
AC 091MB5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3000259;
RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000.";
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346316; AAK62763.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 461 LAVGVLL 468

Db 486 LAVGVLL 493

RESULT 34
091MB2
ID 091MB2 PRELIMINARY; PRT; 501 AA.
AC 091MB2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00-3282;
RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000.";
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346319; AAK62766.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 461 LAVGVLL 468
Db 486 LAVGVLL 493

RESULT 35
091MC2
ID 091MC2 PRELIMINARY; PRT; 501 AA.
AC 091MC2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3000017;
RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000.";
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346309; AAK62756.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVLL 468
|||
486 LAVGVLL 493

Db

RESULT 36

O8JTB5 PRELIMINARY; PRT; 501 AA.

ID O8JTB5

AC O8JTB5: 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Envelope protein (Fragment).

GN E.

OS West Nile virus (WN).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus.

OX NCBI_TaxID=11082;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H-442;

RX MEDLINE=22033887, PubMed=12036314;

RA Beasley D.W., Li L., Suderman M.T., Barrett A.D.;

RT "Mouse neuroinvasive phenotype of West Nile virus strains varies depending upon virus genotype.";

RL Virology 296:17-23(2002).

DR EMBL, AF459403; AAM70028.3; -

DR InterPro; IPR000336; Flavi_glycoprote.

DR Pfam; PF00869; Flavi_glycoprot; 1.

DR ProDom; PD001556; Flavi_glycoprote; 1.

FT NON_TER 1 1

FT NON_TER 501 501

SEQ SEQUENCE 501 AA; 53659 MW; 9899F74E90347286 CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVLL 468
|||
486 LAVGVLL 493

Db

RESULT 37

O91MB7 PRELIMINARY; PRT; 501 AA.

ID O91MB7

AC O91MB7: 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS West Nile virus (WN).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus.

OX NCBI_TaxID=11082;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3000352;

RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,

RT Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;

RT "Partial Genetic Characterization of West Nile Virus Strains, New York State, 2000.";

RL Emerging Infect. Dis. 7:0-0(2001).

DR EMBL, AF346314; AAK62761.1; -

DR InterPro; IPR000336; Flavi_glycoprote.

DR Pfam; PF00869; Flavi_glycoprot; 1.

DR ProDom; PD001556; Flavi_glycoprote; 1.

FT NON_TER 1 1

FT NON_TER 501 501

SEQ SEQUENCE 501 AA; 53659 MW; 9899F74E90347286 CRC64;

DR ProDom; PD001556; Flavi_glycoprote; 1.

FT NON_TER 1 1

FT NON_TER 501 501

SEQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVLL 468
|||
486 LAVGVLL 493

Db

RESULT 38

O91MB4 PRELIMINARY; PRT; 501 AA.

ID O91MB4

AC O91MB4: 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS West Nile virus (WN).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus.

OX NCBI_TaxID=11082;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=00-824;

RX Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,

RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;

RT "Partial Genetic Characterization of West Nile Virus Strains, New York State, 2000.";

RL Emerging Infect. Dis. 7:0-0(2001).

DR EMBL, AF346317; AAK62764.1; -

DR InterPro; IPR000336; Flavi_glycoprote.

DR Pfam; PF00869; Flavi_glycoprot; 1.

DR ProDom; PD001556; Flavi_glycoprote; 1.

FT NON_TER 1 1

FT NON_TER 501 501

SEQ SEQUENCE 501 AA; 53606 MW; FF4F78EE6C22089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVLL 468
|||
486 LAVGVLL 493

Db

RESULT 39

O91MB3 PRELIMINARY; PRT; 501 AA.

ID O91MB3

AC O91MB3: 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS West Nile virus (WN).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus.

OX NCBI_TaxID=11082;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=00-3356;

RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,

RT Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;

RT "Partial Genetic Characterization of West Nile Virus Strains, New York State, 2000.";

RL Emerging Infect. Dis. 7:0-0(2001).
 DR EMBL; AF346318; AK62765.1; -
 DR InterPro; IPR000336; Flavi_glycoprote.
 DR Pfam; PF00869; Flavi_glycoprot; 1.
 DR Pfam; PF02832; Flavi_glycop_C; 1.
 DR ProDom; PD001556; Flavi_glycoprote; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 501 AA; 53646 MW; FF58739D3C1D089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGCVLL 468
 |||||
 Db 486 LAVGCVLL 493

RESULT 40

Q91MCO PRELIMINARY; PRT; 501 AA.
 ID Q91MCO
 AC Q91MCO:
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS West Nile virus (WN).
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 CC Flavivirus.
 OX NCBI_TaxID=11082;
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3000548;
 RA Edzel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kaufman E.B.,
 RA Jones S.A., Young D., Maftel J., Shi P.-Y., Bernard K., Kramer L.D.,
 RT "Partial Genetic Characterization of West Nile Virus Strains, New York
 RT State, 2000.";
 RL Emerging Infect. Dis. 7:0-0(2001).
 DR EMBL; AF346311; AK62758.1; -
 DR InterPro; IPR000336; Flavi_glycoprote.
 DR Pfam; PF00869; Flavi_glycoprot; 1.
 DR Pfam; PF02832; Flavi_glycop_C; 1.
 DR ProDom; PD001556; Flavi_glycoprote; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGCVLL 468
 |||||
 Db 486 LAVGCVLL 493

Search completed: October 2, 2003, 16:05:55
 Job time : 140 secs

2000

DEC

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 15:47:54 ; Search time 29 Seconds
(without alignment)

789.316 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 2922

Sequence: 1 MGWGVQLVLVADCTIFA.....EAEENIDQGETHVEGDY 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5 ,

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents, AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417.5	14.3	628	1 US-08-257-073-9	Sequence 9, Appli
2	120	4.1	1507	3 US-08-929-329-5	Sequence 5, Appli
3	107.5	3.7	1104	2 US-08-327-832-5	Sequence 5, Appli
4	107.5	3.7	1104	2 US-08-828-584-5	Sequence 5, Appli
5	104	3.6	1255	2 US-08-484-438-8	Sequence 8, Appli
6	104	3.6	1255	2 US-08-625-101-2	Sequence 2, Appli
7	104	3.6	1255	2 US-08-356-786-2	Sequence 2, Appli
8	103	3.5	1255	1 US-08-467-083-68	Sequence 6, Appli
9	103	3.5	1255	1 US-08-414-417B-68	Sequence 68, Appli
10	103	3.5	1255	2 US-08-486-348A-68	Sequence 68, Appli
11	103	3.5	1255	2 US-08-468-545B-68	Sequence 68, Appli
12	103	3.5	1255	3 US-08-466-680B-68	Sequence 68, Appli
13	103	3.5	1255	4 US-09-527-487-2	Sequence 2, Appli
14	102.5	3.5	934	3 US-08-929-329-6	Sequence 6, Appli
15	101.5	3.5	467	3 US-09-086-483A-6	Sequence 6, Appli
16	101.5	3.5	467	4 US-09-580-212-6	Sequence 6, Appli
17	101.5	3.5	468	4 US-09-013-895A-2	Sequence 2, Appli
18	101.5	3.5	468	4 US-09-565-918-2	Sequence 2, Appli
19	101.5	3.5	468	4 US-09-448-868-2	Sequence 2, Appli
20	101.5	3.5	468	4 US-10-039-785-1	Sequence 1, Appli
21	97.5	3.3	571	4 US-09-216-393B-327	Sequence 327, App
22	97	3.3	484	2 US-08-252-493C-9	Sequence 9, Appli
23	97	3.3	484	3 US-09-276-197-9	Sequence 9, Appli
24	96	3.3	652	4 US-09-310-463-4	Sequence 4, Appli
25	96	3.3	652	4 US-08-842-248A-4	Sequence 4, Appli
26	95.5	3.3	454	3 US-08-929-329-8	Sequence 8, Appli
27	94.5	3.2	724	1 US-08-121-713D-62	Sequence 62, Appli

28	94.5	3.2	724	1 US-08-835-268-62	Sequence 62, Appli
29	94.5	3.2	724	2 US-09-060-692-62	Sequence 62, Appli
30	94.5	3.2	724	3 US-08-833-391-62	Sequence 2, Appli
31	94.5	3.2	724	4 US-09-060-610-62	Sequence 62, Appli
32	94.5	3.2	724	5 PCT-US94-10151A-62	Sequence 62, Appli
33	93.5	3.2	702	4 US-08-107-512A-5645	Sequence 5645, Ap
34	93.5	3.2	593	5 PCT-US93-07923-11	Sequence 11, Appli
35	93.5	3.2	650	4 US-09-310-463-2	Sequence 2, Appli
36	93.5	3.2	650	3 US-08-842-248A-2	Sequence 22, Appli
37	93.5	3.2	651	4 US-08-985-950-22	Sequence 22, Appli
38	93.5	3.2	651	4 US-09-546-049-22	Sequence 22, Appli
39	93.5	3.2	766	1 US-08-230-491A-3	Sequence 3, Appli
40	93.5	3.2	766	1 US-08-619-280A-3	Sequence 3, Appli
41	93.5	3.2	766	2 US-08-940-391-3	Sequence 1, Appli
42	93.5	3.2	766	4 US-09-794-236-1	Sequence 6, Appli
43	93.5	3.2	766	4 US-10-002-593-6	Sequence 8, Appli
44	93.5	3.2	487	4 US-09-685-462-8	Sequence 2, Appli
45	92.5	3.2	611	3 US-09-370-807-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-257-073-9
; Sequence 9, Application US/08257073
; Patent No. 5766597
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: de Talamo, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,073
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,305
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,183
; FILING DATE: 20-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2570
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELE: 425066 CURTIS
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 628 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

FRAGMENT TYPE: internal
US-08-257-073-9

Query Match 14.3%; Score 417.5; DB 1; Length 628;
Best Local Similarity 26.7%; Pred. No. 5.4e-33;
Matches 152; Conservative 86; Mismatches 214; Indels 117; Gaps 26;

QY 41 GNPFAANVEMKTFMRFLTHHOSGIYVDLGQDEVDGTLVREBAGLCPIMGKHIELOQ 100
DB 107 GNPW-----TEYMAKYDIEEVHSGIRVDLGEDEAVAGTORLPSCGCPVFGKILLEN 160
QY 101 PDRLEPRNNPLEDVTEKEKYKQGNPLPGGFNLNFTPSGORISFPME---LLEKSN 156
DB 161 SN-----TFLTPVATGNOYLKD-----CGFAF---PTEPLMSPTLDEMRHFYKDKY 207
QY 157 IKASTDLCRCAEFAKTYAMDKNNKATKRYPFYVDSKKRLCHILYVSMQMEGKYCSV 216
DB 208 VGNLDELTLCSRHANMI--PNDKNSNYKYPVAVDDKDKCHILYIAAQENNGPRYCN- 264
QY 217 KGEPRDLTWYCKPKRKSTENHHLIYGSAYGEN--PDAFISCPNQAALRGVFGVKKGR 275
DB 265 KDESRRSMFCRPAKDISFQNY-----TYSKNVVDNMEKVCPRKNLQNAKFGLVDSN 319
QY 276 CLDYELTD-TVIERVESKAQCWVKTENDGVASDQPHTP----- 315
DB 320 CEDIHVNEFPALDPE-----CNKLVFELS--ASDQPKYEGHLDYEKIKGFKNKAS 373
QY 316 -LTSQASWMDWP--LHOSDQPHSGGVGNRYFYVDTTGEGKALSDQVPCLVSDSA 372
DB 374 MKSRIRKSAFLPTGAFKADRYKSHGKGYMGNVTEQ--KCEIFNVKPTCLINNSY 430
QY 373 VSTYAGSISETPNF-----IIPSNPSTPTPTPTALQ--CTMDK 411
DB 431 IATTLSPHTEVNNPSCSLYKDEIMKEIERESKRIKLANDNDEGNKTKMLDEFLISDK 490
QY 412 FPDSE-GACDVQ-----ACKROKTSVGGIOISTVDCTA-----DEQNECGSN----- 454
DB 491 --DSLKRCPDEPMVNSNTRCFVCKVERAEVTSNNEVVVVEKYDEADLPEKPTMD 548
QY 455 --TALIAGLAVGVLLALLGGGCPYAKRLDNKGVAAHHEHFOSDRGAKKPSDL 512
DB 549 KKKIILASSAAVAVLATILM---VLYLKR---KGNAEKYDKDDEPDODGKNSR--NDEM 600
QY 513 QEAESFMEAEENIEQDEGTHVMEGDY 541
DB 601 LDPEASFWGEER--RASHTPVLMEKPY 626

RESULT 2
US-08-929-329-5
Sequence 5, Application US/08929329
Patent No. 6120770
GENERAL INFORMATION:
APPLICANT: Adams, John H
APPLICANT: Dalton, John P
APPLICANT: Kappe, Stefan
TITLE OF INVENTION: Plasmidum Proteins Useful for Preparing
TITLE OF INVENTION: Vaccine Compositions
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnes & Thornburg
STREET: 11 S Meridian
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,329

FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 835910-28685
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1507 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Plasmidum yeell1

US-08-929-329-5
Query Match 4.1%; Score 120; DB 3; Length 1507;
Best Local Similarity 18.8%; Pred. No. 0.021;
Matches 87; Conservative 52; Mismatches 151; Indels 172; Gaps 21;

QY 34 TLASASTGNPQAVNEMKTFMERFNLTHH-----OSGIYVDLGQDEVD--- 78
DB 18 TFSIRADNP-----QDFMDRFDILNNHVNIKMTNSGSLAQNLKFDIYDEDNISKL 71
QY 79 -----GTLYREBAGLCPIMGKH-----I 96
DB 72 NSLENARLCPNNEKGNIR--GSCPDKYKFSMDLDKDEYSEDPLNEISLGLNKKLLI 128
QY 97 ELQOPDL-----PYNNPLEDVPTKEY-----KQGNPLPGGFNL 133
DB 129 DVEIPVNMSSGLMYQGLFANCPYDKNHNVDIKNEKEYDMCPKFSNKKD----- 178
QY 134 NFVTPSGORISPFMELEKSNIKA---STDLRCAEFAKTYAMDKNNKATKYRY--- 187
DB 179 ---ISTRIKYP--LISKTYTFSHGLGRLGSNTBEPPLHYNPLENTYQKRPKL 231
QY 188 -----PFVYDSKKRLCHILYVSMQMEGKYCSVK 217
DB 232 VETLEDGSIYHCGICPCDRDFDNKCFRDLVARNHKTKECIIIGTH---EKKTTVCN 287
QY 218 GEPDPLTWYCKPKRKSTENHHLIYGSAYGENPDALFSC--PQOALRGYFV--WKKG 274
DB 288 SDNSRNNRCRFSIHK--EKGDMWTYASFTL--RPD--YETKCPRRYPPLNNSSEFGYFNVYTG 343
QY 275 RCLDVTETDVIKRVESKAQCWVKTENDGVASDQPHTPVLTQASWMDWPLHOSDQ 334
DB 344 NCSEFTKLYD--NSVTSFNECIEKLF--NFYVNAEDPE--EKRNMYLMGVAVLNKKOKL 397
QY 335 HSGVGNRYGFYVDTTGEGKALSDQVPCLVSDSAVSYT 376
DB 398 NS-----MNDLGVCALLKEKPTCVLKKQNYST 426

RESULT 3
US-08-327-832-5
Sequence 5, Application US/08327832
Patent No. 5840832
GENERAL INFORMATION:
APPLICANT: Ono, Santa J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: Transcription Factor Regulating MHC
TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
TITLE OF INVENTION: Retroviral Expression Constructs Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.

CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,832
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107,46362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20-2 508-9153
TELEFAX: 202 508-9239
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-832-5

Query Match 3.7%; Score 107.5; DB 2; Length 1104;
Best Local Similarity 19.7%; Pred. No. 0.23;
Matches 103; Conservative 61; Mismatches 159; Indels 199; Gaps 29;
QY 85 PAGLCPIWGKHIELQDPRLPYRNFLFEDVPTKEKYGSGNPLPGGFNLNFTVPSGORIS 144
DB 579 PCGOTPL-SQLEBGLSSS-----KRTCMDVPVSCG-KVCGKPLPCG-SLDPIHCEKICH 630
QY 145 PFMELLEKNKSNIKASTDLGRCAEFAPKTVAMD--KNNKATKYRYPFYVD--SKKRL 197
DB 631 EGDGVPVSRVSVISC-----RC--SPRTKELPCTSLKSEDAI-----FMCDKRCNKKRL 677
QY 198 CHILYVMQMLEGKKYCSVGKBPDDLTYWCFKPKKSTENHHLIYGSAVYGENDAFIISK 257
DB 678 C-----GHHKNE-----IC-----CVDKEH-----K 694
QY 258 CPNALRGYRFGVWK-----KGRCLDYELTDVIVBESKACQWVTFENDGVASDOP 311
DB 695 CPLNGKRLRCGLHRCSEPRCHGNC-----QTCWQASFDE----- 729
QY 312 HTYPLTSQASWMDWP-----LHOSDOP--HSGG----- 338
DB 730 ---LTHCGASVITYPVPCGTRPRECTOTCARVNECDHPYVHSGHSEKCPCTFLTK 785
QY 339 --VGR---NYGFIYVDTT-----GEGKCALSDOVPCLVSDAASVYTAAGS 380
DB 786 WCMGKHEFRSNIPCHLVDISGLPCSATLPCGMKRCQLCHKGECVLDE----- 834
QY 381 LSEETPNFIISNSVTPPTETALQCTADKFPDSFGACDVQACK-RKSTSCVGGIOIST 439
DB 835 -----PCKOPCTTPRADCGHPCMAPCHTSS--PCPYTACKAVELQCEGCR-RKE 881
QY 440 SVDCTADEONECGSNTALINGLAVGVLLALLGGGCFYAKRLDRNKGVQAANHHNEFQS 499
DB 882 MVIC-----SEASTYQRIAAISMASKITDMQLGGSVEISKLITK-KEVHQARLECDDEC 935
QY 500 DRGAKKRPSPD--LMQEAEP-----SFWDKAENIEOD 530
DB 936 SALKERKKLAFAHISEDSPFNIRSSGSKFSDIKEDARKD 977

RESULT 4
US-08-828-584-5
Sequence 5, Application US/08828584
Patent No. 5908762

GENERAL INFORMATION:
APPLICANT: Ono, Santa J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: Transcription Factor Regulating MHC
Expression, cDNA and Genomic Clones Encoding Same and
TITLE OF INVENTION: Retrieval Expression Constructs Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,584
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107,46362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20-2 508-9153
TELEFAX: 202 508-9239
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-584-5

Query Match 3.7%; Score 107.5; DB 2; Length 1104;
Best Local Similarity 19.7%; Pred. No. 0.23;
Matches 103; Conservative 61; Mismatches 159; Indels 199; Gaps 29;
QY 85 PAGLCPIWGKHIELQDPRLPYRNFLFEDVPTKEKYGSGNPLPGGFNLNFTVPSGORIS 144
DB 579 PCGOTPL-SQLEBGLSSS-----KRTCMDVPVSCG-KVCGKPLPCG-SLDPIHCEKICH 630
QY 145 PFMELLEKNKSNIKASTDLGRCAEFAPKTVAMD--KNNKATKYRYPFYVD--SKKRL 197
DB 631 EGDGVPVSRVSVISC-----RC--SPRTKELPCTSLKSEDAI-----FMCDKRCNKKRL 677
QY 198 CHILYVMQMLEGKKYCSVGKBPDDLTYWCFKPKKSTENHHLIYGSAVYGENDAFIISK 257
DB 678 C-----GHHKNE-----IC-----CVDKEH-----K 694
QY 258 CPNALRGYRFGVWK-----KGRCLDYELTDVIVBESKACQWVTFENDGVASDOP 311
DB 695 CPLNGKRLRCGLHRCSEPRCHGNC-----QTCWQASFDE----- 729
QY 312 HTYPLTSQASWMDWP-----LHOSDOP--HSGG----- 338
DB 730 ---LTHCGASVITYPVPCGTRPRECTOTCARVNECDHPYVHSGHSEKCPCTFLTK 785
QY 339 --VGR---NYGFIYVDTT-----GEGKCALSDOVPCLVSDAASVYTAAGS 380
DB 786 WCMGKHEFRSNIPCHLVDISGLPCSATLPCGMKRCQLCHKGECVLDE----- 834
QY 381 LSEETPNFIISNSVTPPTETALQCTADKFPDSFGACDVQACK-RKSTSCVGGIOIST 439
DB 835 -----PCKOPCTTPRADCGHPCMAPCHTSS--PCPYTACKAVELQCEGCR-RKE 881
QY 440 SVDCTADEONECGSNTALINGLAVGVLLALLGGGCFYAKRLDRNKGVQAANHHNEFQS 499
DB 882 MVIC-----SEASTYQRIAAISMASKITDMQLGGSVEISKLITK-KEVHQARLECDDEC 935

QY 500 DRGAKKRPD---LMOEAP-----SFMDEAENIED 530
Db 936 SALERKKRLAEFHISEDSDPNIRSSGSKPSLIKEDARXO 977

RESULT 5

US-08-484-438-8
Sequence 8, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
GENERAL INFORMATION:
APPLICANT: PLOWMAN, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegal, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-230
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-438-8

Query Match 3.6%; Score 104; DB 2; Length 1255;

Best Local Similarity 22.2%; Pred. No. 0.64; Matches 107; Conservative 45; Mismatches 173; Indels 156; Gaps 27;

QY 81 LVRPAGLCPIWGKHLEQDPLPYRNPLEDPTEKEYKQSGNDLPGG---FNLNFT 137
Db 256 LHPNHSGLC-----ELHCPALVTYNTDFESMN-----PGRTTFGASCVT 297
QY 138 PSQRISPPMELLEKSNIKASTDLGRCAEFA---FTVAMDKNKAKTKRYPPFVDS 193

Db 298 AC-----PYNYL-----STDVGSCTLVGELHNEVTABDGTORCEKSKPCA--- 339

QY 194 KXELCH-----ILYVSMQMBGKRYC-----SVKGEPPDLTWCFKPRK 232

Db 340 --RVCTGLGMEHLREVRATVTSANIQEPAGCKKIFGSLAFLEPFDDGPAINTAPLOEQEL 397

QY 233 SVTENHHLIYGSAYVGENPDAF--ISKPN-QALRG-----YRFGV-WKKGR 276

Db 398 QVFETLEIITGYLYISAMPDLSPLDLSVFQULQVIRGRILHNGAVSLTLQGLISMLGLRS 457

QY 277 LDVTELTDTYIERVESACQCVKTFENDGVASDQ---PHTYPLTSGASNNDKWPLHQSD 332

Db 458 L--RELGSGLALIHNNHLCFVHT---VPWQLFRNPH-----QAL-----LHTAN 498

QY 333 QPHSGVGRMYGFYVDT-----TGEKCALSDQ-----VPCLVSSAASVYTAAG 379

Db 499 RPEDECYBGLACHQOLARALLGSGFTQCVCNSQFLRGCEBCEVCNVLQGLPREYINAR 558

QY 380 SLSEETNFIIPNSVYTPPETALQCTAD-----KPF 412

Db 559 HCLPCHPE-QQPGNGSVTCFGEPE-ADQCVAQAHYKDBPFCVACPSGVKPDLSYMPIWKF 616

QY 413 PDSFGACDVQACRQKTSVCGGQIGTSVDTADEQNECGSNTRALLGLAVGVLALL 472

Db 617 PDEBGAC--QPC---PINTHSCVDLDDKCGPAEQR--ASPLTISVS--AVGILLVVL 667

QY 473 G 473

Db 668 G 668

RESULT 6

US-08-625-101-2
Sequence 2, Application US/08625101

Patent No. 5869445

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE

TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION

TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu

TITLE OF INVENTION: ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/625,101

FILING DATE: 01-APR-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C7

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1255 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-625-101-2

Query Match	3.6%	Score 104;	DB 2;	Length 1255;
Best Local Similarity	22.5%;	Pred. No. 0.64;		
Matches 108;	Conservative 43;	Mismatches 174;	Indels 156;	Gaps 27

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Oy 81 YYREBAGICPIRGKHIIELOQDRLPRNNFLEVPFEKEXKQSGNLPQSG---FNINFVT 137
Db 256 LHFNHSGIC-----ELHCPLVYNTNTTFFSMPN-----PEGRYTFGASCVT 297
Oy 138 PSGORISPPMELLENKSNISKASTDLGRCAEFA---FKTVAMDKNKKATKYRPFVYDS 193
Db 298 AC-----PNYVL-----STDVGSCTLYCPLHNGEVTADGTQRCEKSKPCA--- 339
Oy 194 KKRILCH-----ILVYSMQLMEGKYC-----SVKGEPPDLTWYCEPKRK 232
Db 340 --RVCYGLGMEHLREVRAVATSANIGEFACKCKIFGSLAFLPESFDPPASNTAPLDPEOL 397
Oy 223 SVTEHHLLIYGSAVYGENDPAR--ISKCPN-QALRG-----YRFGV-WKKGRC 276
Db 398 QVFETLEBITTGLYIISAMPDSLPDLVSFONLQVIRGRILHNGAVSYTLQIGISWGLRS 457
Oy 277 LDYTELTDPIRVESKACQWKTFFENDVASDQ-----PHTYLTLSQASNDMWPLHQSD 332
Db 458 L--RELGSGLALIHHTHLCEVHT-----VPMQLFRNPH-----QAL-----LHTAN 498
Oy 333 QPHSGGVGNRYFYVYDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
Db 499 RPEDSCVEBGLACHQLCARGCHCKGPPQTQCVMNSQPLRQGEYCEBGRVLOGLPREVYNAR 558
Oy 360 SLSEBTPNFILIPSNBVPTRPETAQCTAD-----KF 412
Db 559 HCLPCHPE-CQQONSVTCEGPE-ADQVACAHAHYKDPFCVACPSGVKRDLSYMPIWK 616
Oy 413 PDSFACDVQACKRKQKTSCTGVGGIOGSTVDTCTADEONEGSSNTALLAGLAVGVLIALL 472
Db 617 PDEBAC--QPC---PINCTHSCVDLDDKDCPABOR--ASPLTSIIS--AVWGILLVVL 667
Oy 473 G 473
Db 668 G 668

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RESULT 7
 US-08-356-786-2
 Sequence 2, Application US/08356786
 Patent No. 587305
 GENERAL INFORMATION:
 APPLICANT: Huston, James S.
 APPLICANT: Oppermann, Hermann
 APPLICANT: Houston, L. L.
 APPLICANT: Ring, David B.
 TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
 TITLE OF INVENTION: Marker
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESSES:
 ADDRESSSEE: Edmund R. Pitcher, Teesta, Hurwitz, & Thibault
 STREET: Exchange Place, 53 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356,786
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/831,967
 FILING DATE: 06-FEB-1992

```

1  . ATTORNEY/AGENT INFORMATION:
2
3  NAME: Pitcher, Edmund R.
4
5  REGISTRATION NUMBER: 27,829
6
7  REFERENCE/DOCKET NUMBER: CRP-053
8
9  TELECOMMUNICATION INFORMATION:
10
11 TELEPHONE: (617) 248-7000
12
13 TELEFAX: (617) 248-7100
14
15 INFORMATION FOR SEQ ID NO: 2:
16
17 SEQUENCE CHARACTERISTICS:
18
19 LENGTH: 1255 amino acids
20
21 TYPE: amino acid
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23 TOPOLOGY: linear
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25 MOLECULE TYPE: protein
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	Query Match	3.6%	Score 104	DB 2	Length 1255	
	Best Local Similarity	22.5%	Pred. No. 0.64			
	Matches 108	Conservative	43	Mismatches 174	Indels 156	Gaps 27
Qy	81	LYREPAGLCPIWKGHIELOQPDRLPYRNNFLIEDVTEKEKXSGSNPLPGC---	FNLEPVT	137		
Db	256	LHFNHSGIC-----ELHCPALVTYNDFTEESMN-----	DEGRYTFGASCVT	297		
Qy	138	PSGGRISPFPELLEKXSNITAKSDTDLGCAPFA---	FKTYAMDONKATKRYRPVYOS	193		
Db	298	AC-----PYNVL-----STDVSGCTLVCPRLHNOETVAEDGTORCEKSCPCA--		339		
Qy	194	KGRICH-----ILVYSQMLMGKKYCC-----	SVKGEPRDLTWYCFKPRK	232		
Db	340	--RVCYGLMGHLEAVRAVTSANIQEPFGCKKI	FGSLAPLPESFPGDPAISNTAPLPQEDL	397		
Qy	233	SVTENHHLIYSAAYGVNDPAF--ISKPN-QALRG-----	YRFGV-WKGRIC	276		
Db	398	QVFETLEBITGYLIASMPDLSPLDSVPQNQVIRGILHNGAVSLTLOGIGLSWLGERS		457		
Qy	277	LDYIELDITVIEREBSKAQCVKTKFPENDVASDQ---	PHYPLTSQSNMNMWPLHQSD	332		
Db	458	L--RELSSGLALIHNNHLCFVHT-----VWMDQFRRPH-----QAL-----LHTAN		498		
Qy	333	QPHSGGVGRNRYFYVDTTGE-----GKCALSDQ-----	VPDCLVSDSAAVSYTAAG	379		
Db	499	RPEDECGEGLACHQLCARHGCMGRPQCYNCSQFLAQCEVEBECRYLGSLPREVYANR		558		
Qy	380	SLSEETPNFIIPNSPSVTPPTPETALOCTAD-----	KE	412		
Db	559	HCLPCHPE-CQPGNGSVTCFGRPE-ADQCVAACHYKDPFCVABCPGVKPDLSYMPIMKE		616		
Qy	413	PDSFGACDVQACRQKTS CVSGQIOISTSVDTADQNEGGSNTALAGLAVGCVLLALL		472		
Db	617	PDEEGAC--QPC---PIVCHTSQVDLDDKGGPAEQR--ASPLTISIIS--AVVIGILLVVL		667		
Qy	473	G 473				
Db	668	G 668				

RESULT 8
 US-08-467-083-68
 : Sequence 68. Application US/08467083
 : Patent No. 5726023
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Cheever, Martin A.
 : APPLICANT: Diels, Mary L.
 : TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
 : TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 : TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
 :
 : NUMBER OF SEQUENCES: 68
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Seed and Berry
 : STREET: 6300 Columbia Center, 701 Fifth Avenue
 : CITY: Seattle
 : STATE: Washington
 : COUNTRY: US

Db 398 QVFETLEETITGLYISAMPDSLPLDSVFQNLQVIRGRIILHNGAYSLTLQGLISWGLRS 457
Qy 277 LDYTELDTVIERVESKAQCVKTFENDVASDQ---PHTYPLTSQASNDMPHLHOSD 332
Db 458 L--RELGSGLALIHNNHLCFVHT-----VPWDQLFRNPH-----QAL-----LHTAN 498
Qy 333 QPHSGGVGRNYGFYVDT-----TGEGKALSDQ-----VPDCLVSDSAASYTAG 379
Db 499 RPEDECVGEGLACHQLCARCHWGPRPTQCVCNSQFLRGQECVEECRVLQGLPREYVNR 558
Qy 380 SLSEETPNFIIPSNPSVTPTPTALQCTAD-----KF 412
Db 559 HCLPCHPE-COPQNGSVTCFGE-ADQCVACAHYKDPFCVARGSPGVKPDLSYMPIKF 616
Qy 413 PDSFGACDVQACKKQKTSQVSGQISTSVDTADQNECGSNTALILAGLAVGVLLALL 472
Db 617 PDEGAC--QPC---PINCTHSCVDLDDKGCRAEOR--ASPLTSIIS--AVGILLVVL 667
Qy 473 G 473
Db 668 G 668

RESULT 12

US-08-466-680B-68
; Sequence 68, Application US/08466680B
; Patent No. 6075122

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.
APPLICANT: Disig, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,680B
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-466-680B-68

Query Match 3.5%; Score 103; DB 3; Length 1255;

Best Local Similarity 22.5%; Pred. No. 0.81;
Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

Qy 81 LVREPAGLCPITWGHIELOQDRLPYRNNFLEVDPEKEKYQSGNPLPGG---FNLNFT 137
Db 256 LHNHNSGIC-----ELHCPALVTYNTDTFESMPN-----PEGRYTFGASCVT 297
Qy 138 PSQGRISPPMELLEKNISIKASTDLCRCAEFA-----FKTVAMDKNKATKRYPFVYDS 193

Db 298 AC-----PYNVL-----STDVGSCTLVCPILHNEVTAEDGTORCEKSKPCA--- 339
Qy 194 KKRICH-----ILVSMQLMGKKYC-----SVKGRPDLTWCFPRK 232
Db 340 --RVCTGIGMEHLREVAIVTSANIQEFAGCKKIFGSLAFLESPFDGDPASNTAPLOEBOL 397
Qy 233 SVTENHHLIYSAVAVGENPAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
Db 398 QVFETLEETITGLYISAMPDSLPLDSVFQNLQVIRGRIILHNGAYSLTLQGLISWGLRS 457
Qy 277 LDYTELDTVIERVESKAQCVKTFENDVASDQ---PHTYPLTSQASNDMPHLHOSD 332
Db 458 L--RELGSGLALIHNNHLCFVHT-----VPWDQLFRNPH-----QAL-----LHTAN 498
Qy 333 QPHSGGVGRNYGFYVDT-----TGEGKALSDQ-----VPDCLVSDSAASYTAG 379
Db 499 RPEDECVGEGLACHQLCARCHWGPRPTQCVCNSQFLRGQECVEECRVLQGLPREYVNR 558
Qy 380 SLSEETPNFIIPSNPSVTPTPTALQCTAD-----KF 412
Db 559 HCLPCHPE-COPQNGSVTCFGE-ADQCVACAHYKDPFCVARGSPGVKPDLSYMPIKF 616
Qy 413 PDSFGACDVQACKKQKTSQVSGQISTSVDTADQNECGSNTALILAGLAVGVLLALL 472
Db 617 PDEGAC--QPC---PINCTHSCVDLDDKGCRAEOR--ASPLTSIIS--AVGILLVVL 667
Qy 473 G 473
Db 668 G 668

RESULT 13

US-09-527-487-2
; Sequence 2, Application US/09527487
; Patent No. 6528060

GENERAL INFORMATION:

APPLICANT: Nicolette, Charles
TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
FILE REFERENCE: 126881309200
CURRENT APPLICATION NUMBER: US/09/527,487
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 1255
TYPE: PPT
ORGANISM: Homo sapiens
US-09-527-487-2

Query Match 3.5%; Score 103; DB 4; Length 1255;
Best Local Similarity 22.2%; Pred. No. 0.81;
Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;

Qy 81 LVREPAGLCPITWGHIELOQDRLPYRNNFLEVDPEKEKYQSGNPLPGG---FNLNFT 137
Db 256 LHNHNSGIC-----ELHCPALVTYNTDTFESMPN-----PEGRYTFGASCVT 297
Qy 138 PSQGRISPPMELLEKNISIKASTDLCRCAEFA-----FKTVAMDKNKATKRYPFVYDS 193
Db 298 AC-----PYNVL-----STDVGSCTLVCPILHNEVTAEDGTORCEKSKPCA--- 339
Qy 194 KKRICH-----ILVSMQLMGKKYC-----SVKGRPDLTWCFPRK 232
Db 340 --RVCTGIGMEHLREVAIVTSANIQEFAGCKKIFGSLAFLESPFDGDPASNTAPLOEBOL 397
Qy 233 SVTENHHLIYSAVAVGENPAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
Db 398 QVFETLEETITGLYISAMPDSLPLDSVFQNLQVIRGRIILHNGAYSLTLQGLISWGLRS 457
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DB 499 REDEECVGLACHOLCARGHCMPPTQCVNCISQPLRGQECVBEGRVLQGLPREVYNAR 558
QY 380 SLSSEEPNIIISNSVTPPTPETALQCTAD-----KF 412
DB 559 HCLPCHPE-COPONSVTCTFGPE-ADQVCAHAYKDPFCVAPCPGKVPDLSYMPIMKF 616
QY 413 PDSFACDVQACRQKTSVCGGQIOSTVSDCTADEQNEGCSNTALAGLAVGVLTLAL 472
DB 617 PBEERAC--QPC---PINCTHSCVLDLDDKCCPABQR--ASPUTSIVS--AVVGILLVVL 667
QY 473 G 473
DB 668 G 668

RESULT 14
US-08-929-329-6
; Sequence 6, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
; APPLICANT: Adams, John H
; APPLICANT: Dalton, John P
; APPLICANT: Kappe, Stefan
; TITLE OF INVENTION: Plasmidium Proteins Useful for Preparing
; TITLE OF INVENTION: Vaccine Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 S Meridian
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929.329
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 835910-28685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Plasmidium berghei
; US-08-929-329-6

Query Match 3.5%; Score 102.5; DB 3; Length 934;
Best Local Similarity 20.5%; Pred. No. 0.56;
Matches 89; Conservative 49; Mismatches 150; Indels 147; Gaps 23;

QY 34 TISASTSGNPQANV-EKMTMERENLTHHSGIYVLDGQKEVDGITYREPAGLCPIW 92
DB 47 TNSGSLGKDPFKFDIYEDNINSKFNTELSAQ-----LCSNHENDG-IYR---GSCPDY 96

QY 93 GKH-----TELQOPDRL-----PYRNNFL 111
DB 97 GKTFFMNLDKDEYNEDFLNETSLGLNKKLLIDLEI PNMMSGLAMVYQGLFANCFYDKNA 156
QY 112 EDVPTKEKY-----KOS-----GNPLPGGNLNFVTSGORI 143
DB 157 NDIKKEKEDYMCFDKFKYNNKONISTRIKOLLISKTYFGSHGLGRGASN----- 207
QY 144 SPFPELLEKXSNKA-----STDGRCAEFAPKTYAMDKKATKY 185
DB 208 TEYPLHITNPLENYTKQMRYPKLVETLEDOSIYSHCIGPCPD-----RFDNKCFA 259
QY 186 RYFVYDSKRLCHILYVSMOLMEGKTCVSGEPPDLTWYCFKPKRSXTENHHLIYSGA 245
DB 260 DLVAFNKHKTKECIIIGH-----EKKTKKNCSDHSRRNGRCFSSIKK-EKKDKMTYSS 314
QY 246 YVGENPDAPISK-C-PNQLRGYRFGV--WKKGRCLDYTELTD-TVIERVESKAQCWVYKF 301
DB 315 FL--RPD--YETKCPRPYPLNNSFEFGYFNVTGKCESPTKYDNTVI---SFOCTEKLF 367
QY 302 ENDGVASDQPHYPLTQASNDWVPLHQSDQPHSGGVGRNNGFYVDITGSGKALSQ 361
DB 368 -SENYANENPD--QKRSNYLWGAVWLENKONKLN-----MNDLGVCVLLKE 411
QY 362 VPDCLVSDSAVSYT 376
DB 412 RPTCVLKKQNTYSFT 426

RESULT 15
US-09-086-483A--6
; Sequence 6, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086.483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050.936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069.112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid

Db 320 PADL 323

RESULT 18

US-09-565-918-2
Sequence 2, Application US/09565918
Patent No. 6433147
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Ni, Jian
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4
FILE REFERENCE: 1488.1300005
CURRENT APPLICATION NUMBER: US/09/565,918
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,922
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: US 09/013,895
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: US 60/037,829
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: US 60/035,722
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
US-09-565-918-2

Query Match 3.5%; Score 101.5; DB 4; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.23; Indels 75; Gaps 14;
Matches 59; Conservative 27; Mismatches 83;

313 TYPLTSQASWDMW---PL-----HOSDPHSGVGRNYGYVDTTGEKCALSDQ 361
Db 110 TIKHDDSIGTQWHEHSLGELCPGSHRSRP--GACNR-----CTEGVGTNMANN 160
Qy 362 VPDCIVSDSAVSYTAAGSLSEETPNFTIPSPSVTPPTPTALQCTADKPPDSFGACDV 421
Db 161 LFACI-----PCTACKSDEE-----RSPCTT--TRNTAQCCKRGTRFNDSA--- 201
Qy 422 QACKRQKTSVCGGQIOSTSVDTADBEQNEC-----GSN-----TALTAGLAVGV 467
Db 202 EMCRCSTGCGPRGMVKV--DCTPMSDIECVHKGSGNGHNIWLVTVLWVPLLVAVLI 259
Qy 468 LLALLGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFOSDRGARKKR 507
Db 260 VCCIGSGCGGDPKCMDRVCFWRLGLRGPABDNANHEILSNADSLSTFVSEQMESOE 319
Qy 508 PSDL 511
Db 320 PADL 323

RESULT 19

US-09-448-868-2
Sequence 2, Application US/09448868
Patent No. 6461823
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4; Death
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
TITLE OF INVENTION: Superfamily and Binding to Trail (Ap02-L)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-448-868-2

Query Match 3.5%; Score 101.5; DB 4; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.23; Indels 75; Gaps 14;
Matches 59; Conservative 27; Mismatches 83;

313 TYPLTSQASWDMW---PL-----HOSDPHSGVGRNYGYVDTTGEKCALSDQ 361
Db 110 TIKHDDSIGTQWHEHSLGELCPGSHRSRP--GACNR-----CTEGVGTNMANN 160
Qy 362 VPDCIVSDSAVSYTAAGSLSEETPNFTIPSPSVTPPTPTALQCTADKPPDSFGACDV 421
Db 161 LFACI-----PCTACKSDEE-----RSPCTT--TRNTAQCCKRGTRFNDSA--- 201
Qy 422 QACKRQKTSVCGGQIOSTSVDTADBEQNEC-----GSN-----TALTAGLAVGV 467
Db 202 EMCRCSTGCGPRGMVKV--DCTPMSDIECVHKGSGNGHNIWLVTVLWVPLLVAVLI 259
Qy 468 LLALLGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFOSDRGARKKR 507
Db 260 VCCIGSGCGGDPKCMDRVCFWRLGLRGPABDNANHEILSNADSLSTFVSEQMESOE 319
Qy 508 PSDL 511
Db 320 PADL 323

RESULT 20

US-10-039-785-1
Sequence 1, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
US-10-039-785-1

Query Match 3.5%; Score 101.5; DB 4; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.23;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

313 TYPPTSQASWMDW---PL-----HSDPHSGCGVGRNGFYVDTTGSEKALSDQ 361
110 TTKLHDQSIGTOQWHSPIGELCPGSHSRSP--GACNR-----CTEGVGYTNASNN 160
362 VPDCLVSDAAVSYTAAGSLSEETPNFIIPSNPSVTPPETALQCTADKFPDSFGACDV 421
161 LFRACL-----PCTACKSDEER-----RSBCTT--TRNTACQCKPGTFRINDSA--- 201
422 QACKROKTSVCGQIOISTVDTADEQNEC-----GSN-----TALLAGLAVGVYL 467
202 EMCRKSGTSGPRMVAVK--DCTPMGDIQVHKESGNHNIWLVVTLVPLLVAVLVI 259
468 LALLGCG-----CYFAKRLDRNKGVQ-AAHNE-----HEFOSRGRARKKR 507
260 VCCCTGGCGGDPKCMRDVCFMRLGLRGFGAEDNAHETLSNADSLSTFVSEQWESQE 319
508 PSDL 511
320 PADL 323

RESULT 21
US-09-216-393B-327
Sequence 327, Application US/09216393B
Patent No. 6514694
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393B
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 327
LENGTH: 571
TYPE: PRT
ORGANISM: Toxoplasma gondii
US-09-216-393B-327

Query Match 3.3%; Score 97.5; DB 4; Length 571;
Best Local Similarity 24.0%; Pred. No. 0.8;
Matches 42; Conservative 24; Mismatches 58; Indels 51; Gaps 6;

353 EGCALSDQVDPCLVSDAAVSYTAAGSLSEETPNFIIPSNPSVTPPETALQCTADK 412

DB 445 EGEHVPEEIEPE-----GEHVPEEIEPEGEHV--PEEET----- 476
QY 413 PDSFGACVQACKROKTSVCGQIOISTVDTADEQNECGSNTALLAGLAVGVYLALL 472
DB 477 PEGEHAPPEETPAPEET-----EKEEEGVVAIAGGVGVLLINGG 520
QY 473 GGGCYFAFLDRNKGVAHHEHEFOSDRG---ARKRPSDLMQBAEPSFVDEAE 524
DB 521 AGAANYVANO---GGEVAHDEWVFESEEDGTQAGENRESFTVIEIDDAADND 571

RESULT 22
US-08-252-493C-9
Sequence 9, Application US/08252493C
Patent No. 5891645
GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matlis, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,493C
FILING DATE: June 1, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: predicted amino acid sequence of Porcine E-selectin
US-08-252-493C-9

Query Match 3.3%; Score 97; DB 2; Length 484;
Best Local Similarity 22.3%; Pred. No. 0.68;
Matches 73; Conservative 32; Mismatches 131; Indels 92; Gaps 16;

QY 249 ENPDAPISKCPN-----QALRGYRF-----GVW---KKGRCLDYTELDT 285
DB 185 ENPVGAVVYCPQSLPMTTCAFECKEGFELIGPEHLQCTSSGSGMDKKPTCAVT--CDT 242
QY 286 V-----IEVESAQCWVKTFFNDGVASQPHYPTLSQASWMDWMPLOS 331
DB 243 VEHFQNGVDSCHSSIGEPAYKSTCHFTCAEGFQGG--PAQIETAGQMTQAQPVCKA 300
QY 332 -----DQPHSGVGRNGFYVDTTGE-----GKCALSDQVDPCLVSDAAVSYTAAGSL 381

Db 301 VKCPAVSQPKGLVKFTH-----SPTGEFTYKSSCAFSCE-EGFELKRSQAQLCTSGQOW 354
Qy 382 SEETPNFLIPSNBVPPTPETALQCTADKFPDSFGACDVQACKRKQKTSQVGGIOISTSV 441
Db 355 TQEVPSQVQVQSSLEVP-R-EINMSCGEPV---FGAVCTPACPE-----GWMINGSV 403
Qy 442 DCTADEQNECG-----SNTALIAGLAVGVLLALLGGCCYPAKRLDR 484
Db 404 ALT-----CGATGHWSGMLPTCEAPAESKIPLAMGLAAGVSPMTSASFLLMLLKRRLK 457
Qy 485 NKGVQAAHHEHFOSDRGARKRPSDLM 512
Db 458 RAKKFPSSSSECLQPNGS-YQWPSDLI 484

RESULT 23
US-09-276-197-9
Sequence 9, Application US/09276197
Patent No. 6040428

GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matls, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/252,493
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: predicted amino acid sequence of
DESCRIPTION: Porcine E-selectin
US-09-276-197-9

Query Match 3.3%; Score 97; DB 3; Length 484;
Best Local Similarity 22.3%; Pred. No. 0.68;
Matches 73; Conservative 32; Mismatches 131; Indels 92; Gaps 16;

Qy 249 ENPDATSKCPN-----QALRGYR-----GWM--KKGRCLDYTELDT 285
Db 185 ENPANGVATCPQSLPMNTTCAFECKEGLIGPEHLQCTSSGSGDKKPTKAVT--CDT 242
Qy 286 V-----IERVESKACQWVTFTENDVASDPHTYPLTSGQSWNDWMLHQS 331

Db 243 VGHFQNDVSCNHSLSIEFAFKSTCHPTCAEGFELQG--PAQLECTAQOGTQOAPVCKA 300
Qy 332 -----DQPSGGVGRNRYGVYVDTTGE-----GKCALSDQVPCDLVDSAAVSTAAAGSL 381
Db 301 VKCPAVSQPKGLVKFTH-----SPTGEFTYKSSCAFSCE-EGFELKRSQAQLCTSGQOW 354
Qy 382 SEETPNFLIPSNBVPPTPETALQCTADKFPDSFGACDVQACKRKQKTSQVGGIOISTSV 441
Db 355 TQEVPSQVQVQSSLEVP-R-EINMSCGEPV---FGAVCTPACPE-----GWMINGSV 403
Qy 442 DCTADEQNECG-----SNTALIAGLAVGVLLALLGGCCYPAKRLDR 484
Db 404 ALT-----CGATGHWSGMLPTCEAPAESKIPLAMGLAAGVSPMTSASFLLMLLKRRLK 457
Qy 485 NKGVQAAHHEHFOSDRGARKRPSDLM 512
Db 458 RAKKFPSSSSECLQPNGS-YQWPSDLI 484

RESULT 24
US-09-310-463-4
Sequence 4, Application US/09310463A
Patent No. 6384203

GENERAL INFORMATION:
APPLICANT: Cosman, David J.
APPLICANT: Anderson, Dirk M.
APPLICANT: Borges, Luis
TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
FILE REFERENCE: 2624-A
CURRENT APPLICATION NUMBER: US/09/310,463A
CURRENT FILING DATE: 1999-05-12
EARLIER APPLICATION NUMBER: 08/842,248
EARLIER FILING DATE: 1997-04-24
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 652
TYPE: PRT
ORGANISM: human
US-09-310-463-4

Query Match 3.3%; Score 96; DB 4; Length 652;
Best Local Similarity 20.4%; Pred. No. 1.4;
Matches 50; Conservative 32; Mismatches 95; Indels 68; Gaps 6;

Qy 293 KAQCWVTFENDGVASDPHTYPLTSGQSWNDWMLHQSQDPHSGVGRNRYGVYVDTTG 352
Db 347 QSQGMQGT-----LLTKEGAADDPRLRSTYQSK----- 377
Qy 353 EGKCALSDQVPCDLVDSAAVSTAAAGSLSE-----TPNFIISNSVTPPTETA 404
Db 378 -----YQAEPPMGVPTSAAHGYRCYGSQSKPYLLTHPDPLELVVSGSGGSSPTTG 432
Qy 405 LQCTADKFPDSFGACDVQACKRKQKTSQVGGIOISTSVDTADEQNEGSNTALIAGLAVG 464
Db 433 -----PTTSAGBEDQPLPTGSDPSSGGRHGVIGLIVA 469
Qy 465 GVLLALLGGCCYPAKRLDRNKGVQAAHHEHFOSDRGARKRPSD--LMQEAEPSPWDE 522
Db 470 VILLILLILLFLLRHRQGKHWTSQRYADFGHAGVGPETRDGLQWRSSPALA-DA 528
Qy 523 AEENI 527
Db 529 QEENL 533

RESULT 25
US-08-842-248A-4
Sequence 4, Application US/08842248A
Patent No. 6448035
GENERAL INFORMATION:

APPLICANT: Cosman, David J.
TITLE OF INVENTION: Family of Immunoregulators Designated
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
OPERATING SYSTEM: Microsoft Word 7.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,248A
FILING DATE: April 24, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-842-248A-4

Query Match 3.3%; Score 96; DB 4; Length 652;
Best Local Similarity 20.4%; Pred. No. 1.4;
Matches 50; Conservative 32; Mismatches 95; Indels 60; Gaps 6;

QY 293 KACQWVKTENDGVASDOPHTYPLTSQASWMDWMPHQSODPHSGVGNNGFYVDTTG 352
DB 347 GQGWMTF-----LTREGAADPWRLRSTYQSK----- 377

QY 353 ESKCALSDVDPCLVSDSAVSTYAGSISE-----TNFIIPSNPSTPRPETA 404
DB 378 -----YQAEFPMGPVTSAAHAGTYRCYSSQSKRYLLTHPSDPLELVSGSPSGPSPPTTG 432

QY 405 LQCTADKFPDSFGACVQACQKQKTSQVSGQIQSTSVDCSTADEQNECGSNTALLIAGLAVG 464
DB 433 -----PTSTAGPREDPQLTPGSDPSGLGHLGVIGILVA 469

QY 465 GVLLALLGGGCFYAKRLDRNKGVQAAHNEHFQSDRGARKKRPD-LMQEAEPGFME 522
DB 470 VILLILLILLFLILHRROGKMTSTQKADQHPAGAVGPEPTDRGLQWSSPA-DA 528

QY 523 ASENT 527
DB 529 QEENL 533

RESULT 26
US-08-929-329-8
Sequence 8, Application US/08929329
GENERAL INFORMATION:
APPLICANT: Adams, John H
APPLICANT: Dalton, John P
APPLICANT: Kappel, Stefan
TITLE OF INVENTION: Plasmidum Proteins Useful for Preparing
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: Barnes & Thornburg
STREET: 11 S Meridian
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,329
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 835910-28685
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Plasmidum falciparum
US-08-929-329-8

Query Match 3.3%; Score 95.5; DB 3; Length 454;
Best Local Similarity 21.1%; Pred. No. 0.87;
Matches 94; Conservative 46; Mismatches 144; Indels 161; Gaps 25;

QY 56 RPNLTHHOSGTYVDL---GQDKVDTGLYREPA-GLCPIGKTHLQDPRLPYRNNFL 111
DB 21 KNIISNTAGTSOSLFHNYDKTCCPNHYVSGRAHSGCPNYGKALIVQ-----NLL 71

QY 112 EDVPEKEXYKQSGNPLPGFNLNFTP--SGQRSPF--PMELKSNINIKASTDLGRCA 167
DB 72 GE-----EYDKN-----FNLNFTNERTIGTLNKFKKQDVETSIENSGIAMHNNMLASC 119

QY 168 E-----FAKTVAMDKNKATK--YRYPFV--YDSKKRLCHILVSMQLMEG--- 210
DB 120 PVHNEBKLFVKT--DYNYKMKCKSLFSNRFTWKEVDPKTRL--FMVYGLYGGRLG 174

QY 211 -----KXY-----CSYKGEPRDLTWYCFPR----- 230

DB 175 ANIKRDKKQKKEKYEENITLPMKNPBLIKNLPDCSIS-----YCLAPCLSENSGNKCF 227

QY 231 RKSVTENHLIYGAVGENPDATISKCPNQLRGYRFGWKKGRCGLDYTELDTVIERV 290
DB 228 RNLPAVYNHLTNECVILGTHQERTNSCRRTKEK-----KKPNCOLIKRTD----- 275

QY 291 ESKACQWVKTENDGVASDOPHTYPLTSQASWMDWMPHQS-----DQPHSGGV--- 339
DB 276 -SKDWTYVSSFRPDYETKCPRPYLPKSKV-----FGTFDQTKGCKSLMDKAYEYGINKF 330

QY 340 -----GRN--YGFYVDTT-----GEGKCALSDQVDDCLVSDSA 371
DB 331 SVCLEYFLVSPKDLVNSGRNNYWGIMADHSVNNENIEIANGKCYHLVVKTCVIXEN 390

QY 372 AVSYTAAGSLSEETPNFIIPSNPV 396
DB 391 HPSFTA---LTANTYDF---NQSV 408

RESULT 27

US-08-121-713D-62
Sequence 62, Application US/08121713D
Patent No. 5639856
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-713D-62

Query Match 3.2%; Score 94.5; DB 1; Length 724;
Best Local Similarity 20.3%; Pred. No. 2.4;
Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

QY 51 KTFMERFLTH-----HHQSGIYVDLGQDKEVDGTLVREPAGL 88
DB 156 KDVIYANLTLPRSEYVIGVGLGIACPYDPLDNSTAIYENG-----NPGGL 204
QY 89 CPIW-GKIIIELOQPRRLPYRNNFLEDVPTKEKYKSGNPLPGCFNLNFTVPSGQRISSFP 147
DB 205 PGLVSGTNAETKATDVIFRTDLVNTSAKRLKYK-----FKRTLLKYD 246
QY 148 MELLEKSNITASTDLGRCAEFAPKTVAMDKN--KATKYRYPFYDSKRLCH-----199
DB 247 SKWLDK-PNFVGSFPIGEGYVFFPRETAVEYINCKA-----VYSRIARVCKKDVCGK 298
QY 200 --ILVSNQMEGKKYCSVKGEPPDLTWYCFKPRKSV-----TENHHLIYG 243
DB 299 NLNHNATYIKALRNCISGSEFP---FYNEIQSVYQLPSDKSRFPATFTTSTNGLIG 354
QY 244 SA-----YVGENPDPAISKCPNOLRGYRFGW-----KKGRL-DYTELTDTVI 287
DB 355 SAVCSFHINEIQAFNGKFKGQSSN---SAMLPLVLSNRVPEPRGTCVNDTSLNLPDTVL 411
QY 288 ERVES 292
DB 412 NFIRS 416

RESULT 28

US-08-835-268-62
Sequence 62, Application US/08835268
Patent No. 5807826
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,268
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-835-268-62

Query Match 3.2%; Score 94.5; DB 1; Length 724;
Best Local Similarity 20.3%; Pred. No. 2.4;
Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

QY 51 KTFMERFLTH-----HHQSGIYVDLGQDKEVDGTLVREPAGL 88
DB 156 KDVIYANLTLPRSEYVIGVGLGIACPYDPLDNSTAIYENG-----NPGGL 204
QY 89 CPIW-GKIIIELOQPRRLPYRNNFLEDVPTKEKYKSGNPLPGCFNLNFTVPSGQRISSFP 147
DB 205 PGLVSGTNAETKATDVIFRTDLVNTSAKRLKYK-----FKRTLLKYD 246
QY 148 MELLEKSNITASTDLGRCAEFAPKTVAMDKN--KATKYRYPFYDSKRLCH-----199
DB 247 SKWLDK-PNFVGSFPIGEGYVFFPRETAVEYINCKA-----VYSRIARVCKKDVCGK 298
QY 200 --ILVSNQMEGKKYCSVKGEPPDLTWYCFKPRKSV-----TENHHLIYG 243
DB 299 NLNHNATYIKALRNCISGSEFP---FYNEIQSVYQLPSDKSRFPATFTTSTNGLIG 354
QY 244 SA-----YVGENPDPAISKCPNOLRGYRFGW-----KKGRL-DYTELTDTVI 287
DB 355 SAVCSFHINEIQAFNGKFKGQSSN---SAMLPLVLSNRVPEPRGTCVNDTSLNLPDTVL 411
QY 288 ERVES 292

Db 412 NFIRS 416

RESULT 29
US-09-060-692-62

Sequence 62, Application US/09060692

Patent No. 5935865

GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.

APPLICANT: Matthes, David

APPLICANT: Bentley, David R.

APPLICANT: O'Connor, Timothy

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 Bush Street, Suite 3200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/060,692

FILING DATE:

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/121,713

FILING DATE: 13-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oseman, Richard A.

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: B94-002-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)343-4341

TELEFAX: (415)343-4342

TELEX:

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 724 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-060-692-62

Query Match 3.2%; Score 94.5; DB 2; Length 724;

Best Local Similarity 20.3%; Pred. No. 2.4;

Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

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QY 51 KTFMERFNLTH-----HHOSGIYVDLGDQKVEDGTLNREPAGL 88
   ||:|||||
Db 156 KQYVIVANLTHLPRSEYVIGVGLGIAKCPYDPLDNSTAIYENG-----NPGGL 204
   ||:|||||
QY 89 CPIW-GKHIELQOPRLPYRNPNLEDPVTEKEYKOSGNPLPGGFNLNFTVPSGORISPP 147
   ||:|||||
Db 205 PGLYSTNNEFTKADIVIFRTDLYNTSAKRLKLVK-----FKRTLKWD 246
   ||:|||||
QY 148 MELLEKNSTIKASTDLGRCAEFAFKTVAMDKN--KATKYRVPFYDSKRLCH----- 199
   ||:|||||
Db 247 SKMLDK-PNFVGSFDIGEVYVFFRETAVEYINCGKA-----VYSRIARVCKKDVGSK 298
   ||:|||||
QY 200 --ILVSNQLMGKCKYCSVKGEBPDLTWCCEKPKRSV-----TENHHLIYG 243
   ||:|||||
Db 299 NLLAHNMAWTLKARLNCISISGEFP-----FYFNEIOSVYQLPSDKSRFPATFTTSTNGLIG 354
   ||:|||||
QY 244 SA-----YVGENPDPAFISKCPNQLARGYRGVW-----KKGRCL-DYTELDTVI 287
   ||:|||||
Db 355 SANCSHINIEIOAFAFGKFKEGSSN---SAMLPLVNSRVPEBRPGTCVNDTSLNLDPTVL 411
   ||:|||||
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QY 288 ERVES 292
Db 412 NFIRS 416RESULT 30
US-08-833-391-62

Sequence 62, Application US/08833391

Patent No. 6013781

GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.

APPLICANT: Matthes, David

APPLICANT: Bentley, David R.

APPLICANT: O'Connor, Timothy

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 Bush Street, Suite 3200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,391

FILING DATE:

CLASSIFICATION: 530

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/121,713

FILING DATE: 13-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oseman, Richard A.

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: B94-002-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)343-4341

TELEFAX: (415)343-4342

TELEX:

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 724 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-391-62

Query Match 3.2%; Score 94.5; DB 3; Length 724;

Best Local Similarity 20.3%; Pred. No. 2.4;

Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

```
QY 51 KTFMERFNLTH-----HHOSGIYVDLGDQKVEDGTLNREPAGL 88
   ||:|||||
Db 156 KQYVIVANLTHLPRSEYVIGVGLGIAKCPYDPLDNSTAIYENG-----NPGGL 204
   ||:|||||
QY 89 CPIW-GKHIELQOPRLPYRNPNLEDPVTEKEYKOSGNPLPGGFNLNFTVPSGORISPP 147
   ||:|||||
Db 205 PGLYSTNNEFTKADIVIFRTDLYNTSAKRLKLVK-----FKRTLKWD 246
   ||:|||||
QY 148 MELLEKNSTIKASTDLGRCAEFAFKTVAMDKN--KATKYRVPFYDSKRLCH----- 199
   ||:|||||
Db 247 SKMLDK-PNFVGSFDIGEVYVFFRETAVEYINCGKA-----VYSRIARVCKKDVGSK 298
   ||:|||||
QY 200 --ILVSNQLMGKCKYCSVKGEBPDLTWCCEKPKRSV-----TENHHLIYG 243
   ||:|||||
Db 299 NLLAHNMAWTLKARLNCISISGEFP-----FYFNEIOSVYQLPSDKSRFPATFTTSTNGLIG 354
   ||:|||||
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Oy 244 SA-----YVGNPDAFISKCPNALRGYRFGW-----KKGRCL-DYTELTDTVI 287
Db 355 SAVCSFHINEIOAFAFGKFKXQSSSN---SAMLPLYNSRVBEPRGTCVNDTSLNLPDVL 411
Oy 288 ERVES 292
Db 412 NFIRS 416

RESULT 31

US-09-060-610-62

; Sequence 62, Application US/09060610
; Patent No. 6344544
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matches, David R.
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-060-610-62

Query Match 3.2%; Score 94.5; DB 4; Length 724;

Best Local Similarity 20.3%; Pred. No.2.4; Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

Oy 51 KTFMERFNLTH-----HHOSGIYVDLGQDKVEDTLVREPAGL 88
Db 156 KDVIYIANLTHLPSEVYIGVGLGIAKCPDPLDNSTAIYVENG-----NPGGL 204
Oy 89 CPPIV-GKHIELQOPDRLEPYRNNPLEADVTEKEYKQSGNPLPGGFNLNFTPSGORISBP 147
Db 205 PGLVSGTNAEFTKADTVIFRTDLVNTSAKRLKYK-----FKRTLKYD 246
Oy 148 MELLEKSNINIKASTDLGRCAEFAPKTVAMDKN--KATKRYPPVYDSKKRLCH----- 199
Db 247 SKWLDK-PNFGVSGFDIGEVYVFFRETAVEYINGKA-----VYSRIARVCKKDVGGK 298
Oy 200 --ILVSMQLMGKKYGSVKGEPPDLTWYCFKPRKSV-----TENHHLIYG 243

Db 299 NLAHNATYIKALNCSISGEFP-----FYFNEIQSVYQLPSDKSRFPATFTSTNGLIG 354
Oy 244 SA-----YVGNPDAFISKCPNALRGYRFGW-----KKGRCL-DYTELTDTVI 287
Db 355 SAVCSFHINEIOAFAFGKFKXQSSSN---SAMLPLYNSRVBEPRGTCVNDTSLNLPDVL 411
Oy 288 ERVES 292
Db 412 NFIRS 416

RESULT 32

PCT-US94-10151A-62

; Sequence 62, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: PP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-10151A-62

Query Match 3.2%; Score 94.5; DB 5; Length 724;

Best Local Similarity 20.3%; Pred. No.2.4; Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

Oy 51 KTFMERFNLTH-----HHOSGIYVDLGQDKVEDTLVREPAGL 88
Db 156 KDVIYIANLTHLPSEVYIGVGLGIAKCPDPLDNSTAIYVENG-----NPGGL 204
Oy 89 CPPIV-GKHIELQOPDRLEPYRNNPLEADVTEKEYKQSGNPLPGGFNLNFTPSGORISBP 147
Db 205 PGLVSGTNAEFTKADTVIFRTDLVNTSAKRLKYK-----FKRTLKYD 246
Oy 148 MELLEKSNINIKASTDLGRCAEFAPKTVAMDKN--KATKRYPPVYDSKKRLCH----- 199
Db 247 SKWLDK-PNFGVSGFDIGEVYVFFRETAVEYINGKA-----VYSRIARVCKKDVGGK 298
Oy 200 --ILVSMQLMGKKYGSVKGEPPDLTWYCFKPRKSV-----TENHHLIYG 243
Db 299 NLAHNATYIKALNCSISGEFP-----FYFNEIQSVYQLPSDKSRFPATFTSTNGLIG 354
Oy 244 SA-----YVGNPDAFISKCPNALRGYRFGW-----KKGRCL-DYTELTDTVI 287

Db 355 SAVCSFHNEIOAFNGKFEQSSSN---SAWLPLYNSRVPERRPOTCVNDSNLPJVL 411
QY 288 ERVES 292
Db 412 NFIRS 416

RESULT 33
US-09-107-532A-5645
Sequence 5645, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: LYNN A DUCETTE-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Maltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariandello, Pamela Dencke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5645:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...702
SEQUENCE DESCRIPTION: SEQ ID NO: 5645:
US-09-107-532A-5645

Query Match 3.2%; Score 94; DB 4; Length 702;
Best Local Similarity 21.6%; Pred. No. 2.5;
Matches 80; Conservative 33; Mismatches 117; Indels 140; Gaps 18;

QY 107 RNFL--EVP-----TEKEYKSGNPLPGF-----NINFTYPSQR-I 143
Db 55 KNNFIIPKDVPNAKTIITVNGASKYKVVHDANKGGFTDDYGLVGNKNIRYPSFOKEY 114
QY 144 SEPEMLEKSNIXASTDLGRCAEPAFIV-----AMDKNKATK 184
Db 115 GEINIVLEBVTNTKYNIDYKIGTYNGKKVNIKVLVSNHLYSDTLPNLNDNNTYTKH 174
QY 185 YR-----YPFVYDSKRLCHILVYVSMQJMEGKKYCSVKGPPDLTWYCFKPKSVTEN 237
Db 175 FDDGKYNNGAMSKSKRT--VLWISDLVFSGIY-----HSTQKN 214

QY 238 HHLIYGAAYGENP-----DAFIS-KCPNQA-----LRGYRFGWKKGRCLDYTELDT 285
Db 215 VQLV--ATYEDGSPVQPSGDTFFISNLSNPAGKSTDLKG--EYAHYDKMNTTDMVVRDT 271
QY 286 VIERVESRAQCQVMTFENDGVAADPHYPLTSQASNDWMLHOSDQPHSGGVRNYGF 345
Db 272 VLSEFKS-----FYNNLANVVGHPGGS SKLTQAD -NDFNNLH----- 307
QY 346 YVDTGKCALSDQVDCVSDSAVSYRAAGSLSEFTNFIIPSP----- 394
Db 308 --DXLGDPKRGQG-----TVSEKISBANPLFYIGSSNVOTWFTLSAT 348
QY 395 --SVTPPTPE 402
Db 349 IFSVDPDPE 358

RESULT 34
PCT-US93-07923-11
Sequence 11, Application PC/TUS9307923
GENERAL INFORMATION:
APPLICANT: Morimoto, Chikao
APPLICANT: Schlossman, Stuart F.
APPLICANT: Tanaka, Yoshiaki
TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2894
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
FILING DATE: 19930819
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,162
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: 07/832,211
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/055002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 593
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07923-11

Query Match 3.2%; Score 93.5; DB 5; Length 593;
Best Local Similarity 20.8%; Pred. No. 2.1;
Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

QY 1 MGLVGVQVLV-VLVADCIIFASGLSSSTR--GRESOTLSASTSGNPFQANVEKTEMERPN 58
Db 9 LGLLGAALAVTTITVPVLLNKGTDDATADSKTYTLT-----DYKNTYRIKLKLSLKI 63
QY 59 LTHHSGIYVDLGDQKVDGTLVREPAGLCPHWKHTELQOPRLLPYRNN--FLEDVPT 116

Db 64 SDHEX-----LYKQENNIIVF-----NAEYGNSSVPLEN-ST 94
Qy 117 EKEKYQSGNPLRGFNLFVTPSGORISPPMELLEKSNIKASTDLCRCAPAFKTYAM 176
Db 95 FDEFGHSINDYS-----ISPDGQFI-----LLE----- 117
Qy 177 DKNKATKYRYPF-----VYDSKKRLCHILVYSMOLMECKKYCVKGEPPDLTWYCFKPR 231
Db 118 --YNYVQMRHSYTA SYDIYDLNKR-----QLITEERL-----PNNQWTWMS- 159
Qy 222 KSVTENHLYGSAVYGENPDAFISCKPQALRGYRGVWKKGKCLDYTELTDTYIER-- 289
Db 160 ---VGHXL-----AYVMYN-DIYVXIEBP--LPSYRI-TWTKEDI IYNGITDWMYEEBV 207
Qy 290 VESKAQCWVKTFENDGVASDQPHTYPLTSQASMNWM-WPLHOSDQPHSGVGRNNGFYV 348
Db 208 FSAVSAALN--WSPNGT-----FLVYAOFNDETVLE-----YSFYSD 243
Qy 349 DTGEGKALSDQVDPCLVSDSAVSYTAAGSLSEETPNFIIIPSNPSVTPTPTALQCT 408
Db 244 E-----SLQYP-----KTVRVPYPAQAVN-PTVKFFVVTNDLSLSTVNATSIQT 288
Qy 409 ADKFPDSF-----GACDVQACRKQKTSYVG-GQIYSTSVDTADPQNECGSNITALIA 459
Db 289 A---PASHMLIGDHYLCDVTWATQERISLQWLRRIQNYGSMIDCYDESGRWNCIIVA 342

RESULT 35
US-09-310-463-2
; Sequence 2, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
; FILE REFERENCE: 2624-A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: US/09/310,463A
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 650
; TYPE: PRT
; ORGANISM: human
; US-09-310-463-2

Query Match 3.2%; Score 93.5; DB 4; Length 650;
Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 51; Conservative 34; Mismatches 91; Indels 69; Gaps 7;

Qy 293 KAQCWVKTFENDGVASDQPHTYPLTSQASMNWMWPLHOSDQPHSGVGRNNGFYVVDTTG 352
Db 347 OSQGMQTF-----LITKEGADDPMLRLRSTYOSK----- 377
Qy 353 EGKCALSDQVDPCLVSDSAVSYTAAGSLSEB-----TPNFIIIPSNPSVTPTPTETA 404
Db 378 -----YQAEFPMGPVTSAHAGTYRCYGSQSKPYLLTHPSRDLVLVSGSGSPESPTTG 432
Qy 405 LQCTADKRPDSFGADVQACRKQKTSYVGQIYSTSVDTADPQNECGSNITALIAGLAVG 464
Db 433 -----PTSTSGPDPQPLT-PTGSDPQSGLRHLGVLIGIIVA 468
Qy 465 GVLLTALLGGCGCYFAKRLDRNKGVQAAHHEHFQSDRGARKRPSD--LMQEAEPSPWDE 522
Db 469 VILLILLILLFLIRHRROGKHWTSYORKADFGHPAGAVPEPFDRLQWRSSPAA-DA 527
Qy 523 AEENI 527
|||:

Db 528 OEENL 532

RESULT 36
US-08-842-248A-2
; Sequence 2, Application US/08842248A
; Patent No. 6448035
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Family of Immunoregulators Designated
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Janis C. Henry, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM/PC Compatible
; SOFTWARE: Microsoft Word 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,248A
; FILING DATE: April 24, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-842-248A-2

Query Match 3.2%; Score 93.5; DB 4; Length 650;
Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 51; Conservative 34; Mismatches 91; Indels 69; Gaps 7;

Qy 293 KAQCWVKTFENDGVASDQPHTYPLTSQASMNWMWPLHOSDQPHSGVGRNNGFYVVDTTG 352
Db 347 OSQGMQTF-----LITKEGADDPMLRLRSTYOSK----- 377
Qy 353 EGKCALSDQVDPCLVSDSAVSYTAAGSLSEB-----TPNFIIIPSNPSVTPTPTETA 404
Db 378 -----YQAEFPMGPVTSAHAGTYRCYGSQSKPYLLTHPSRDLVLVSGSGSPESPTTG 432
Qy 405 LQCTADKRPDSFGADVQACRKQKTSYVGQIYSTSVDTADPQNECGSNITALIAGLAVG 464
Db 433 -----PTSTSGPDPQPLT-PTGSDPQSGLRHLGVLIGIIVA 468
Qy 465 GVLLTALLGGCGCYFAKRLDRNKGVQAAHHEHFQSDRGARKRPSD--LMQEAEPSPWDE 522
Db 469 VILLILLILLFLIRHRROGKHWTSYORKADFGHPAGAVPEPFDRLQWRSSPAA-DA 527
Qy 523 AEENI 527
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RESULT 37
US-08-985-950-22
; Sequence 22, Application US/08985950
; Patent No. 6140076

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GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-950-22

Query Match          3.2%; Score 93.5; DB 3; Length 651;
Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 51; Conservative 34; Mismatches 91; Indels 69; Gaps 7;

QY 223 KAQCWKTFENDGVASDDQHTVPLTSQASWMDMPLHSDQPHSGVGGRNYGVYVDTTG 352
DB 347 OSQGMWQTF-----LITKGAADDPKRLRSTYOSK----- 377
QY 353 EKGKALSDQVDPCLVSDSAVSYTAAGSLSE-----TNPFIIPSNPSVTPPTPETA 404
DB 378 -----YQAEFPMGPRTSAHAAGTYRCGSSSKRPYLTHPSDPLLVSGSPGSPPTTG 432
QY 405 LQCTADKPPDSFGACDVQACRKQKTSYVGGQIQSTSVDTCTADEQNECGSNRLALIGLAVG 464
DB 433 -----PTSTGSPEDQPLT-PTGSDPQSGLRHLGLVIGILVA 468
QY 465 GVLLALALGGCYFAKRLDRNKGVQAAHNEHFOSDRGARKKRPSP--LMOEABSPFWE 522
DB 469 VILLILLILLFLILHRROGKHWTSYRKADPQHPAGAVGPEPTDRRLQMRSSPA-DA 527
QY 523 AEENI 527
DB 528 QEENL 532

RESULT 38
US-09-546-049-22
Sequence 22, Application US/09546049
Patent No. 6479638

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GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
Meynard, Linde
Gorman, Daniel M.
McClanahan, Terrill K.
Zurawski, Sandra M.
Zurawski, Gerard
Lanter, Lewis L.
Phillips Jr., Joseph H.
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
Related Reagents
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,049
FILING DATE: 10-APR-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-546-049-22

Query Match          3.2%; Score 93.5; DB 4; Length 651;
Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 51; Conservative 34; Mismatches 91; Indels 69; Gaps 7;

QY 223 KAQCWKTFENDGVASDDQHTVPLTSQASWMDMPLHSDQPHSGVGGRNYGVYVDTTG 352
DB 347 OSQGMWQTF-----LITKGAADDPKRLRSTYOSK----- 377
QY 353 EKGKALSDQVDPCLVSDSAVSYTAAGSLSE-----TNPFIIPSNPSVTPPTPETA 404
DB 378 -----YQAEFPMGPRTSAHAAGTYRCGSSSKRPYLTHPSDPLLVSGSPGSPPTTG 432
QY 405 LQCTADKPPDSFGACDVQACRKQKTSYVGGQIQSTSVDTCTADEQNECGSNRLALIGLAVG 464
DB 433 -----PTSTGSPEDQPLT-PTGSDPQSGLRHLGLVIGILVA 468
QY 465 GVLLALALGGCYFAKRLDRNKGVQAAHNEHFOSDRGARKKRPSP--LMOEABSPFWE 522
DB 469 VILLILLILLFLILHRROGKHWTSYRKADPQHPAGAVGPEPTDRRLQMRSSPA-DA 527
QY 523 AEENI 527


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Db 528 OEENL 532

RESULT 39

US-08-230-491A-3
Sequence 3, Application US/08230491A

Patent No. 5587299

GENERAL INFORMATION:

APPLICANT: Rettig, Wolfgang J.; Scanlan, Matthew J.;

APPLICANT: Garin-Chesa, Pilar; Old, Lloyd J.

TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR

TITLE OF INVENTION: FIBROBLAST ACTIVATION PROTEIN, AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FELFE & LYNCH

STREET: 805 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE 3.5 inch 1.2 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT - ASC II

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/230,491A

FILING DATE: 20-APRIL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5587299man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 330

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 766 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-230-491A-3

Query Match 3.2%; Score 93.5; DB 1; Length 766;

Best Local Similarity 20.8%; Pred. No. 3.3; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Db 1 MGLVGVQVLL-VLVADCTIFASGLSSSTR-SRESQTLASSTSGNPFQANVEMKTFMERFN 58

Db 9 LGLLGAALVLTITVPVLLNKGTDDATADSRKTYTLT-----DYLNKTYRLKLYSLRWI 63

Db 59 LTHHHQSGIYVDLQGDKEVDGTLVREPAGLCPWGHKIELOQDRLPYRNN--FLEDPVT 116

Db 64 SDHEY-----LYKQENNIIVF-----NAEYGNSSVPLEN-ST 94

Db 117 EKEYKQSGNPLPGGFNLVTPSGORISPPFMELLEKNKSNIKASTDLGRCAEFAKTYAM 176

Db 95 FDEFGHSINDYS-----ISPDQGYI-----LLE----- 117

Db 177 DKNNAKATKYRPF-----VYDSKKRLCHILVSMQLMGKKYCSVKGEPPDLTWYCFKPR 231

Db 118 --YVVKQMRHSYSTASYDIYDLNKR-----QLITEERI-----PNNQVNTWSP- 159

Db 232 KSVTENHLLIYGSAVGENPDAPFISKCPNOLRGYRFGVWKKGRCLDYTELTDVIER-- 289

Db 160 ---VGHKL-----AYVANN-DIYVKIEBN--LPSYRI-TWTGKEDIYNGITDWYEEBV 207

Db 290 VESKACQCVTKTFENDGVASDQPHYPLTISOASNDNM-WPLIOSDOPHSGGIVGRNTGYTV 348

Db 208 FSAYSALM--WSPNGT-----FLAIVAQFNDETVLE-----YSFYSD 243

Qy 349 DTGEGKALSDQVDPCLVSDSAVSYTAAGSLSEETPNFIIPNSPVTPTPETALQCT 408

Db 244 E-----SLQYF-----KTVRVVPYPKAGAVN-PTVKFVNVVTDLSLSTVNTSIQIT 288

Qy 409 ADKEPDSF-----GACDYQACKRQKTSVVG-GQIQSTSVYDCTADAEONCGSNTALIA 459

Db 289 A---PASMLIGDHYLCDTWATQERISLQWLRIQNVNSVMDICDYDESSGWNCLVA 342

RESULT 40

US-08-619-280A-3

Sequence 3, Application US/08619280A

Patent No. 5767242

GENERAL INFORMATION:

APPLICANT: Zimmermann, Rainer; Park, John E.;

APPLICANT: Rettig, Wolfgang; Old, Lloyd J.

TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN

TITLE OF INVENTION: ALPHA, AND USES THEREOF

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/619,280A

FILING DATE: 18-MARCH-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/230,491

FILING DATE: 20-APRIL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5767242man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5330.1

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 766 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-619-280A-3

Query Match 3.2%; Score 93.5; DB 1; Length 766;

Best Local Similarity 20.8%; Pred. No. 3.3;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Db 1 MGLVGVQVLL-VLVADCTIFASGLSSSTR-SRESQTLASSTSGNPFQANVEMKTFMERFN 58

Db 9 LGLLGAALVLTITVPVLLNKGTDDATADSRKTYTLT-----DYLNKTYRLKLYSLRWI 63

Db 59 LTHHHQSGIYVDLQGDKEVDGTLVREPAGLCPWGHKIELOQDRLPYRNN--FLEDPVT 116

Db 64 SDHEY-----LYKQENNIIVF-----NAEYGNSSVPLEN-ST 94

Db 117 EKEYKQSGNPLPGGFNLVTPSGORISPPFMELLEKNKSNIKASTDLGRCAEFAKTYAM 176

Db 95 FDEFGHSINDYS-----ISPDQGYI-----LLE----- 117

Db 177 DKNNAKATKYRPF-----VYDSKKRLCHILVSMQLMGKKYCSVKGEPPDLTWYCFKPR 231

Db 118 --YVVKQMRHSYSTASYDIYDLNKR-----QLITEERI-----PNNQVNTWSP- 159

Db 232 KSVTENHLLIYGSAVGENPDAPFISKCPNOLRGYRFGVWKKGRCLDYTELTDVIER-- 289

Db	160	----	VGHKL----	ATVMNN-DIYVXIERN--	LPSTRI--TWTKEDIIYNGITDWMYEEBV	207
Qy	290	----	VESKAQCWKTPENDGVASDOPHTYPLTSQASMDM-WPLHOSDQPHSGVGGRNYGFYV			348
Db	208	----	FSAYSALW---WSPNGT-----	FLAYAQFNDTEVPLIE-----	YSFYSD	243
Qy	349	----	DTTGEGKCALSDQVDPDCLVSDSAVSYTAAGSLSEETPNFIIPSNPSVTPTPETALQCT			408
Db	244	----	B-----SLOYP-----	KTVRVYPRAGAVN-PTVKFVYNTDLSSTVNTATSIQIT		288
Qy	409	----	ADKPPDSF-----	GACDVQACKROKTS CVG-GQIOSTSVDTADEQNECGSNTALIA		459
Db	289	----	A---PASMIGDHYICDVTWATQERISLQWLRIONYSVMDICDYDESSGRNCLVA			342

Search completed: October 2, 2003, 15:53:02
 Job time : 35 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 15:39:04 ; Search time 83 seconds

(without alignments)
1034.591 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 2322
Sequence: 1 MGLGVQVLLVADCTIFA.....EAEENIEODGETHVVEGDY 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452	15.5	86	24	ABP56991
2	431	14.8	622	10	AAp91632
3	420.5	14.4	563	12	AAr10551
4	418	14.3	622	13	AAr27532
5	418	14.3	622	16	AAr68840
6	412	14.1	622	23	AAU93159
7	410	14.0	622	23	AAU99360
8	404	13.8	478	24	ABR99416
9	403	13.8	654	23	ABG70931

10	395	13.5	561	10	AAp91588	Rhoptry membrane a
11	391	13.4	1807	22	AAr85697	Recombinant protei
12	391	13.4	2028	22	AAr85698	Recombinant protei
13	357	12.2	489	12	AAr10935	Plasmodium vivax 6
14	120	4.0	1507	21	AAr24128	Plasmodium yoelii
15	118	4.1	2519	22	ABG16636	Novel human diagno
16	113	3.9	996	22	AAr39322	Human polypeptide
17	113	3.9	1023	22	ABG22883	Novel human diagno
18	113	3.9	1023	22	AAU79772	Human protein SEQ
19	113	3.9	1023	22	AAU79773	Human protein SEQ
20	113	3.9	1023	22	AAU41108	Human polypeptide
21	113	3.9	1076	23	AAU74355	Human cytoskeleton
22	113	3.9	1581	22	AAU78788	Human protein SEQ
23	107.5	3.7	1104	17	AAr24957	NP-X1 DNA-binding
24	104	3.6	355	23	ABR97742	Human procathepsin
25	104	3.6	1200	21	AAr21208	Human HER-2/neu pr
26	104	3.6	1213	23	ABP25604	Streptococcus poly
27	104	3.6	1255	17	AAW01111	Human HER-2/neu on
28	104	3.6	1255	20	AAW92406	Human HER-2/neu pr
29	104	3.6	1255	21	AAr21198	Amino acid sequenc
30	104	3.6	1255	21	AAr24780	Human HER-2/neu pr
31	104	3.6	1255	22	AAr85458	Human HER-2/neu pr
32	104	3.6	1255	22	AAr88267	Human cytoskeleton
33	104	3.6	1255	23	AAr24057	Human Her-2 protei
34	104	3.6	1255	23	AAr20479	Human Her-2/neu pr
35	104	3.6	1255	23	AAW51143	Human Her-2/neu on
36	104	3.6	1255	23	AAU77114	Human Her-2/neu po
37	104	3.6	1433	14	AAr39568	Sequence of c-erbB
38	103.5	3.5	365	21	AAr3307	Human colon cancer
39	103.5	3.5	365	22	AAr5613	Human breast cance
40	103	3.5	1223	23	AAU98923	Human heregulin 2
41	103	3.5	1255	21	AAU82620	Human tyrosine kin
42	103	3.5	1255	22	AAr21230	HER2 transgene pla
43	103	3.5	1255	22	AAr60167	Human HER-2 protei
44	103	3.5	1255	23	AAr26349	Human Her2 antigen
45	103	3.5	1255	23	AAr26366	Human Her2 antigen

ALIGNMENTS

RESULT 1	ABP56991	standard; Peptide: 86 AA.
ID	ABP56991	
XX	ABP56991	
AC	10-APR-2003	(first entry)
DT	10-APR-2003	
XX		
DE	Toxoplasma gondii	AMA1 amino acid sequence fragment.
XX		
KW	Elmeria maxima; 250 kDa antigen; sporozoite; merozoite; infection;	
KM	vaccine; antiparasitic; gene therapy.	
XX		
OS	Toxoplasma gondii.	
XX	Synthetic.	
XX		
XX	W02003004684-A2.	
XX		
PD	16-JAN-2003.	
XX		
PF	03-JUL-2002; 2002MO-US21237.	
XX		
PR	06-JUL-2001; 2001US-303670P.	
XX		
PA	(WITC/) WITCOMBE D.	
PA	(SMIT/) SMITH N C.	
PA	(WALL/) WALLACH M.	
XX		
PI	Witcombe D, Smith NC, Wallach M;	
XX		
DR	WPI; 2003-201556/19.	
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[illegible]

[illegible]

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QY 430 SCV--GGQIQIS-----VDCIADQNECGSN--TALLAGLAVGVLLALLGGGCTPK 480
DB 450 NCVEKRAIKENNEVIIKEEFKEDYENPDGKHKKMLIIIGTVGAVCVVAASLFYFRK 509
QY 461 RLDRKKGVAQAHHEHEFQSDRGARKRPSPDLMOEAEPSPFWDPAEENIEODGETHWVEGD 540
DB 510 KAQDK-----YDKKIDQAEAYGKTANTRKDEMLDPEASFWGDEK---RASHTTPLVMKRP 561
QY 541 Y 541
DB 562 Y 562

RESULT 4
AAR27532
ID AAR27532 standard; Protein; 622 AA.
XX
XX AAR27532;
AC
XX
XX 25-MAR-2003 (updated)
DT 08-MAR-1993 (first entry)
XX
XX Plasmodium falciparum AMA1 antigen.
DE
XX
XX Recombinant poxvirus; antimalarial vaccine; malaria; immunise;
KW immunogen.
XX
XX Plasmodium falciparum.
OS
XX
XX MO9216616-A1.
PN
PD 01-OCT-1992.
XX
XX 19-MAR-1992; 92MO-US02207.
XX
XX 20-MAR-1991; 91US-0672183.
XX PR 18-MAR-1992; 92US-0852305.
XX
XX (VIBRO-) VIROGENETICS CORP.
PA
PI De TAISNE C, Paolucci E, Tine JA;
XX
XX WPI; 1992-349203/42.
DR N-PDB; AAQ29189.
XX
XX Recombinant poxvirus - contg. Plasmodium DNA, useful as
PT antimalarial vaccine
PS
XX
XX Example 4; Fig 5; 74pp; English.
XX
CC This sequence is the Plasmodium falciparum AMA1 antigen.
CC cDNA encoding it was cloned into vaccinia donor plasmids
CC before being inserted into the vaccinia virus to be used in a
CC vaccine to stimulate an antimalarial immunological response, or for
CC in vitro prodn. of gene prods. for use as immunogens. As plasmodium
CC genes are conserved among P. falciparum strains, they are widely
CC effective in a vaccine.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC
XX
XX Sequence 622 AA;

Query Match 14.3%; Score 418; DB 13; Length 622;
Best Local Similarity 26.5%; Pred. No. 6.3e-30;
Matches 151; Conservative 88; Mismatches 207; Indels 124; Gaps 26

QY 41 GNPFQANVEMKTFMERFNLTHHDSGIYVDLGQDKVNDGTLYREBAGLCPIWGHIELQO 100
DB 107 GNPF-----TEVMAKYDIEEVHSGINVDLGEDAEVAGTGYRLPSGKCPVGGKIIEN 160
QY 101 PDRLPYRNKFLFEDVTEKEKYKQSGNPLDGGFPLNVTVTSGGARISFPME---LLEKSN 156
DB 161 SN-----TTFLLPVATGQYELKD---GGFAF--PTEPLMSVTLDEMKNHFKDKNY 207

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QY 157 IKASTDLGRCAEFKATVAMDKNKATKRYRPFYVDSKRLCHILYVSMQLMGKKYCSV 216
DB 208 VKNDELTLTCSRHAGNM1--PDNDKSNYKYPAYVDDDKCHILYIAQENNGRYCN- 264
QY 217 KGEPPDLTWYCFKPKRSYVTENHLLYGSAYYGEN-PDAFISKCPNQAALRGYRFGVWKGR 275
DB 265 KDESERNMFCFRPAKDISFQNY-----TYSKVVVDWMEKVCPRKNLQNAKFGIMVDGN 319
QY 276 CLDYTELTD-TVIERVESKACQWKTFFENDGVASDQPHYTP--LTSQASNDWMP----- 327
DB 320 CEDIPHVEFPALIDFE---CNKLVFELS--ASDQPKQYEQHLTDYEKIKGKGFKNKAS 373
QY 328 -----LHSDQPHSGGVGRNYGFYVDTTGEKCALSDQVPCLVSDSAVSYTA 377
DB 374 MIKSAFLPTGAFKADRYKSHGKYNMGNYTETQ--KCEIFNVKPTCLINSSYIATTA 430
QY 378 AGSLSEETPNF-----IIPNSVTPPTPETAQ--CTADKFPDSF 416
DB 431 LSHPIEVENNFCPSLYKDEIMKEIERESKRITLNDNDGKNKIMLQEFLLSDDK--DSL 488
QY 417 -GACDVQ-----ACRQKQTSYVGGQIOSTSV-----CTADEQNEC 451
DB 489 KRPCDPEWVNSSTCFEYVCKVERAEVTSNNEVVVKEEYDEYADIPENKPTIDKMKII 548
QY 452 GSNTALLIAGLAVGVLLALLGCGCYFAKRLDRNKGVOAHHNEHFOSDRGARKKRPDDL 511
DB 549 IASSARAVLAVT--ILMV-----YLYKR-----KGNMEKYDKMDEPDQYGSNSR-NDE 594
QY 512 MQEAPSPFWDEAEENIEODGETHWVVEGDY 541
DB 595 MLDPEASFWGEK---RASHTTPVLMEXKY 621

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RESULT 5
AAR68840
ID AAR68840 standard; Protein; 622 AA.
XX
AC AAR68840;
XX
DT 25-MAR-2003 (updated)
DT 24-AUG-1995 (first entry)
XX
DE Plasmodium falciparum AMA-1 gene protein.
XX
KM Plasmodium falciparum AMA-1 gene; recombinant poxvirus;
KW multicomponent multistage malarial vaccines; immunogens;
KW malaria diagnosis.
XX
OS Plasmodium falciparum (3D7).
XX
PN WO9428930-A1.
XX
PD 22-DEC-1994.
XX
PF 10-JUN-1994; 94WO-US06652.
XX
PR 11-JUN-1993; 93US-0075783.
PR 09-JUN-1994; 94US-0257073.
XX
PA (VIRO-) VIROGENETICS CORP.
XX
PI De Taiene C, Paolucci E, Tine JA;
XX
DR N-PSDB; AAQ80910.
XX
PT Recombinant poxvirus contg. Plasmodium DNA in non-essential
PT Plasmodium immunogens
XX
PS Clatm 3; Fig 5; 183pp; English.
XX
CC AAQ80910 encodes AAR68840 the P. falciparum AMA-1 gene product. New

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recombinant poxviruses containing either the SERA, ABRA, Pf8ap70, CC AMA-1, Pf8a25, GFP, Pf8SP2, LSA-1, LSA-1 repeats, MSA-1, CC MSA-1 (N-terminal p83 or C-terminal gp42) genes, or a combination CC of these in non-essential regions of their genomes are claimed. CC These poxviruses (pref. with a virulence reducing genomic CC deletion or disruption) can be used as vaccines against malaria CC and for the prodn. of Plasmodium immunogens. These viruses CC provide multicomponent, multistage vaccines due to their expression CC of sporozite, liver stage, blood stage and sexual stage proteins. CC (Updated on 25-MAR-2003 to correct PN field.)

Sequence 622 AA;

Query Match 14.3%; Score 418; DB 16; Length 622;
 Best Local Similarity 26.5%; Pred. No. 6,3e-30;
 Matches 151; Conservative 88; Mismatches 207; Indels 124; Gaps 26;

```

QY 41 GNPQANVEMKTFMERFNLTHHSGIYVDIGQKEVDGTYREPAICLPWGHIELOQ 100
DB 107 GNPW-----TEYMAKYDIEVHSGIRVDGEDAEVAGTQYRLPSGKCPVFGKILLEN 160
QY 101 PDRLPYRNPFEDYPTKEKYKQSGNPLRGFNLMFVTPSGRISPFWE-----LLEKSN 156
DB 161 SN-----TTFLLPVATGNQYIKD-----GGFAP--PTEPLMSPTLDEMRHFFYKDKY 207
QY 157 IKASTDLGRCAEFKATVAMDKNKATKRYRPFYVDSKRLCHILYVSMQLMGKKYCSV 216
DB 208 VKNDELTLTCSRHAGNM1--PDNDKSNYKYPAYVDDDKCHILYIAQENNGRYCN- 264
QY 217 KGEPPDLTWYCFKPKRSYVTENHLLYGSAYYGEN-PDAFISKCPNQAALRGYRFGVWKGR 275
DB 265 KDESERNMFCFRPAKDISFQNY-----TYSKVVVDWMEKVCPRKNLQNAKFGIMVDGN 319
QY 276 CLDYTELTD-TVIERVESKACQWKTFFENDGVASDQPHYTP--LTSQASNDWMP----- 327
DB 320 CEDIPHVEFPALIDFE---CNKLVFELS--ASDQPKQYEQHLTDYEKIKGKGFKNKAS 373
QY 328 -----LHSDQPHSGGVGRNYGFYVDTTGEKCALSDQVPCLVSDSAVSYTA 377
DB 374 MIKSAFLPTGAFKADRYKSHGKYNMGNYTETQ--KCEIFNVKPTCLINSSYIATTA 430
QY 378 AGSLSEETPNF-----IIPNSVTPPTPETAQ--CTADKFPDSF 416
DB 431 LSHPIEVENNFCPSLYKDEIMKEIERESKRITLNDNDGKNKIMLQEFLLSDDK--DSL 488
QY 417 -GACDVQ-----ACRQKQTSYVGGQIOSTSV-----CTADEQNEC 451
DB 489 KRPCDPEWVNSSTCFEYVCKVERAEVTSNNEVVVKEEYDEYADIPENKPTIDKMKII 548
QY 452 GSNTALLIAGLAVGVLLALLGCGCYFAKRLDRNKGVOAHHNEHFOSDRGARKKRPDDL 511
DB 549 IASSARAVLAVT--ILMV-----YLYKR-----KGNMEKYDKMDEPDQYGSNSR-NDE 594
QY 512 MQEAPSPFWDEAEENIEODGETHWVVEGDY 541
DB 595 MLDPEASFWGEK---RASHTTPVLMEXKY 621

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RESULT 6
 AAU93359
 ID AAU93359 standard; Protein; 622 AA.
 XX
 AC AAU93359;
 XX
 DT 26-SEP-2002 (first entry)
 XX
 DE Synthetic P. falciparum AMA-1 ectodomain (FVO Pf83syn) protein.
 XX
 KW Apical membrane antigen-1; AMA-1; protozoacide;
 KW Plasmodium, ectodomain; malaria; parasite; vaccine; immune response;
 KW epitope; FVO Pf83syn; mutant; mutcin.
 XX
 OS Plasmodium falciparum.

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OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..622
FT /label= Mature_FVO_Pf83syn
FT Misc-difference 162
FT /note= "Wild-type Asn substituted by Lys"
FT Misc-difference 288
FT /note= "Wild-type Thr substituted by Val"
FT Misc-difference 373
FT /note= "Wild-type Ser substituted by Asp"
FT Misc-difference 422
FT /note= "Wild-type Asn substituted by Asp"
FT Misc-difference 423
FT /note= "Wild-type Ser substituted by Lys"
XX WO200252014-A2.
XX 04-JUL-2002.
XX 21-DEC-2001; 2001WO-NL00934.
XX 22-DEC-2000; 2000EP-0204697.
XX (BIOM-) STICHTING BIOMEDICAL PRIMATE RES CENT.
XX Kocken CHM, Thomas AW, Blackman MJ, Withers-Martinez C, Holder AA,
XX WPI; 2002-575381/61.
XX N-PSDB; ABK89028.
XX
XX Producing mRNA encoding Plasmodium AMA-1 ectodomain in yeast cell,
XX useful for preparing vaccines for treating or preventing malaria,
XX comprises providing the yeast cell with a nucleic acid encoding the
XX ectodomain
XX
XX Example 1; Fig 1; 42pp; English.
XX
XX The invention discloses the production of mRNA encoding Plasmodium
XX apical membrane antigen-1 (AMA-1) ectodomain, its functional part,
XX derivative and/or analogue in a yeast cell, which has been modified to
XX use the yeast's codon usage. Plasmodium falciparum (Pf) is the most
XX important human malaria parasite. At present there is no effective
XX vaccine against human malaria, but studies have indicated that the AMA-1
XX family of molecules are a target for protective immune responses. The
XX proteins have a predicted ectodomain and cytoplasmic domain and evidence
XX has identified that protection invoked by AMA-1 is directed at
XX conformational epitopes located in the ectodomain. The Plasmodium AMA-1
XX ectodomain, its functional part, derivative and/or analogue and the
XX proteinaceous molecule are useful for diagnosing and preparing vaccines
XX or medicaments for preventing malaria caused by Plasmodium falciparum. Pf
XX AMA-1 has an unusually high A+T content and N-glycosylation sites which
XX make expression and deglycosylation in yeast difficult. The method
XX provides an efficient production of Plasmodium falciparum, strain FVO,
XX AMA-1 ectodomain in high amounts due to its effective expression in the
XX yeast Pichia pastoris. This is achieved by mutating the gene sequence
XX (FVO Pf83syn) to utilise the yeast's codon usage and remove the
XX N-glycosylation sites, which are not conserved in Plasmodium. The FVO
XX Pf83syn can be used to create vaccines against Plasmodium induced
XX malaria. The sequence presented is the synthetic P. falciparum AMA-1
XX ectodomain (FVO Pf83syn) protein.
XX
XX Sequence 622 AA;
XX
XX Query Match 14.1%; Score 412; DB 23; Length 622;
XX Best Local Similarity 26.0%; Pred. No. 2,3e-29;
XX Matches 149; Conservative 79; Mismatches 215; Indels 110; Gaps 25;
XX
XX 41 GNPFPANVEMKTFMRFLTHHSGIYVDGQKVEVDGTLRPAAGLCPTWKGKRIELQ 100
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 107 GNPM-----TEYMAKYDIEEVHGSGIRVDLGEDEAVAGTGYRLPSGKCPVFGKIIEN 160

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QY 101 PDRLPYRNPLFLEDPVT-EKEYKOSGNPLPGGFNLNFTVPSGORISPPFM-----ELLEKNS 155
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 161 S-----KTFPLKPAVATNGQDKDGGFAFP-----FTNPILSPMTLNGMRPFYKNE 206
QY 156 NIKASTDIGRCAEFAFTVAMDKNKATKTRYPYPSKKRLCHILYVSNOLMGSKYCS 215
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 207 YVKNLDELTLCSRAAGN--NMPDNDKNSNYCPAVDYNDKCHILYLAODENNGPRYCN 264
QY 216 VKGEPDLTWYCFPRK-SVTENHLLYGSAYVEN-PDAFISCPNALRGYRGVWK 273
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 265 -KDSKNSMFCFRPADKLFENY-----VLSKNVVDNVEVCPKRNLSNAKFLGLWVD 317
QY 274 GRCLDYELTDVTVIERVESKAQCWKTFFENDVASDQPHYTP--LTSQASNMWMP----- 327
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 318 GNCEIDPIRVNPF-----SANDLFECKLTFELS--ASDPKQVEQHLTDVEKIKEGPKKNKA 372
QY 328 -----LHSDQPHSGVGVRNYGFYVDTTGEGKALSQVDPDCLVSDAASVYT 376
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 373 DMKSAFLPTGAFADRYKSHGKGYNMGVNYRETQ---KCEIFVWKPTCLINDKSYIATY 429
QY 377 AAGSLSETPRPIIPSN-----PSTVPTPTETA 404
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 430 ALSHPTEVENP--PCSLYKDEIKKEIERESKRIKLNDDNDEGNKKIIAPRIFTSDDKS 487
QY 405 LQCTADKFPDSFGACDVQACKRQKTSQVGGQIQSTST-----VDCTAD--EQNECG 452
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 488 LKCPDPEBMSQSICRFFVCK-----CVERAETSNNEVVKREYDEYVIDEHNKPT 542
QY 453 SNTALI---AGLAVGVLLALLGGCYFAKRLDRNKGVQAAHHEFGSDRGARKRP 508
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 543 DNMKIIIASNAVAVLAILMV-----YLYKR---KG-NARKYDKMDQVGHYKSTSR 591
QY 509 SDLMQEAEPSPFDEAEINBDGETHYMVEDY 541
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 592 NDEMLDPEASFWGEEK--RASHTTPVLMEXY 621
XX
XX RESULT 7
XX AAU99360
XX ID AAU99360 standard; Protein; 622 AA.
XX
XX AAU99360;
XX AC
XX
XX 26-SEP-2002 (first entry)
XX
XX DE P. falciparum apical membrane antigen-1 (AMA-1) ectodomain protein.
XX
XX XX Apical membrane antigen-1; AMA-1; protozoacide; Plasmodium; ectodomain;
XX KW malaria; parasite; vaccine; immune response; epitope; FVO Pf83syn.
XX
XX OS Plasmodium falciparum.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT Protein 25..622
XX FT /label= Signal_peptide
XX FT /label= Mature_AMA-1
XX
XX WO200252014-A2.
XX
XX 04-JUL-2002.
XX 21-DEC-2001; 2001WO-NL00934.
XX 22-DEC-2000; 2000EP-0204697.
XX (BIOM-) STICHTING BIOMEDICAL PRIMATE RES CENT.
XX Kocken CHM, Thomas AW, Blackman MJ, Withers-Martinez C, Holder AA,
XX WPI; 2002-575381/61.
XX

```

PT Producing mRNA encoding Plasmodium AMA-1 ectodomain in yeast cell,
PT useful for preparing vaccines for treating or preventing malaria.
PT computer providing the yeast cell with a nucleic acid encoding the
PT ectodomain -

XX Example 1; Page -; 42pp; English.

CC The invention discloses the production of mRNA encoding Plasmodium
CC apical membrane antigen-1 (AMA-1) ectodomain, its functional part,
CC derivative and/or analogue in a yeast cell, which has been modified to
CC use the yeast's codon usage. Plasmodium falciparum (Pf) is the most
CC important human malaria parasite. At present there is no effective
CC vaccine against human malaria, but studies have indicated that the AMA-1
CC family of molecules are a target for protective immune responses. The
CC proteins have a predicted ectodomain and cytoplasmic domain and evidence
CC has identified that protection invoked by AMA-1 is directed at
CC conformational epitopes located in the ectodomain. The Plasmodium AMA-1
CC ectodomain, its functional part, derivative and/or analogue and the
CC proteinaceous molecule are useful for diagnosing and preparing vaccines
CC or medicaments for preventing malaria caused by Plasmodium falciparum. Pf
CC AMA-1 has an unusually high A+T content and N-glycosylation sites which
CC make expression and deglycosylation in yeast difficult. The method
CC provides an efficient production of Plasmodium falciparum, strain FVO,
CC AMA-1 ectodomain in high amounts due to its effective expression in the
CC yeast *Pisichia pastoris*. This is achieved by mutating the gene sequence
CC (FVO Pf83syn) to utilise the yeast's codon usage and remove the
CC N-glycosylation sites, which are not conserved in Plasmodium. The FVO
CC Pf83syn can be used to create vaccines against Plasmodium induced
CC malaria. The sequence presented is the P. falciparum AMA-1 ectodomain
CC which was used to create the synthetic P. falciparum AMA-1 ectodomain
CC (FVO Pf83syn) protein (AAU9359).
CC Note: This sequence is not shown in the specification, but was created
CC by the indexer from information given in example 1.

XX Sequence 622 AA:

Query Match 14.0%; Score 410; DB 23; Length 622;
Best Local Similarity 26.0%; Pred. No. 3.6e-29;
Matches 149; Conservative 80; Mismatches 214; Indels 130; Gaps 25;

QY 41 GNPFOANVEMKTFMERFNLTHHSGIYVDLGQKEVDGTLYPEAGLCPIMGKHIELQ 100
DB 107 GNPW-----TEYMAKYDIEEVHSGIRVDLGDAEVAAGTQRLPSGKCPVFGKGIIBN 160
QY 101 PRLPRNNFLDVP-EKEYKQSGNPPLPGGFVNLNVTSGQRISFPF-----ELLEKRS 155
DB 161 SN-----TFLKPVATGNODLKDGFAPF-----PTNPLISPMTLNGMRDFYKNE 206
QY 156 NIKASTDLGRCAEFARCTVAMDKNNKATYRYPFYVDSKKRLCHILYVMQIMEGKKYCS 215
DB 207 YKKNDELTLCSRHAN--MNPNDKNSNYKIPAVDYNDKCHILYIAQENNGRYCN 264
QY 216 VKEPPEDLTWYCFKPKR-SVTENHMLIYSAYVGEN-PDAFISKCPNALRGYRGVWK 273
DB 265 -KDQSRNMFGRPAKDKLFENY-----TYLSKVNVNMEVECPKRLLENAKFGLAWD 317
QY 274 GRCGLDTLDTVYIEVESKACQWTFPNDGVAASQPHYTP--LTSQASNDMW---- 327
DB 318 GNCEBIPHYNEF--SANDLFECKNLVFEIS--ASQDPQYEOHLDYKIKIEGFKNKQA 372
QY 328 -----LHSDPHSGGVRNRYGFYVDTTEGKCALSDVDCIVSDSAVSYT 376
DB 373 SMIKSAFLPTGAFAKADRYKSHGKGYMGVYNRETO--KCEIFNVFPTCLINNSYIATT 429
QY 377 AAGSLSEETPNFTIPSN-----PSVTPPTETA 404
DB 430 ALSHPLEVEHNF--PCLYKDEIKIEIERESKRILKINDDEGNKKIIPRIISDDXS 487
QY 405 LOCTADKFPDSFGACVQACCKOKTSCVGGQOSTS-----VDCIAD--EENEG 452
DB 488 LKCPDCEPMVSOSTCFVCK-----CVERRAEVTSNNEVVEEYKDEYADIPKPKPT 542
QY 453 SNTALI-----AGLAVGVLLMLLGGGCFAPAKLDENKGVQAHHHEFQSDRGAKKAP 508

DB 543 DNMKTIISAAVAVLATILAV-----YLKR-----KG-NAEKYDKMDQPHYKSTSR 591
QY 509 SDLMQEAAPSFWDEAEENIEDQGETHWVEDY 541
DB 592 NDEMIDPEASFWGEK--RASHTTPLYMEKPY 621

RESULT 8
ABB99416
ID ABB99416 standard; Protein; 478 AA.

AC ABB99416;

DT 29-JAN-2003 (first entry)

DE Amino acid sequence of AMA-1 ectodomain protein.

KW Apical membrane antigen-1; AMA-1; ectodomain protein; AMA1/E;
KW membrane protein; apical rhoptry; merozoite; vaccine; malaria.

OS Plasmodium falciparum.

FH Key Location/Qualifiers

FT Peptide 1..18 /note= "His tag"

FT Misc-difference 294 /note= "Thr encoded by AGC"

FT Peptide 468..478 /note= "His tag"

PN W02027195-A2.

PD 03-OCT-2002.

PF 25-MAR-2002; 2002WO-US09406.

PR 26-MAR-2001; 2001US-278616P.

PA (REED-) REED ARMY INST RES WALTER.

PI Lanar DE, Dutta S, Ware LA, Nair LPV;

DR WPI: 2003-029928/02.

PS N-PSDB; ABV72528.

PT New Plasmodium falciparum apical membrane antigen-1 (AMA-1) ectodomain
PT protein, useful as a diagnostic reagent, for producing antibodies, as a
PT vaccine, or for inducing a protective immune response to malaria
PT infection -

PS Claim 10; Page 88; 88pp; English.

XX The present sequence represents a Plasmodium falciparum apical membrane
XX antigen-1 (AMA-1) ectodomain protein, consisting of amino acids 83-531
XX of AMA-1, and designated AMA1/E. AMA-1 is an integral membrane protein,
XX localised in the apical rhoptries of the merozoites present within the
XX late stage schizont. The AMA1/E polypeptide comprises an Escherichia
XX coli codon bias. The AMA1/E polypeptide is useful as a diagnostic
XX reagent, for producing antibodies, and as a vaccine. It is useful for
XX diagnosing malaria antibodies, monitoring malaria infection or prognosing
XX the response to treatment of patients suffering from malaria infection,
XX or for inducing a protective immune response to malaria infection.

XX Sequence 478 AA:

Query Match 13.8%; Score 404; DB 24; Length 478;
Best Local Similarity 27.0%; Pred. No. 8.7e-29;
Matches 123; Conservative 71; Mismatches 163; Indels 98; Gaps 18;

QY 41 GNPFOANVEMKTFMERFNLTHHSGIYVDLGQKEVDGTLYPEAGLCPIMGKHIELQ 100
DB 43 GNPW-----TEYMAKYDIEEVHSGIRVDLGDAEVAAGTQRLPSGKCPVFGKGIIBN 96

QY 101 PDRLPYRNNFLEADVTEKEYKQGNPLPGCFNLNFTPSGORISPPME---LLEKNSN 156
 Db 97 SN-----TTFLLPVATGNQYLKD-----GGFAF---PPTBPLMSPTLDEMRHFYKDKY 143
 QY 157 IKASTDLGRCAEFKATVAMDKNNKATKRYRPFYVDSKKRLCHILLYSMOLMEGKKYCSV 216
 Db 144 VKNIDELTLCRRHAGNM1--PDNDKNSNYKYPAYVDDKCKCHILYIAQENNGRKYCN- 200
 QY 217 KGEPPDLTWYCFKPKRSVTENHLLIYGSAYVGEN--PDAFISKCPNOALRGYRFGVWKKGR 275
 Db 201 KDEGRNSMFCFRPKAKDISPQNY-----TYSKRVVDMEKVCPRKQLQNAKFGLMVDGN 255
 QY 276 CLDYTELTD-TVIERVESKACQWVTFENDGVASDQPHYTP--LTSQASWMDMP----- 327
 Db 256 CEDIPHVNEPAIDLFE---CNKLVFELS--ASDQPRQYEQHLTDYEKIKEGFKNKQAS 309
 QY 328 -----LHOSQPHSGVGRNYGYVDTTGEKCALSDQVPCDCLVSDSAVSYTA 377
 Db 310 MIKSAFLPTGAFKADRYKSHGKGYMGNVNTETO---KCEIFNVKPTCLINSSYIATTA 366
 QY 378 AGSLSEETPNFPIPSN-----PSYTPPTPETAL 405
 Db 367 LSHPIEVNNF--PCSLYKDEIMKEIERESKRITLNDNDDEGNKTIAPRIFISDDKSL 424
 QY 406 QCTADKPPDSFGACDVQACRQKTSYVGGQIOSTS 440
 Db 425 KCPDPEWVSQSTCRFVCK-----CVERRAEVTS 454

RESULT 9
 ABG70931
 ID ABG70931 standard; protein; 654 AA.

XX AC ABG70931;

XX DT 11-DEC-2002 (first entry)

XX DE Plasmodium AMA-1/MSP-1 fusion protein PFCP-1.

XX KM Malaria; merozoite surface protein-1; MSP-1; AMA-1; PFCP-1; apical membrane antigen-1; vaccine; antimalarial; protozoacide.

XX OS Plasmodium falciparum.
 OS Synthetic.

XX PN WO200272625-A1.

XX PD 19-SEP-2002.

XX PF 01-FEB-2002; 2002WO-CN00049.

XX PR 01-FEB-2001; 2001CN-0105292.

XX PA (UTSE-) UNIV SECOND MILITARY MEDICAL.

XX PI Pan W;

XX DR WPI; 2002-723317/78.

XX PT Preparation of fusion protein from Plasmodium merozoite surface protein-1 and Plasmodium apical membrane antigen-1, for use in anti-malarial vaccines for treatment of malaria -

XX PS Claim 3; Page 29-31; 39pp; Chinese.

XX CC The invention relates to a fusion protein comprising the amino acid sequence of the Plasmodium apical membrane antigen 1 (AMA-1), that of the Plasmodium merozoite surface protein-1 (MSP1) and the connection peptide between these amino acid sequences. Also included are; (1) an isolated DNA molecule encoding the fusion protein; (2) a vector containing the DNA molecule; (3) a host cell containing the vector; (4) producing the fusion protein by culturing the host cells to express

CC the protein before isolation; and (5) anti-malarial vaccines containing the fusion protein or its encoding DNA molecule. The fusion antigen is useful for anti-malarial vaccines for treatment of malaria. The fusion protein has superior immunogenicity and can cause an effective immune response against Plasmodium. The present sequence is the AMA-1/MSP-1 fusion protein PFCP-1.

XX Sequence 654 AA;

Query Match 13.8%; Score 403; DB 23; Length 654;
 Best Local Similarity 27.9%; Pred. No. 1.8e-26;
 Matches 127; Conservative 68; Mismatches 162; Indels 98; Gaps 20;

QY 41 GNPFQAVNEMKTEMERNLTHHOSGIYVDGQDEYDGLYRBPAGLCPIWKGHIEQQ 100
 Db 91 GNPF-----TEWAKKDIEVHSGIRYDGEAFAVAGTQRLPSGKCPVFGGIIEN 144
 QY 101 PDRLPYRNNFLEADVTEKEYKQGNPLPGCFNLNFTPSGORISPPME---LLEKNSN 156
 Db 145 S-----OTTFLLPVATGNQYLKD-----GGFAF---PPTBPLMSPTLDEMRHFYKDKY 191
 QY 157 IKASTDLGRCAEFKATVAMDKNNKATKRYRPFYVDSKKRLCHILLYSMOLMEGKKYCSV 216
 Db 192 VKNIDELTLCRRHAGNM1--PDNDKNSNYKYPAYVDDKCKCHILYIAQENNGRKYCN- 248
 QY 217 KGEPPDLTWYCFKPKRSVTENHLLIYGSAYVGEN--PDAFISKCPNOALRGYRFGVWKKGR 275
 Db 249 KDEGRNSMFCFRPKAKDISPQNY-----TYSKRVVDMEKVCPRKQLQNAKFGLMVDGN 303
 QY 276 CLDYTELTD-TVIERVESKACQWVTFENDGVASDQPHYTP--LTSQASWMDMP----- 321
 Db 304 CEDIPHVNEPAIDLFE---CNKLVFELS--ASDQPRQYEQHLTDYEKIKEGFKNKQAS 357
 QY 322 W--NDWMP--LHOSQPHSGVGRNYGYVDTTGEKCALSDQVPCDCLVSDSAVSYTA 377
 Db 358 MIKSAFLPTGAFKADRYKSHGKGYMGNVNTETO---KCEIFNVKPTCLINSSYIATTA 414
 QY 378 AGSLSEETPNFPIPSN-----PSYTPPTPETAL 405
 Db 415 LSHPIEVNNF--PCSLYKDEIMKEIERESKRITLNDNDDEGNKTIAPRIFISDDKSL 472
 QY 406 QCTADKPPDSFGACDVQACRQKTSYVGGQIOSTS 440
 Db 473 KCPDPEWVSQSTCRFVCK-----CVERRAEVTS 502

RESULT 10
 AAP91588
 ID AAP91588 standard; protein; 561 AA.

XX AC AAP91588;

XX DT 25-MAR-2003 (updated)

XX DT 25-JAN-1990 (first entry)

XX DE Rhoptry membrane antigen-1.

XX KM Malaria; rhoptry membrane antigen-1; antibodies.

XX OS Plasmodium chabaudi adami DS.

XX PN WO8907645-A.

XX PD 24-AUG-1989.

XX PF 10-FEB-1989; 89WO-AU00056.

XX PR 12-FEB-1988; 88AU-0006743.

XX PA (SARA-) SARAFANE PTY LTD.

XX PI Peterson MG, Crewther PE, Smythe JA, Marshall VM, Silva A;

DR WPI, 1989-263714/36.
 DR N-PSDB; AAP91632.
 XX RhoPrty membrane antigen of Plasmodium falciparum
 PT - used for producing antibodies and in immunisation,
 PT diagnostic and treatment methods for malaria.
 XX
 PS Disclosure; Fig 3; 46pp; English.
 CC Predicted mol. wt. is 63901 D. This shows great similarity to
 CC P. falciparum RMA-1 protein (sequence in specification-claimed).
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 561 AA;
 Query Match 13.5%; Score 395; DB 10; Length 561;
 Best Local Similarity 25.7%; Pred. No. 7.8e-28;
 Matches 147; Conservative 86; Mismatches 202; Indels 138; Gaps 24;
 QY 42 NPFQANVEMKTFMERFNLTHHSGIYVDLQDKEVDGTLYPEAGLCPTGKHIELQDP 101
 DB 53 NPWE-----KEMEKYDIEKVGSGIRVDLGEDARVENQDRIPSGKCPVWGKITONS 106
 QY 102 DRLRYRNNFLDVPPT-EKEYKQSGNPLDGFNINFTPSGGRISFPFWE-----LLEKXSN 156
 DB 107 -----KVSFLTRVATGNQKVRGGGLAPP-----QTDVNISFTITDNLKMKQKHKE 152
 QY 157 IKASTDLRCGAEPFAFTVAMDKNKATKRYRPFYVDSKKRLCHILYVSMQMEGKKYCSV 216
 DB 153 ILALNDSLCAKHA--SFYVGOTNVNTVRRHAYVDKSNKTCYILYVAAGNMGPRYCS- 209
 QY 217 KGEPPDLTWYCFKPKKSVTEHHLLIYGSAYVGENPDATISKCPNALGIRFGWKKRC 276
 DB 210 NEEDNENQPCFTPEKK--DEYKNLSYLTKNLRED--WETSCPNKSIONAKFGWVDGYC 265
 QY 277 LDY--TELTPVIEVESKAQCVMTFENDGVAASDPHTY----- 314
 DB 266 SEYQKKEVHND---KTLLEBNOIVFNES--ASDQPKQYEGHLEDTAKIRRGIVDRNGK 318
 QY 315 -----PLTSQASWNDWMLPHQSDQPHSGGVGRNYGFYVDTTGEKCALSDQVPLCLV 367
 DB 319 LIGELMLLIGS-----YRADQVSKGKGVWAWYDKKTK--KCYIFNKKKPTCLII 365
 QY 368 SDSAAVSTYTAAGSLSEETPNFTIPSN-----PSVTPTPT 400
 DB 366 NDKDVAATATLSSL-EEGFQESFPDIIYKKKIAEBIKVMNNRNNNGNDTIKFPRIITSD 424
 QY 401 PETALQCTADKRPDSFGACDVQACKRKQTSVGGIQTSTVDTADEONEGCSNTA---- 456
 DB 425 DKESINCPCEPTQLTOSTCKFFVC---NCEVERK-QPISNNVEVLEIDEFKSEYAESEPI 478
 QY 457 -----LIAGLAVGVLLALLLGGGCVFAKRLDRNKGVAQHHEHFEQSDRGARKKRP 508
 DB 479 NKPRQLMIIIIIIAIGALIASLII---FYFFK---SNK--PGDDVDYKMGQADTYGKAQAR 530
 QY 509 SDLWQEAEPSPWDEAEENIEDQGEITHVMEGY 541
 DB 531 KDEMLDPEVSWGEGDK---RASHTTPVLMEKPY 560
 RESULT 11
 AAB85697
 ID AAB85697 standard; Protein; 1807 AA.
 XX
 AC AAB85697;
 XX
 DT 29-OCT-2001 (first entry)
 XX
 DE Recombinant protein v1vac1p.
 XX
 KM Multivalent protein; immune response; Plasmodium vivax; parasite;
 XX protozoacide; vaccine; malaria; recombinant; v1vac1.

OS Synthetic.
 OS Plasmodium vivax.
 XX
 PN WO200155181-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-US02937.
 XX
 PR 31-JAN-2000; 2000US-0179213.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Lal AA, Xiao L, Zhou Z;
 XX
 DR WPI, 2001-514557/56.
 DR N-PSDB; AAH47058.
 XX
 PT New recombinant multivalent protein comprising antigenic determinants
 PT derived from more than one stage in a life cycle of Plasmodium vivax,
 PT useful as a vaccine for treating, preventing and reducing malarial
 PT infection -
 XX
 PS Claim 5; Page 39-45; 59pp; English.
 CC The invention relates to recombinant multivalent proteins (I) that
 CC stimulate an immune response to Plasmodium vivax. (I) comprises antigenic
 CC determinants, fragments or conservative substitutions, derived from more
 CC than one stage in a life cycle of a Plasmodium vivax parasite. (I) is
 CC useful as a vaccine for stimulating an immune response, specifically a
 CC protective immune response that confers increased resistance to infection
 CC by Plasmodium parasites, such as P. vivax. (I) is especially useful in
 CC the treatment, prevention and reduction of malarial infection, as
 CC research or diagnostic reagents for the detection of Plasmodium species
 CC in a biological sample, and for conferring immunity against multiple
 CC stages of the malarial parasite. The antibodies produced are useful for
 CC the detection or measurement of antigenic epitopes derived from one or
 CC more stages in a life cycle of a parasite, particularly P. vivax. The
 CC vaccine comprising the recombinant protein, is cost-effective, health-
 CC promoting intervention for controlling, preventing or treating the
 CC incidence of malaria. The present sequence represents the amino acid
 CC sequence of the recombinant protein v1vac1p, a multivalent and
 CC multistage vaccine against P. vivax.
 XX
 SQ Sequence 1807 AA;
 Query Match 13.4%; Score 391; DB 22; Length 1807;
 Best Local Similarity 26.3%; Pred. No. 1.2e-26;
 Matches 132; Conservative 73; Mismatches 182; Indels 114; Gaps 22;
 QY 5 GVQULVIVVACCTIFASGL-----SSSTRS-----RESQTLASST-SGNPQANVEMK 51
 DB 339 GIYIIFLSAQLVHIGCGNQRPSRLTRANNVLEKGTVERSTRMSPW-----K 392
 QY 52 TFERFNLTHHSGIYVDLQDKEVDGTLYPEAGLCPTGKHIELQDPRLPYRNNFL 111
 DB 393 AFMEKTYDIERHSSGVRLDGEDAEVENAKRIRAGRPVGVKGIENSD-----VSFL 447
 QY 112 EDVPT-EKEYKQSGNPLDGFNINFTPSGGRISFPFWELEKSNITAST---DLGRC 166
 DB 448 RPVATGDKLKQGGFAFPN-----ANDHISPMTLANKERYKDNVETMKLNDIALC 498
 QY 167 AEFAPKTY-ANDKNNKATKRYRPFYVDSKKRLCHILYVSMQMEGKKYCSVGEPPDLTW 225
 DB 499 RTHAASFVWAGDQN---SSYHPAYDEKERTCHMLYLSAQENNGPRYCSPPAQNRDVA- 554
 QY 226 YCFKPKRSVT-ENHLLIYGSAYVGENPDATISKCPNALRGIRFGWKKGRCLDYTELTD 284
 DB 555 FCFKPKDKIESFEN--LVLSLKNVRNDND---KKCPKRLGNAGKGLWVGNCBEPYVKE 609
 QY 285 TVIERVESKAQCVMTFENDGVAASDPHTYPLTQASWNDWMLHQ----- 330
 DB 610 V---EAEDLRECNRLVF--GASASDPQTY-----EEETDYOKIQCGFRONNREMIKSAF 660

QY 331 -----SDPHSGVGRNRYGYVDTTGGKCALSDQVPCLVSDSAVSYTAAGSLSE 383
 Db 661 LPVGAFNSDNFKSKRGFMNMF---DSVKKCYIFNFKPCLINDKNFIATLASHQE 717
 QY 384 ---ETPNFIIPSN-----PSVTPEPTALQCTADKPPDSF 416
 Db 718 VDLEPPCSITYDEIERIKKOSRMNLYSVDERIVLPRIIFSNDKESIKCSCEPERISN 777
 QY 417 GACDVQACKROKTSQVGGQIQ 437
 Db 778 STCNFYVC-----NCEKRVK 793

RESULT 12
 AAB85698
 ID AAB85698 standard; Protein; 2028 AA.

AC AAB85698;

DT 29-OCT-2001 (first entry)

DE Recombinant protein ViVac2p.

KM Multivalent protein; immune response; Plasmodium vivax; parasite;
 KW protozoacide; vaccine; malaria; recombinant; ViVac2.

OS Synthetic.

XX Plasmodium vivax.

PN WO200155181-A2.

XX 02-AUG-2001.

PD 29-JAN-2001; 2001WO-US02937.

PF 31-JAN-2000; 2000US-0179213.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Lal AA, Xiao L, Zhou Z;

PI WPI; 2001-514557/56.

DR N-PSDB; AAH47055.

PT New recombinant multivalent protein comprising antigenic determinants
 derived from more than one stage in a life cycle of Plasmodium vivax,
 useful as a vaccine for treating, preventing and reducing malarial
 infection

PS Claim 5; Page 48-55; 59pp; English.

XX The invention relates to recombinant multivalent proteins (I). that
 CC stimulate an immune response to Plasmodium vivax. (I) comprises antigenic
 CC determinants, fragments or conservative substitutions, derived from more
 CC than one stage in a life cycle of a Plasmodium vivax parasite. (II) is
 CC useful as a vaccine for stimulating an immune response, specifically a
 CC protective immune response that confers increased resistance to infection
 CC by Plasmodium parasites, such as P. vivax. (I) is especially useful in
 CC the treatment, prevention and reduction of malarial infection, as
 CC research or diagnostic reagents for the detection of Plasmodium species
 CC in a biological sample, and for conferring immunity against multiple
 CC stages of the malarial parasite. The antibodies produced are useful for
 CC the detection or measurement of antigenic epitopes derived from one or
 CC more stages in a life cycle of a parasite, particularly P. vivax. The
 CC vaccine comprising the recombinant protein, is cost-effective, health-
 CC promoting intervention for controlling, preventing or treating the
 CC incidence of malaria. The present sequence represents the amino acid
 CC sequence of the recombinant protein ViVac2p, a multivalent and
 CC multistage vaccine against P. vivax.

XX Sequence 2028 AA;

Query Match 13.4%; Score 391; DB 22; Length 2028;
 Best Local Similarity 26.3%; Pred. No. 1.4e-26;
 Matches 132; Conservative 73; Mismatches 182; Indels 114; Gaps 22;

QY 5 GVOVLVIVADCTFASGL-----SSSTRG-----RESOTLAST-SGNPFOANVEMK 51
 Db 560 GIYYIIFLSAQLVHIGKCGNOKPSRLTRSANVYLEKGTPTVERSTMSNPW-----K 613
 QY 52 TEMERFNLTHHSGIYVDTGODKEVDGTLREBPAGLCPIGKHIELQOPRLPFRNPL 111
 Db 614 AFMEKTYDERTHSSGVRLDEDAEENAKYRIIPGRCPVGGKGIIVNSD-----VSFL 668
 QY 112 EDVPT-EKEYKQSGNPLPGGFNLVPTPSGORISPPFMELLEKNINIKAST-----DLGRC 166
 Db 669 RPAVATGDKLDGGFAFEN-----ANDHISPMTLANKERYKONVERTMKINDIALC 719
 QY 167 AEFAPKTY-AMDKNNKATKYRPPYDSKRLCHILYVSNQLMGKTKCSYKGEPPDLTW 225
 Db 720 RTHAASFVMAQDQ---SSYRHPAVYDEKERTCHMLYLSAQBNNMGPFCSPDAQNRDAV- 775
 QY 226 YCFPKRSKVT-ENHHLIYGSAYVGENPDPAFISKCPNOALRGYRFGVWKGRCLDYTELTD 284
 Db 776 FCFKPDKNSEFEN--LVYLSKNVRNDWD--KKCPKRLGNAKTGLVNDGNCBILPYKE 830
 QY 285 TVIERVESKACQWYKTFENDVASDQPTPTPLTSQASNDWMPPLHQ----- 330
 Db 831 V---EADLRRCNNRIVF--GASASDQPTQY---EBEETDVOKIQQGRQNNREMIKSAF 881
 QY 331 -----SDPHSGVGRNRYGYVDTTGGKCALSDQVPCLVSDSAVSYTAAGSLSE 383
 Db 882 LPVGAFNSDNFKSKRGFMNMF---DSVKKCYIFNFKPCLINDKNFIATLASHQE 938
 QY 384 ---ETPNFIIPSN-----PSVTPEPTALQCTADKPPDSF 416
 Db 939 VDLEPPCSITYDEIERIKKOSRMNLYSVDERIVLPRIIFSNDKESIKCSCEPERISN 998
 QY 417 GACDVQACKROKTSQVGGQIQ 437
 Db 999 STCNFYVC-----NCEKRVK 1014

RESULT 13
 AAR10935
 ID AAR10935 standard; Protein; 489 AA.

AC AAR10935;

DT 25-MAR-2003 (updated)

DT 17-DEC-2001 (updated)

DT 15-APR-1991 (first entry)

DE Plasmodium vivax 66KD merozoite antigen protein partial sequence.

XX Plasmodium merozoite antigens; malaria vaccine.

XX Plasmodium vivax.

PN USN7483516-N.

XX 15-JAN-1991.

PD 22-FEB-1990; 90US-0483516.

PF 22-FEB-1990; 90US-0483516.

PR (USSH) NAT INST OF HEALTH.

PA (USDC) US SEC OF COMMERCE.

PI Waters AP, McCutchan TF;

XX WPI; 1991-044381/06.

DR N-PSDB; AAQ10869.

XX

Plasmodium merozoite antigen proteins and DNA sequences - useful
 in vaccine prodn., anti-malarial drug design, and in diagnostics

Disclousure; fig 1; 31pp; English.
 This protein is encoded by a recombinant DNA molecule comprising
 the complete P. vivax merozoite antigen gene and e.g. a pUC19
 or vaccinia virus vector sequence and regulatory elements. This
 allows efficient expression of the antigen on transformation of
 host cells. It is useful in an anti-malarial vaccine for con-
 ferding immunity against the merozoite form of the parasite and
 preventing infection of uninfected red blood cells.
 See also AAQ10418.
 (Note: Revised entry submitted to correct the patent number format of
 US Government-owned NTIS applications to prevent clashes with ongoing US
 granted patent numbers. For further information please visit the Derwent
 web site at www.derwent.com/dwpi/updates/ntis_us.html.)
 (Updated on 25-MAR-2003 to correct PA field.)

Sequence 489 AA:

Query Match 12.2%; Score 357; DB 12; Length 489;
 Best Local Similarity 25.6%; Pred. No. 2,4e-24;
 Matches 138; Conservative 75; Mismatches 208; Indels 118; Gaps 24;

QY 70 DLGQKEVDGTYRBPAGLCPTWGHIEIQOPDRLEPRNNEEDVPT-EKEKQSGNPLP 128
 DB 1 DLGEADVENAKYRIIPAGKCPVFGKIVENSDB---VSFLRPATGQKDKGCFAPF 55
 QY 129 GGFNINFTVPSGORISFPFM---ELLEKNSNIKASTDLGCAEPAFKTV-AMDKNKAT 183
 DB 56 N-----ANGHSPTMLANKERYKNVEMKMLNDALCRTBAASVMAAGDN---S 103
 QY 184 KYRPFVYDSKRLCHILVSNQLMGKRYCSVKKEPPDLTYCEPKRSVTENHLLYG 243
 DB 104 SYRHAVVDEKKEKCHMLYLSAQENMGPRYCSPDQNRDAV-FCFKPDNGESFD-NLVYL 161
 QY 244 SANYVENPAPFISKCPNOLRGYRFGVMKKGRCLDTLTIVIERVES--KAQGMVKT 301
 DB 162 SKNVNNDMD---KCCPRKNLGNAGKGLWADGNCEEL---DYVKEVEAGDLRECNRIYE 213
 QY 302 ENDGVAASDOPHTYPLTSQASMDMWPPLHQ-----SDQPHSGVG 340
 DB 214 ---GASASDOPROX---EEEMTDYQIKIQGFRONNREMKASFLPGAGNSDNFSGKRG 267
 QY 341 RNYGYVYDVTGEGKALSQVPCIVSDSAAVSYTAAGLSLSE---ETPNFTIPSN--- 393
 DB 268 FVMAMF---DSYKNKCYIFNTKPTCLINDKNFIATATLASHPOEVDLEFPCSIYKDEIERE 324
 QY 394 -----PSVTPTPTALQCTADKFPDSFGACDVQACKROKTSVC- 432
 DB 325 IKKQSRNNMLYSVDGERIVLPRIFISNDKESIKPCPEPRISNSTGNFYVC---NCEV 379
 QY 433 -----GGOIQSTSVDTADEONECGSN---TALTAGLVAGVLLALLAGGCGYPAKL 482
 DB 380 KRAEIKENNQVVLKEFRNYENGESKYNKMLIIIGI-TGVVCVVA-LASMAFYRKA 437
 QY 483 DRNKGVQAHHHEHFEQSDRGARKKRPDLMQEAEPSEFMDAEENIEQDCETHVMYEGDY 541
 DB 438 NNIDK-----YDKMDQAEYEGYKPTNTRKDEMLDPEASFMEGDEK---RASHTTPLVLEKPY 488

RESULT 14

AAAB24128 ID AAB24128 standard; Protein; 1507 AA.

AC AAB24128;

DT 29-JAN-2001 (first entry)

DE Plasmodium yoelii YM MAEBL protein sequence SEQ ID NO:5.

KW Plasmodium; malaria; parasite; adhesion molecule; MAEBL; vaccine;

KW erythrocyte binding protein; protozoacide; infection.

XX Plasmodium yoelii.

OS US6120770-A.

XX 19-SEP-2000.

XX 12-SEP-1997; 97US-0929329.

XX 12-SEP-1997; 97US-0929329.

XX (UNOT) UNIV NOTRE DAME DU LAC.

PI Adams JH, Dalton JP, Kappe S;

XX WPI; 2000-593710/56.

DR N-PSDB; AAA99265.

XX New erythrocyte binding protein (MAEBL) useful as a vaccine against

PT malaria, for enhancing cell's resistance to infection or for

XX alleviating symptoms associated with the disease

PS Example 4; Column 25-34; 31pp; English.

XX The present invention describes an isolated polypeptide (I) comprising

CC a Plasmodium parasite (malaria parasite) erythrocyte binding protein

CC (MAEBL). Also described is an immunogenic composition comprising an

CC amino acid sequence, which includes a MAEBL protein cysteine domain.

CC MAEBL polypeptides and compositions containing them are useful as

CC vaccines against malaria, to enhance a cell's resistance to infection

CC by Plasmodium parasites or to alleviate the symptoms associated with

CC the disease. The present sequence represents a MAEBL protein, which is

CC used in the exemplification of the present invention.

XX Sequence 1507 AA;

QY Query Match 4.1%; Score 120; DB 21; Length 1507;

DB Best Local Similarity 18.8%; Pred. No. 0.26;

XX Matches 87; Conservative 52; Mismatches 151; Indels 172; Gaps 21;

QY 34 TLASASTSGNPQAVNEMTFMERFNLTHH-----QSGIYVLDQDKEVD--- 78

DB 18 TPTSTALINP-----QEDFMDRFDILNNHVNIMKTNSGSLAQGLKFDIVEDNISKL 71

QY 79 -----GLTYRBPAGLCPTWGHIEIQOPDRLEPRNNEEDVPT-EKEKQSGNPLP 128

DB 72 NSLENARLCPNNKKNIVR---GSCPDYKTFMSMDLQDEYSEDFLNEISGLNKLKLI 128

QY 97 ELQOPDRLEPRNNEEDVPT-EKEKQSGNPLP 128

DB 129 DVEIFVNNNSGLAMQGLFANCPYDKHVNNDIKNELEYDMCDKPYSNKOD----- 178

QY 134 NEVTPSGORISFPFMLELKNKSNIKV---STDGRCAPFAKTVAMDKNKATKYRY--- 187

DB 179 -----ISIRIKYR-LSKTYTFSGHGLGRLGNTSEYPLHIYPIEYRQKARYPL 231

QY 188 -----PRVYDSKRLCHILVSNQLMGKRYCSVKKEPPDLTYCEPKRSVTENHLLYG 243

DB 232 VETLEDGSIYSHCLGPCFDRDQDNKCFRDLPAFAHMKKECTIIIGTH---EKKTYTCN 287

QY 218 GEPDLTYVCFKPRKSVTENHLLIGSAYVGENPDAFISK-PNOALRGYRFGV---MKKG 274

DB 288 SUNSNRNGRCFSGSIK-EKGDWYASSFL-RPD-YETKCPRIPLANNSEFGYRNYNTG 343

QY 275 RCLDYTELTDVIERVESKAQCVKTFENDGVAASDOPHTYPLTSQASNDMMWPLHQSDOP 334

DB 344 NCESEPTKLYD---NSVISFNECTIEKLF-NFNVANDBPE-EKRNMYLNGVWVLGKKNKL 397

QY 335 HSGGVGRNYGYVYDVTGEGKALSQVPCIVSDSAAVSYT 376

DB 398 NS-----MNDLGVCALALKERKPTCVLKQNYVSFT 426

RESULT 15
ABG16636
ID ABG16636 standard; Protein; 2519 AA.
XX
AC ABG16636;
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #16627.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS80823.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 20; SEQ ID NO 46995; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2519 AA;
Query Match 4.0%; Score 118; DB 22; Length 2519;
Best Local Similarity 19.4%; Pred. No. 0.9;
Matches 129; Conservative 66; Mismatches 222; Indels 248; Gaps 28;
OY 15 DCTIFASGLSSSTMRRESQTLASSTGNGPQANVEMKTFMRPNLTTHHOGIYVDLQD 74
DB 1809 DMSLYASTSEKVSLEBGEKLSPKSDISP-----LTPRESSPLVSPTFSD 1853
OY 75 -----KEVDGTLTY-----REPAG-----LCPIWGHIELOQPDRLPYRNINFLD 113

DB 1854 STSAVKEKATACHSSSPPIDAASAEPPGFASVLPDTMCHHLALNR-----D 1901
OY 114 VPEKEVKQSGNPNLPDGGFNINFTVPPSGQRISP-----FPMELLEKNS----- 155
DB 1902 LSTPGLKEDSGCKTPGGPSYAVQKPEETTRSPDEEDYDYESYEKTRTSDVGYYEKIE 1961
OY 156 -NIRASTDLGRCAEFAFEKV-----AMDKNKATK----- 184
DB 1962 RTTSPSDSGSYETIGTKITTPEDGDYSYIEIKTRTPREGGYSYDISKTTSPPEVS 2021
OY 185 -YRYPFV-----YDSKRLCHIL-----YVSNQMEKKY-CSVK 217
DB 2022 GSYEKTERSRRLDDISNGYDSEDCGHTLGDPSSYETTEKITSPSESGSYETSTK 2081
OY 218 -GEPPLTWYCFKRKRSVTEHHHLYSAYGENPDPAFISCKPQALRGVFGVKKRC 276
DB 2082 TTRTPDSTYCYETAEKTRTPQ-----ASTSYETSD----- 2114
OY 277 LDYTELDITVIERVESKAQCWVTFENDGVASDQPHTYPILT--SOASWN-----DMW----- 326
DB 2115 LCYTAEEKSPSEANQDVLCLVSCF-----YKHPTELSPFTINPPLMFASAE 2165
OY 327 PLHQSDQP--HSGGVGNNGFYVDTTGEKCALSDQVPDCLVSDA----- 371
DB 2166 PTESEKPLTQSGGAPPPG-----GKQGRQCDEFPPTVSSESAPSDTSDVPETE 2218
OY 372 -AVSYTAAGSISETPFIIPSNPSVT-----PPTPEALQCTADKPPDSGACDVQAC- 424
DB 2219 ECPSTITDANIDSEBETITPTDKTYTKMDPPAPVQDPSPPRHPD--VSNVDPFLA 2277
OY 425 -----KROKTSVGGIOISTSVDCADQNEGSGNTALVAGVGLLA 470
DB 2278 IEQNLGALKKDLKEXKTKTKPGTKTKSSSVYKSD-----GSKPPLAASPKPAGL----- 2328
OY 471 LGGGCVFARKLDNRKGVQAHHHEHFQSDRGARKKPPSLMOGAEPSPFME--AEENIE 528
DB 2329 -----KESDVKVSRVASPKKESVEKAAPTTTPEVKAARGEE 2366
OY 529 QDGET 533
DB 2367 KDKET 2371
RESULT 16
ID AAM39322 standard; Protein; 996 AA.
XX
AC AAM39322;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2467.
XX
KW Human; nocutropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-052317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.
 DR N-PSDB; AA158478.

XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -

XX Example 4; SEQ ID NO 2467; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA158642-AA1642213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilization of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 996 AA;

XX Query Match 3.9%; Score 113; DB 22; Length 996;

XX Best Local Similarity 20.9%; Pred. No. 0.63; Mismatches 170; Indels 104; Gaps 18;

XX Matches 87; Conservative 55; Mismatches 170; Indels 104; Gaps 18;

QY 100 QPRLPYNNF--LEDVTEKEYKQSG-----NPLPGFNLFVT-----PSQRIISP 145

DB 139 EKKSTPPNNLVNPNVQELTERVRKAPAPVLSPTKGVNENTVSAGKDLSTSPKSP 198

QY 146 PMELLEKNSNITKASTDLGRCAEFAPKTVAMDKNKATYRYRPFYVDSKKRLCHILYISM 205

DB 199 IPSPLVGRKRNASQSL-LWCKE-----VTKNYRGVK-----ITNFTT 235

QY 206 QMEGKKYCSYKGE-PPDLTWYCFKPKRSVTENHHLIY-GSAYVG-----ENPDAFISK 258

DB 236 SRRNGSLFCALIHHPERDLIDYKSLNPDIKENKKAIVGFSIGISRLLEPSDVLAI 295

QY 259 PNO-----ALRGYRFGVWKKGRCLDYTELTLDYIERVESKAQCMVTFENDGAS-D 309

DB 296 PKLTMVLYQIRAHFSG-----QELNVVQIEENSKSYTKVGNVETDNTSSVD 345

QY 310 QHTTYPPLTSQASNMWMLHQSDQPHSGVG--RNYGYVYVDTTGGKCALSDQVPCIV 367

DB 346 QEKFY-----AELSLDKREPELQOPISGAVDFLSQDSVFVNDVSGESESSEHQTPDDHL 400

QY 368 SSSANSY-----TAAGSLSEETPNFIIPSNSVTPTPTPALQC----- 407

DB 401 SPSSTASPYRRTKSDTEPKSQSQSGRTSGSDPGICSNVDTSTQAVLLGKRLKAEFL 460

QY 408 -----TADKFPDSFG--ACDVQACGRQKTSQVGGQIQ-----STSVCTADEON 449

DB 461 ELSDLYVSKKKDMSPPFCEETDEBOKLTLDIGSLNLEKKEKLENSLSLCRSDPES 516

RESULT 17
 ABG22883

ID ABG22883 standard; Protein; 1023 AA.

XX AC ABG22883;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22874.

XX Human: chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AA87070.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnosis, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity -

XX Claim 20; SEQ ID NO 53242; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX CC and gene mapping, and in recombinant production of (II). The

XX CC polynucleotides are also used in diagnostics as expressed sequence tags

XX CC to restore normal activity of (II) or to treat disease states involving

XX CC (II). (II) is useful for generating antibodies against it, detecting or

XX CC quantitating a polypeptide in tissue, as molecular weight markers and as

XX CC a food supplement. (II) and its binding partners are useful in medical

XX CC imaging of sites expressing (II). (I) and (II) are useful for treating

XX CC disorders involving aberrant protein expression or biological activity.

XX CC The polypeptide and polynucleotide sequences have applications in

XX CC diagnostics, forensics, gene mapping, identification of mutations

XX CC and to produce other types of data and products dependent on DNA and

XX CC amino acid sequences. ABG00010-ABG30377 represent novel human

XX CC diagnostic amino acid sequences of the invention.

XX CC Note: The sequence data for this patent did not appear in the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1023 AA;

XX Query Match 3.9%; Score 113; DB 22; Length 1023;

XX Best Local Similarity 20.9%; Pred. No. 0.65; Mismatches 170; Indels 104; Gaps 18;

XX Matches 87; Conservative 55; Mismatches 170; Indels 104; Gaps 18;

QY 100 QPRLPYNNF--LEDVTEKEYKQSG-----NPLPGFNLFVT-----PSQRIISP 145

DB 166 EKKSTPPNNLVNPNVQELTERVRKAPAPVLSPTKGVNENTVSAGKDLSTSPKSP 225

QY 146 PMELLEKNSNITKASTDLGRCAEFAPKTVAMDKNKATYRYRPFYVDSKKRLCHILYISM 205

DB 226 IPSPLVGRKRNASQSL-LWCKE-----VTKNYRGVK-----ITNFTT 262

QY 206 QMEGKKYCSYKGE-PPDLTWYCFKPKRSVTENHHLIY-GSAYVG-----ENPDAFISK 258


```

Db      263 SWRNGLSFCAILHFRPDLIDKXSLNPDIKNNKKAADGFASIGISRLLEPSDMVLAI 322
Oy      259 PNO-----ALRGYFGVWKKGRCIDYTELDTIVIRVSKACQWKTENGVAS-D 309
Db      323 PDKLTVMYLYQIRAHFSG-----QELNVQIENSSTKYKXGNETDINSVD 372
Oy      310 QPHTYPLTSQASWMDWPHLHSDQPHSGVG--RNYGYVYDTTGEKCALSDQVPCLV 367
Db      373 QEKFY-----AELSDLKREPELQPIGAVDFLSQDSDSVFVNDGVSSESEHQTDPDHL 427
Oy      368 SDSAAVSY-----TAAGSLSEETPNFIISNPSVTPPTETALQC----- 407
Db      428 SPSTASPYCRRRTKSDTEPQKSGQSSGRTSGSDPDCICNTDSTQAVLLGKKRLKAEYL 487
Oy      408 -----TADKFPDSFG--ACDVQACKROKTSQVGGQIQ-----STVDCIADEN 449
Db      488 ELSDLVSDKXKXMSPPFICETDEQKQTLIDIGSNLEKELENSRLSECRSDPES 543

RESULT 21
AAU74355
ID      AAU74355 standard; Protein; 1076 AA.
AC      AAU74355;
DT      12-MAR-2002 (first entry)
XX      Human cytoskeleton-associated protein (CYSKP) #26.
XX      Human; cytoskeleton-associated protein; CYSKP; autoimmune disorder;
XX      cell proliferative disorder; inflammatory disorder; prion disease;
XX      vesicle trafficking disorder; gastrointestinal disorder; muscle disorder;
XX      neurological disorder; cell motility disorder; reproductive disorder;
XX      spinal cord disease; central nervous system disorder; mental disorder;
XX      gene therapy; cancer.
XX      Homo sapiens.
XX      OS
XX      MO200185942-A2.
XX      15-NOV-2001.
XX      03-MAY-2001; 2001WO-US14355.
XX      05-MAY-2000; 2000US-201960P.
XX      08-MAY-2000; 2000US-202729P.
XX      05-JUN-2000; 2000US-209705P.
XX      07-JUN-2000; 2000US-210149P.
XX      21-JUN-2000; 2000US-213215P.
XX      (INCY-) INCYTE GENOMICS INC.
XX      Yue H, Tang YT, Au-Young J, Lu DAM, Baughn MR, Hillman JL,
XX      P1 Azimzai Y, Lal P, Yao MG, Bandman O, Burford N, Batra S;
XX      P1 Kearney L, Policky JL;
XX      WPI: 2002-062248/08.
XX      DR N-PSDB; AAS99915.
XX      New cytoskeleton-associated proteins and polynucleotides, useful for
XX      diagnosing, preventing and treating cell proliferative, autoimmune,
XX      inflammatory, neurological, cell motility, reproductive and muscle
XX      disorders -
XX      Claim 1; Page 153-155; 194pp; English.
XX      The invention relates to human cytoskeleton-associated polypeptides
XX      (CYSKP) and their associated polynucleotide sequences. The sequences are
XX      useful in the treatment of disorders associated with overexpression or
XX      underexpression of CYSKP in a patient. The disorders include cell
XX      proliferative disorders (such as cancer, actinic keratosis,
XX      arteriosclerosis, cirrhosis, hepatitis and psoriasis),

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CC      autoimmune/inflammatory disorders (such as, asthma, atherosclerosis,
CC      osteoporosis, Crohn's disease, rheumatoid arthritis, diabetes mellitus
CC      and anaemia), vesicle trafficking disorders (such as
CC      hypercholesterolaemia, diabetes insipidus, Graves' disease and goitre),
CC      gastrointestinal disorders, prion diseases, neurological disorders (such
CC      as epilepsy, stroke, cerebral neoplasms, Alzheimer's disease,
CC      Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis
CC      and other motor neuron disorders), cell motility disorders, reproductive
CC      disorders (such as endometriosis and polycystic ovary syndrome), muscle
CC      disorders (such as myoarthritis, migraine, hypertension, hypoglycaemia,
CC      myocardial infarction, epilepsy and muscular dystrophy), spinal cord
CC      diseases, central nervous system disorders (such as Down syndrome and
CC      cerebral palsy) and mental disorders (such as anxiety and schizophrenia).
CC      Sequences AAU74330-AAU74363 represent human CYSKP of the invention.
XX      SO
XX      Sequence 1076 AA;
XX      Query Match 3.9%; Score 113; DB 23; Length 1076;
XX      Best Local Similarity 20.9%; Pred. No. 0.71;
XX      Matches 87; Conservative 55; Mismatches 170; Indels 104; Gaps 18;

Oy      100 QPDLPLRYNNF---LEDVPEKEYKQSG-----NPLRGNNLNPV-----PSGQRI 145
Db      219 EPKSTPPNNLVNDVQLETERRYKRAAPAPVLSPTGVNENTVSAKDLSIPKSP 278
Oy      146 PMELLEKNINIKASTDLGCAEFAFTVAMDKNKATKRYRPVYDSKKRLCHILVSM 205
Db      279 IPSVVGKRPVASSL-LWCKE-----VTKRYRGV-----ITNFTT 315
Oy      206 QLMGKKYCSYKGB-PDDLTYWYCPKPKSVTENHLLY-GSAVVG-----ENPDATSKC 258
Db      316 SWRNGLSFCAILHFRPDLIDYKSLNPDIKNNKKAADGFASIGISRLLEPSDMVLAI 375
Oy      259 PNO-----ALRGYFGVWKKGRCIDYTELDTIVIRVSKACQWKTENGVAS-D 309
Db      376 PDKLTVMYLYQIRAHFSG-----QELNVQIENSSTKYKXGNETDINSVD 425
Oy      310 QPHTYPLTSQASWMDWPHLHSDQPHSGVG--RNYGYVYDTTGEKCALSDQVPCLV 367
Db      426 QEKFY-----AELSDLKREPELQPIGAVDFLSQDSDSVFVNDGVSSESEHQTDPDHL 480
Oy      368 SDSAAVSY-----TAAGSLSEETPNFIISNPSVTPPTETALQC----- 407
Db      481 SPSTASPYCRRRTKSDTEPQKSGQSSGRTSGSDPDCICNTDSTQAVLLGKKRLKAEYL 540
Oy      408 -----TADKFPDSFG--ACDVQACKROKTSQVGGQIQ-----STVDCIADEN 449
Db      541 ELSDLVSDKXKXMSPPFICETDEQKQTLIDIGSNLEKELENSRLSECRSDPES 596

RESULT 22
AAU78788
ID      AAU78788 standard; Protein; 1581 AA.
AC      AAU78788;
DT      06-NOV-2001 (first entry)
XX      Human protein SEQ ID NO 1450.
XX      Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX      vaccine; peptide therapy; stem cell growth factor; haematopoietic;
XX      tissue growth factor; immunomodulatory; cancer; leukaemia;
XX      nervous system disorder; arthritis; inflammation.
XX      Homo sapiens.
XX      OS
XX      MO200157190-A2.
XX      09-AUG-2001.
XX      05-FEB-2001; 2001WO-US04098.

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03-FEB-2000; 2000US-0496914.
 PR 27-FEB-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YF, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,
 PI Zhao Q, Wang D, Zhang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 XX WPI, 2001-476283/51.
 DR N-PSDB; AAKS1921.
 XX
 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 3716-3718; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoietic regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 CC
 SQ Sequence 1581 AA;
 Query Match 3.9%; Score 113; DB 22; Length 1581;
 Best Local Similarity 20.9%; Pred. No. 1.3;
 Matches 87; Conservative 55; Mismatches 170; Indels 104; Gaps 18;
 QY 100 QPRLPYRNRF--LEDVTEKEYKQSG-----NPLPGENLNFVT-----PSGORISP 145
 DB 212 BKSTPPPNLNVNPVQELTERVRVKAKAPVLSPTGVLNMENTVSAGKDLSTSPKPS 271
 QY 146 FMELEKKSNIKASPDLCRCAEFKATVAMDKNNKATRYRPFVDSKKRLCHILYGM 205
 DB 272 TSPVLYGRPNASQSL-LWCKE-----VTNNYGVK-----ITNFTT 308
 QY 206 QLMGKKYKSVKGE--PPDLTWYCFKPKKSVTENHLLIY-GSAVVG-----ENPDAFISK 258
 DB 309 SMRNGSLFCAILHFRPDLIDYKSLNPQIKENKKAAYGFASIGISRLLEPSDWLAI 368
 QY 259 PNO-----ALRGYRFGVKKGRCLDYELTDVTIERVESGAQGVKTFENDGAS-D 309
 DB 369 PKRLTWMTLYOIRAHFSG-----QELNVVQIEENSSKSTYKVNAYETDNTSSVD 418
 QY 310 QHTHTYLTQSANNWMLHQSOPHSGVG--RNVGFYVDTTGSGKALSDQVDDCUV 367
 DB 419 QEKFY-----AELSDIKREPELQOPTSGAVDFISODSVFVNDGSGESBSEHQDPDH 473
 QY 368 SDSAAVSY-----TAAGSLSEETPNFIIPNSPVTPPTETALOC----- 407
 DB 474 SPSSTAPYCRRTKSTDEPQKSSGRTSGSDDPGICNSTDSTQAVLIGKKRLKAEKL 533
 QY 408 -----TADKFPDSFG--ACDVQACKRKQKTSVCGGQIQ-----STSVDCETADEQN 449
 DB 534 ELSDLYVSKKKMSPFICEETDEOKLTLDIGSNLEKEKLENSRLSECRSDPS 589

RESULT 23
 AAR94957
 ID AAR94957 standard; Protein: 1104 AA.
 XX
 XX AAR94957;
 AC
 XX
 DT 17-AUG-1996 (first entry)
 XX
 XX NF- κ B DNA-binding protein.
 DE
 XX NF- κ B1; transcription factor; major histocompatibility complex; MHC;
 KW allergy; DNA-binding protein; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 430..900
 FT /label= Cysteine-rich_domain
 FT Region 417..468
 FT /label= Cysteine-rich_repeat
 FT Region 473..521
 FT /label= Cysteine-rich_repeat
 FT Region 533..583
 FT /label= Cysteine-rich_repeat
 FT Region 599..647
 FT /label= Cysteine-rich_repeat
 FT Region 688..737
 FT /label= Cysteine-rich_repeat
 FT Region 799..839
 FT /label= Cysteine-rich_repeat
 FT Region 840..890
 FT /label= Cysteine-rich_repeat
 PN MO9612823-A1.
 XX
 PD 02-MAY-1996.
 XX
 PF 20-OCT-1995; 95WO-US12749.
 XX
 PR 21-OCT-1994; 94US-0327832.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (UYGO) UNIV JOHNS HOPKINS.
 XX
 PI Ono SJ, Strominger JL;
 DR WPI, 1996-230621/23.
 DR N-PSDB; AAT18813.
 XX
 PT Transcription factor, NF- κ B and DNA encoding it - used in regulation
 PT of MHC class II expression and in treatment of allergic disease
 XX
 PS Claim 6; Page 55-58; 93pp; English.
 XX
 CC Human NF- κ B1 (AAR94957) is a new DNA-binding protein which regulates
 CC expression of major histocompatibility complex (MHC) class II
 CC molecules. The sequence was deduced from a cDNA clone (AAT18813)
 CC isolated from Raji cells. NF- κ B1 is a cysteine-rich polypeptide
 CC which interacts specifically with the conserved κ 1 box regulatory
 CC element (AAT18812) found in the proximal promoters of class II MHC
 CC genes. It contains a cysteine-rich domain (see also AAR94955-56)
 CC required for both sequence-specific binding and effector function.
 CC Overexpression of NF- κ B1 specifically represses transcription of
 CC the HLA-DRA gene. NF- κ B1 can be obtd. by expression in transformed
 CC host cells and is useful in the treatment of allergic disease.
 XX
 SQ Sequence 1104 AA;
 Query Match 3.7%; Score 107.5; DB 17; Length 1104;
 Best Local Similarity 19.7%; Pred. No. 2.4; Indels 199; Gaps 29;
 Matches 103; Conservative 61; Mismatches 159;
 QY 85 PAGLCPIWGKIHLEQDPRLPYRNFLLEDVTEKEYKQSGNPLPGGFNLNFVTPSGORIS 144


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Db      579 PCCGTPPL-SQLLELSSSS-----RKTCDMPVPSCG--KVCGRPLPG-SLDFIHRCXKCH 630
Qy      145 PFMPELEKSNINIKASTDLGRCAEFATVAMD-----GNKATKRYRFVVD---SKRL 197
Db      631 EGGDGPVSRIVTISC-----RC--SFRTKEIPCTSLKSDAT-----FMCDKCKNKKRL 677
Qy      198 CHILVSNQMLEGKKYCSVKGEPPDLTWYCFKPKRSVTENHLLYGSAYGVENPDATISK 257
Db      678 C-----GRHKNE-----IC-----CVDKEH-----X 694
Qy      258 CPNOALRGYRFGWK-----KGRCLDTLDTLTYIEVESKACQWKTENDGVASDQ 311
Db      695 CPLNGCRRLRCGLHRCSEPCRHGNC-----QTQWQASFDE----- 729
Qy      312 HTYPLTQASWMDMP-----LHQSQP--HSGG----- 338
Db      730 ----LTCGASVYRPVPCGTRPECTQTCAVHECHPYHSHSEKCRPCTFLTK 785
Qy      339 --VGR-----NYGFYVDTT-----GEGKCALSDVPDLVSDSAVSYTAGS 380
Db      786 WCMGHEFRSNIPCHLVDISGLPESATLPCGMHKCGLCHKGECLVDE----- 834
Qy      381 LSEETPNFIIPSNSVTPPTETALQCTADKFPDSFGACDVQACK-ROKTSCVGGQIQST 439
Db      835 -----PCQPCITPRADCGHPCWAPCHTS--PCPYTACAKVLELQCEGGR-RKE 881
Qy      440 SVDCTADQNEGCSNTALAGLAVGVLLALLGGCCVFAKRLBNKGVQAHHNEHROS 499
Db      882 MVIC-----SEASSTYQRIAIISMASKITDMQLGGSVESIKLITK-KEVHQAELCEDEC 935
Qy      500 DRGARKKRPSD---LMQEAEP-----SFWDEAEENIED 530
Db      936 SALEKKKRLAEAFHISEDSPFNIRSSGSKFSDSLKEARD 977

RESULT 24
ABB97742
ID      ABB97742 standard; Protein; 355 AA.
XX
AC      ABB97742;
XX
DT      11-JUN-2002 (first entry)
XX
DE      Human procathepsin W epitopes related protein.
XX
KW      Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.
XX
OS      Homo sapiens.
XX
PN      WO200226831-A1.
XX
PD      04-APR-2002.
XX
PF      09-JUN-2001; 2001WO-EP07877.
XX
PR      29-SEP-2000; 2000DE-1048727.
XX
PA      (LABS-) LABSOFT DIAGNOSTICS AG.
XX
PI      Weber E;
XX
WI      2002-330095/36.
XX
PT      New hybridoma cell lines that produces antibodies specific for human
XX      cathepsin W, useful e.g. for diagnosis, therapy and drug targeting
XX
PS      Disclosure; Page 17-19; 23pp; German.
XX
CC      The present invention relates to hybridoma cell lines that produce
XX      monoclonal antibodies directed against a defined epitope of human
XX      (pro)cathepsin W, which are produced by fusing myeloma cells with spleen
XX      cells from an animal that has been immunised with recombinant

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CC      procathepsin W. The antibodies produced are useful for analysis,
CC      diagnosis (detection of human (pro)cathepsin W), purification of
CC      (pro)cathepsin W (also for clarifying processing of the precursor and
CC      functional significance of the mature protein), for drug targeting and
CC      for therapeutic use. The present sequence is a human protein shown in the
CC      exemplification of the invention.
CC      Note: No further information about this sequence is given in the
CC      specification.
XX
SQ      Sequence 355 AA;
XX
Query Match 3.6%; Score 104; DB 23; Length 355;
Best Local Similarity 21.7%; Pred. No. 0.88;
Matches 83; Conservative 44; Mismatches 141; Indels 114; Gaps 19;

Qy      18 IFASGLSSSTRSRESQTLASTSGNPRQAVENKTFMERNTLTHHSGIYVDLQDKEV 77
Db      44 IFAHNLAQARLQEDIDGTAIEFGVTPLS-----DLTEEFGLYG----- 83
Qy      78 DGLTYREPAGLCPIWGKHILAQOQDRLPYRNNELEDVPEKEYKQSG--NPLPGFNLN 134
Db      84 ----YRDAAGVPSMGRFISEEPE-----ESVPFCDMRKVAGALSPIDQKCN 130
Qy      135 ---FVTPSGRISPPFMELLEKN-----NIKASTDLGRCAE-----FAKTVAM 176
Db      131 CWMAMAAAGN-----IETLMRISFMDFVDSVYHELDCRCGCGCHGFVMDAFITV-L 183
Qy      177 DKNNKATKRYVPPFYDSKRLCHILVSNQMLEGKKYCSVKGEPPDLTWYCFKPKRSVTE 236
Db      184 NNSGLASEKQIPFGQKRAHRC-----PKTKQK-----AM--IDQFIMLON 224
Qy      237 NHHLI-----YGSAYGVENPDATISKCPNOALRGYFGWKKGRCLDTLDTLTVI--- 287
Db      225 NEHRIAGYLAITYGITYTIN-----MKPLQLYKKGIYKATPTTCDDQLVDHSLVLV 275
Qy      288 -ERVESKACQWKTENDGVASDQHTYPL-TSQASWMDMPLHOSDQPHSGGVGNNG 344
Db      276 GFGSVKSEEGIMAEIVASQS-QQPPHPTPYWILKNSGMQAMEKGYFRLHRS----- 328
Qy      345 FYVYDTTGEGRKALSDV--PD 364
Db      329 ---NTGITKFPPLTARQKPD 346

RESULT 25
AAB21208
ID      AAB21208 standard; Protein; 1200 AA.
XX
AC      AAB21208;
XX
DT      12-JAN-2001 (first entry)
XX
DE      Human HER-2/neu protein.
XX
KW      Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
XX      breast cancer; prostate cancer; ovarian cancer; lung cancer;
XX      colon cancer.
XX
OS      Homo sapiens.
XX
PN      WO200044899-A1.
XX
PD      03-AUG-2000.
XX
PF      28-JAN-2000; 2000WO-US02164.
XX
PR      29-JAN-1999; 99US-0117976.
XX
PA      (CORI-) CORIXA CORP.
XX      (SMIK ) SMITHKLINE BEECHAM.
XX
PI      Cheever MA, Gheysen D;
XX

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DR MPI: 2000-505976/45.
 DR N-PSDB; AAA89736.
 PT HER-2/neu extracellular domain/phosphorylation domain fusion proteins
 PT useful for vaccinating against breast, ovarian, colon, lung and
 PT prostate cancers -
 XX
 PS Disclosure; Fig 15; 128bp; English.
 XX
 CC The present sequence is the human HER-2/neu protein. It is a member
 CC of the tyrosine kinase family of receptor-like glycoproteins and shows
 CC homology to the epidermal growth factor receptor (EGFR). It probably
 CC plays a part in cell growth and/or differentiation. The HER-2/neu
 CC gene is an oncogene. An HER-2/neu fusion protein comprising a
 CC HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation
 CC domain may be used to treat or prevent cancer by eliciting or
 CC enhancing an immune response to the HER-2/neu protein. It may be used
 CC to treat malignancies such as breast, ovarian, colon, lung and
 CC prostate cancers, and may be used as an antigen to vaccinate against
 CC these neoplasias.
 CC
 XX Sequence 1200 AA;
 SQ
 Query Match 3.6%; Score 104; DB 21; Length 1200;
 Best Local Similarity 22.5%; Pred. No. 5; 9;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;
 QY 81 LVREPAAGLPVIGKHEIQPDRLPYRNNFLEVDPEKEKYKSGNPLPG---ENLNFYT 137
 DB 256 LHFNSHGIC-----ELHCPALVTYNTDTFESMPN-----PGRGYTFGASCVT 297
 QY 138 PSGQRISPPMELKSNIKASTDLGRCAEFA---FKTVAMDKNNKATKRYPPVDS 193
 DB 298 AC-----PYNVL-----STDVGSCLVCPHNGEVTAEADGTORCEKSKPCA--- 339
 QY 194 KKRLLCH-----ILVVMQMLEGKXYC-----SVKGEPPDLTWYCFKPRK 232
 DB 340 --RVCCGLGMEHREVRATYSANIOFPAQCKIFGSLALPESFPDPAISNTAPLQPEQL 397
 QY 233 SYTENHLLIYGSAYGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRG 276
 DB 398 QVFETLEITGYLYISAMPDSLPLDSVFQNLQVIRGRILHNGAYSLTLOGLSWLGSR 457
 QY 277 LDVTELTIVIERVESKACQWVTFENDGVASDQ---PHTYPLTSQASNMWMLHOSD 332
 DB 458 L--RELGGSLALIHNTHLCEVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
 QY 333 QPHSGGVGRNYGFYVDTTGE-----GKCALSDQ-----VPDLVSDSAVSYTAAG 379
 DB 499 RPEDDEVGEGLAGHQICARGHCWGPPTQCVNCSQFLRQGECEBGRVLQGLPREVYNAR 558
 QY 380 SLSEETPNFIIPNSVTPPTPTALQCTAD-----KF 412
 DB 559 HCLPCHPE--QOPONGSVTCFGRPE--ADQCAVCAHYKDPFCVAPCSGVXPDLSYMPIMWF 616
 QY 413 PSFGACDVQACRKQKTSQVCGIOGSTVDTADEQNEGSGNALLAGLAVGSVLLALL 472
 DB 617 PDEEGAC--QPC--PINCTHSCVDDDDKGCPEAQR--ASPLTSLTS--AVGILLVVL 667
 QY 473 G 473
 DB 668 G 668
 RESULT 26
 ID ABR25604
 ABP25604 standard; Protein; 1213 AA.
 AC ABR25604;
 XX
 XX 02-JUL-2002 (first entry)
 DT
 XX Streptococcus polypeptide SEQ ID NO 384.

XX
 KM Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 XX (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Frazer C,
 PI Tettelin H;
 DR MPI: 2002-352536/38.
 DR N-PSDB; ABN66235.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 PS Claim 1; Page 3194; 4525bp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus (GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antinflammatory
 CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
 CC antibodies that bind (1) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a
 CC biological sample. (1) is used to determine whether a compound binds to
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (1) may be used to recombinantly produce (1) and may be
 CC used in gene therapy. Antibodies to (1) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 CC
 XX Sequence 1213 AA;
 SQ
 Query Match 3.6%; Score 104; DB 23; Length 1213;
 Best Local Similarity 19.3%; Pred. No. 6;
 Matches 91; Conservative 55; Mismatches 165; Indels 160; Gaps 22;
 QY 115 PTEKEYKSGNPLPGGFNLNFTVPSGRISPPFM-ELLEKN--SNIRK----- 159
 DB 349 PTLKMY-OCGVREMAIEI-----FKFPVREIYAKAYAGVAKAKMVERGDERI 398
 QY 160 -----STDIGRCAEFAFKTVAMDKNNKATKRYPPV-----YDSKK 195
 DB 399 WDLIEVIEKHEPVLLNRAPTLHRLGIDQAFEPVLID--GKALRL-HPLVCEAVNADFDQDQ 455
 QY 196 RICHILVYSQMLEGKXYCSYKGEPPDLTWYCFKPRKS---VTENHLLIYGSAYV----- 247
 DB 456 MAIHV-PLSEEAQAEARLLMLAAE-----HILNPKDKSPVTPSQDWLGNVYLTMEDA 508
 QY 248 GENPDAPFSKCNQALRGVRGVWKKGRCLDYTELTIVIERVESKACQWVTFENDGVA 307
 DB 509 GREGGGMIFKDKDEAVMAYRRNG-----YAHLSRY-----GIA 541
 QY 308 SDQPTVPLTSQASNMWMLPHOSDQPHSGGVGRNYGFYVDTTGEGKCALSDQVPLCLV 367

```

Db      542 VDSMNKP-----WKD-----NQRHK-----INVTVGKLFNDIMP----- 573
Qy      368 SDSAAVSATAGSLSEETPNFIIPSNPSVTPTPTALQCTADKPPDSFGACDVQACKRO 427
Db      574 -----EDLPYLOEPNNANITEGTPDKYFLPEGODIQEVIDRLDIVNPKK 618
Qy      428 KTSVCGG-----QIGTSVDCCTADEONEGCSNTALAGLAVGVLLALLGGCCYPAK 480
Db      619 KN--LGNIIAETFKRFRRTETSAFLDLKDLGYVSTLAGLVGIADIPVI----- 667
Qy      461 RLDNRKG--VQAAHHEHFQSDRGARKKRPSPLMGEAEPSPFDEAEENIEQ 529
Db      668 ---DNKAEIIDAHAHREINKAFRGLMTDDRYVAVTTWRAKALEK 715

```

RESULT 27

AAW01111
ID AAW01111 standard; Protein, 1255 AA.

XX AAW01111;

DT 01-JAN-1997 (first entry)

DE HER-2/neu protein.

KM HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;

KM breast cancer; ovary cancer; colon cancer; lung cancer;

KM prostate cancer; immunisation; tumour; vaccine; vector.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 676..1255

FT /label= Intracellular_domain

FT /note= "Claimed domain, useful for immunisation"

PN W09630514-A1.

PD 03-OCT-1996.

XX 28-MAR-1996; 96WO-US01689.

XX 31-MAR-1995; 95US-0414417.

PA (UNIW) UNIV WASHINGTON.

PI Cheever MA, Disis ML;

XX MPI, 1996-455361/45.

DR N-PSDB; AAT40739.

PT DNA encoding HER-2/neu poly:peptide(s) - used for prevention or

PT treatment of malignancies with which the HER-2/neu oncogene is

PT associated

PS Claim 2; Page 56-61; 71pp; English.

XX Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is

CC the product of the HER-2/neu oncogene (see also AAT40739). The

CC protein is over-expressed in various cancers, including breast,

CC ovarian, colon, lung and prostate. The intracellular domain of the

CC which the oncogene is associated. The polypeptide can be produced

CC in transfected host cells for use in immunisation. Alternatively,

CC animal cells are transfected in vivo or ex vivo with a viral vector

CC that directs expression of the polypeptide.

XX Sequence 1255 AA;

Query Match 3.6%; Score 104; DB 17; Length 1255;

Best Local Similarity 22.5%; Pred. No. 6.3;

Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

```

Qy      81 LYRPBAGLCPIWKGKIEIQDRLPYRNFLFEDVPTKEKYQSGNPLPG--FNLFVY 137
Db      256 LHFHNSGIC-----ELHCPALVTYNTDTRESNPN-----PEGYTGASCVT 297
Qy      138 PSGORISFPFELLEKSNINASTDLGRCAFA---FKTYAMDKNNKATKYRPFVYDS 193
Db      298 AC-----PYNVL-----STDVGSCTLVCPHLHNOEVTABDGTORCEKSRPCA--- 339
Qy      194 KKRLLCH-----ILVSMQLMGKKYC-----SVKGEPPDLTWYCFKPRK 232
Db      340 --RVCYIGCMHLEBRAVTSANTIQERFAGCKKIGSLAFLEPESPDGDASTATAPLQEPQL 397
Qy      233 SVTNNHLYGSAVYGENPDAF--ISKCPN-QALRG-----YRPGV-WKKGRC 276
Db      398 QVFETLEETITGYLISAMPDSLPLDSVFNQLQVIRGRIINHGAVALTLQGLIGLIGLRS 457
Qy      277 LDVTELDVTIERYVESKAQCVKTFPNDGVASDQ---PHTYPLTSQASNDMPHLQSD 332
Db      458 L--RELGSGLALIHNNTHLCFVHT---VWDQLFRNPH-----QLTAN 498
Qy      333 QPHSGGVGRNNGFYVDTGB-----GKCALSDQ-----VPDCLVSDSAASYTAG 379
Db      499 RPEDECVGEGLAGCHQLCARHCWGPPTQCVCVCSQPLRGQCEVBECEVLOGLPREYVNA 558
Qy      380 SLSEETPNFIIPSNPSVTPTPTALQCTAD-----KF 412
Db      559 HCLFCHPE-CQPGQSGYTCFGE-ADQCVAHAHKDPPFCVARGSGVKPPLSYMPWK 616
Qy      413 PDSFGACDVQACKRKQKTSVCGGQIGTSVDCCTADEONEGCSNTALAGLAVGVLLALL 472
Db      617 PDEGAC--QPC---PINCTHSCVDLDKCGPAEQR--ASPLTSIIS--AVGILLVVL 667
Qy      473 G 473
Db      668 G 668

```

RESULT 28

AAW92406
ID AAW92406 standard; Protein, 1255 AA.

XX AAW92406;

DT 21-APR-1999 (first entry)

DE Human HER-2/neu oncogene protein.

KM HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;

KM malignancy; treatment; tumour.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 676..1255

FT /note= "region which elicits immune response"

PN US5869445-A.

PD 09-FEB-1999.

XX 01-APR-1996; 96US-0625101.

XX 01-APR-1996; 96US-0625101.

XX 17-MAR-1993; 93US-0033644.

XX 12-AUG-1993; 93US-0106112.

XX 31-MAR-1995; 95US-0414417.

PA (UNIW) UNIV WASHINGTON.

PI Cheever MA, Disis ML;

XX MPI, 1999-152835/13.

DR N-PSDB; AA01912.

XX Use of HER-2/neu polypeptides - for eliciting an immune response to

PT an HER-2/neu associated malignancy, particularly for treating or

PT preventing tumours

XX

PS Claim 3, Column 31-38; 26pp; English.

XX

CC This sequence represents the human HER-2/neu oncogene protein. A fragment

CC of this protein is used in a method for eliciting or enhancing an immune

CC response to HER-2/neu protein. The polypeptide can stimulate T cells and

CC B cells to produce an immune response to the HER-2/neu protein. The

CC method can be used for immunisation against a malignancy in which the

CC HER-2/neu oncogene is associated and in the treatment of an existing

CC tumour, or to prevent tumour occurrence or recurrence.

XX

SQ Sequence 1255 AA;

Query Match 3.6%; Score 104; DB 20; Length 1255;

Best Local Similarity 22.5%; Pred. No. 6.3; Mismatches 174; Indels 156; Gaps 27;

Matches 108; Conservative 43;

QY 81 LYREPAGLCPWKGKIELOQPDRLPYRNPLEDVPTEKEYKQGNPLPGG---FNLNFVT 137

DB 256 LHFHNSGIC-----ELHCPALVTYNTDTFESMPN-----PEGRTFGASCVT 297

QY 138 PSGQRISPPMELLEKNKSNITKASTDGRCAEPA---FKTVAMDKNKATKYRPFVYDS 193

DB 298 AC-----PNYVL-----STDVGSCTLVCPPLHNOEVTADGTORCEKSKPCA--- 339

QY 194 KKRLLCH-----ILVSMQMEGKKYC-----SVKGEPPDLTWYCFKPRK 232

DB 340 --RVCTGLGMEHLREVRVAVTSANIOEPACCKIFGSLAFLESFPGDPSNTAPLOPQL 397

QY 233 SVTENHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRG 276

DB 398 QVFETLEITGYLYISAMPDSLPLDSVFONLVIRGRILHNGAYSLTLQGLISWLGDS 457

QY 277 LDYTELTDTVIERVESKACQWKTFENDVASDQ---PHYPLTQSASNDMWLHOSD 332

DB 458 L--RELGSGLALIHNTHLCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498

QY 333 QPHSGGVGRNGYFYVDVTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379

DB 499 RPEDECVGEGSLACHQICARGHCWGPGPTQVCNCSQFLRGQCEVECRVLQGLPREYVNAK 558

QY 380 SLSEETPNFIIPSNPSVTPTPETALQCTAD-----KF 412

DB 559 HCLPCHPE--CQPNQSVTCFGEPE--ADQCVACAHYKDPFCVACPSGVKPDLSYMPIWK 616

QY 413 PDSFACDVQACKRKQKTSVGGQIOGSTVDTADEQNEGCSNTALIAGLAVGVLLALL 472

DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKGCPEAQR--ASPLTITS--AVVGILLVVL 667

QY 473 G 473

DB 668 G 668

RESULT 29

AA021198

ID AAB21198 standard; protein; 1255 AA.

XX

AC AAB21198;

XX

DT 12-JAN-2001 (first entry)

XX

DE Human HER-2/neu protein.

XX

KW Human; HER-2/neu; oncogene; tyrosine kinase; cytosolic; vaccine;

KM breast cancer; prostate cancer; ovarian cancer; lung cancer;

XX colon cancer.

OS Homo sapiens.

XX

PN WO200004899-A1.

XX

PD 03-AUG-2000.

XX

PF 28-JAN-2000; 2000WO-US02164.

XX

PR 29-JAN-1999; 99US-0117976.

XX

PA (CORI-) CORIYA CORP

PA (SMIK) SMITHLINE BEECHAM.

XX

PI Cheever MA, Gheysen D;

XX

DR WPI, 2000-505976/45.

DR N-PSDB; AAA89736.

XX

PT HER-2/neu extracellular domain/phosphorylation domain fusion proteins

PT useful for vaccinating against breast, ovarian, colon, lung and

PT prostate cancers -

XX

PS Claim 52, Fig 7, 128pp; English.

XX

CC The present sequence is the human HER-2/neu protein. It is a member of

CC the tyrosine kinase family of receptor-like glycoproteins and shows

CC homology to the epidermal growth factor receptor (EGFR). It probably

CC plays a part in cell growth and/or differentiation. The HER-2/neu

CC gene is an oncogene. An HER-2/neu fusion protein comprising a

CC HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation

CC domain may be used to treat or prevent cancer by eliciting or

CC enhancing an immune response to the HER-2/neu protein. It may be used

CC to treat malignancies such as breast, ovarian, colon, lung and

CC prostate cancers, and may be used as an antigen to vaccinate against

CC these neoplasias.

XX

SQ Sequence 1255 AA;

Query Match 3.6%; Score 104; DB 21; Length 1255;

Best Local Similarity 22.5%; Pred. No. 6.3; Mismatches 174; Indels 156; Gaps 27;

Matches 108; Conservative 43;

QY 81 LYREPAGLCPWKGKIELOQPDRLPYRNPLEDVPTEKEYKQGNPLPGG---FNLNFVT 137

DB 256 LHFHNSGIC-----ELHCPALVTYNTDTFESMPN-----PEGRTFGASCVT 297

QY 138 PSGQRISPPMELLEKNKSNITKASTDGRCAEPA---FKTVAMDKNKATKYRPFVYDS 193

DB 298 AC-----PNYVL-----STDVGSCTLVCPPLHNOEVTADGTORCEKSKPCA--- 339

QY 194 KKRLLCH-----ILVSMQMEGKKYC-----SVKGEPPDLTWYCFKPRK 232

DB 340 --RVCTGLGMEHLREVRVAVTSANIOEPACCKIFGSLAFLESFPGDPSNTAPLOPQL 397

QY 233 SVTENHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRG 276

DB 398 QVFETLEITGYLYISAMPDSLPLDSVFONLVIRGRILHNGAYSLTLQGLISWLGDS 457

QY 277 LDYTELTDTVIERVESKACQWKTFENDVASDQ---PHYPLTQSASNDMWLHOSD 332

DB 458 L--RELGSGLALIHNTHLCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498

QY 333 QPHSGGVGRNGYFYVDVTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379

DB 499 RPEDECVGEGSLACHQICARGHCWGPGPTQVCNCSQFLRGQCEVECRVLQGLPREYVNAK 558

QY 380 SLSEETPNFIIPSNPSVTPTPETALQCTAD-----KF 412

DB 559 HCLPCHPE--CQPNQSVTCFGEPE--ADQCVACAHYKDPFCVACPSGVKPDLSYMPIWK 616

QY 413 PDSFACDVQACKRKQKTSVGGQIOGSTVDTADEQNEGCSNTALIAGLAVGVLLALL 472

DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKGCPEAQR--ASPLTITS--AVVGILLVVL 667

Qy 473 G 473
 Db 668 G 668
 RESULT 30
 AAY84780
 ID AAY84780 standard; Protein; 1255 AA.
 XX
 AC AAY84780;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Amino acid sequence of the SPLICE erB-2 receptor protein.
 XX
 KM SPLICE erB-2 receptor protein; cell transformation disorder; cancer;
 KM tumor cell proliferation; tissue degeneration; arthropathy;
 KM bone resorption; inflammatory disease; degenerative disorder;
 KM wound healing.
 XX
 OS Homo sapiens.
 XX
 PN WO200020579-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 01-OCT-1999; 99WO-CA00912.
 XX
 PR 02-OCT-1998; 98US-0165192.
 XX
 PA (UYMC-) UNIV MCMASTER.
 PI Muller WJ, Siegel PM;
 XX
 PI WPI; 2000-303768/26.
 DR N-PSDB; AAA14812.
 XX
 PT Nucleic acid encoding an erB-2 receptor protein designated SPLICE
 erB-2, inhibitors of the protein are useful for treatment of cancer -
 XX
 PS Claim 3; Fig 2; 60pp; English.
 XX
 CC The present sequence represents a SPLICE erB-2 receptor protein. The
 CC protein has an in-frame deletion of 16 amino acids, 2 of which are
 CC conserved cysteine residues, compared to the unspliced protein. The
 CC erB-2 polynucleotide is used to construct probes for detecting
 CC disorders of cell transformation such as cancer. Antibodies to the
 CC protein may be used to detect SPLICE erB-2 in a sample. Agents
 CC (e.g. antisense oligonucleotides) which inhibit the expression of
 CC SPLICE erB-2 are useful for reducing tumor cell proliferation and
 CC treating cancer. Substances which stimulate SPLICE erB-2 are useful
 CC for treating conditions involving damaged cells including conditions
 CC in which degeneration of tissue occurs, such as arthropathy, bone
 CC resorption, inflammatory diseases, degenerative disorders of the
 CC central nervous system and wound healing.
 XX
 SQ Sequence 1255 AA;
 Query Match 3.6%; Score 104; DB 21; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 6.3;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;
 Qy 81 LYREBAGLCPIWKGKIHIEQOPDRLPYRNPFEDVPTKEVYQSGNPLFG--FNLNRYT 137
 Db 256 LHPHSGIC-----ELHCPALVYVNDTFESMN-----PEGVYTGASCVT 297
 Qy 138 PSGORISPPMELLEKSNIRASTDLGRCAEFA-----FKTVAMPKNNKATYRYPFYVDS 193
 Db 298 AC-----PYNVL-----STDVGSCTLVCPHNOEVAHBDGTGCEKCSPCA--- 339
 Qy 194 KKRLLCH-----ILVVSQMLMGKKYTC-----SYKGEPPDLTWYCFKPRK 232

Db 340 --RVCYGLGMEHLREVRVATSVANIQEFAGCKKIFGSLAFLPESFDGPASNTAPLQPEQL 397
 Qy 233 SVTENHHLIYGSAYVGENPDFA--ISKCPN-QALRG-----YRFGV-WKKGRC 276
 Db 398 QVEFTLEITGYLYISAMPDPLSLPQNLQVIRGRILHNKGVSLTLOGIGISMLGRS 457
 Qy 277 LDYTELDTVILERVESKAQCWKTFENDGVAADQ-----PHTYPLTSQAAMNDMPHLQSD 332
 Db 458 L-RELQSGLALIHNNHLCFVHT-----VPWDLQFNPNH-----QAL-----LHTAN 498
 Qy 333 QPHSGVGRNRYGFYVUTTGE-----GKCALSDQ-----VPDCLVSDSAVSYRAAG 379
 Db 499 RPEDECVEGLACHQLARCGHCGPGPTQCVNCSQFLRGQECVECECVLQGLPREYVNA 558
 Qy 380 SLSEETNFIIPSNVSTPPTPETALQCTAD-----KFA 412
 Db 559 HCLPCHPE-COPONGSYTCGFE-ADCCVACAHKDPFCVAPRSPGVKPLSYMPWKF 616
 Qy 413 PDSFGACDVQACKRQKTSVCGGQIOSTSVDTADEQNECGSNTALAGLAVGVLLALL 472
 Db 617 PDEEGAC--QPC---PINCCHSCVDLDDKCGPAEQR--ASPLTSIIS--AVVGILIVVL 667
 Qy 473 G 473
 Db 668 G 668
 RESULT 31
 AAB85458
 ID AAB85458 standard; Protein; 1255 AA.
 XX
 AC AAB85458;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human HER-2/neu protein.
 XX
 KM Antigen-presenting cell; immunogenic; immune response; HER-2/neu;
 KM oncogene; cancer; cytostatic; vaccine; p185; c-erbB2.
 XX
 OS Homo sapiens.
 XX
 PN WO200153463-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 19-JAN-2001; 2001WO-US01850.
 XX
 PR 21-JAN-2000; 2000US-0177545.
 XX
 PA (CORI-) CORIAX CORP.
 PI Cheever MA, Hand-Zimmermann S;
 XX
 PI WPI; 2001-476112/51.
 DR N-PSDB; AAB23392.
 XX
 PT New antigen-presenting cells, useful as vaccines for eliciting or
 PT enhancing an immune response to HER-2/neu protein, particularly useful
 PT for treating or preventing cancer, e.g. breast cancer -
 XX
 PS Claim 2; Page 41-46; 49pp; English.
 XX
 CC The invention provides an isolated antigen-presenting cell, which
 CC expresses at least an immunogenic portion of a polypeptide that produces
 CC an immune response to HER-2/neu protein. The antigen-presenting cells are
 CC useful as vaccines for eliciting or enhancing an immune response to
 CC HER-2/neu protein, particularly in treating or preventing malignancies in
 CC which the HER-2/neu oncogene is associated. Specifically, these are
 CC useful for treating or preventing cancer, e.g. breast cancer, ovarian,
 CC colon, lung or prostate cancers. The present sequence represents
 CC the human HER-2/neu protein (also known as p185 or c-erbB2).

Db 668 G 668

RESULT 33
AAE24067
ID AAE24067 standard; Protein; 1255 AA.

XX AAE24067;
AC AAE24067;
XX 23-SEP-2002 (first entry)
XX
XX Human Her-2 protein.
DE Human Her-2 protein.
XX Human; Her-2; epidermal growth factor receptor 2; infection; cancer;
KW hyperproliferative disorder; prophylaxis; inflammation; antisense;
KW tumour; gene therapy; phosphorothioate backbone.
XX Homo sapiens.
OS
XX WO200222636-A1.
PN
XX 21-MAR-2002.
PD
XX 12-SEP-2001; 2001WO-US28572.
PE
XX 15-SEP-2000; 2000US-0663834.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Bennett CF, Cowseert LM;
PI
XX WPI; 2002-471192/50.
DR
XX N-PSDB; AAD38904.
DR

Novel antisense oligonucleotide which modulates the expression of Human Epidermal Growth Factor receptor, Her2, is useful for treating tumors

PT Inflammation or to prevent infection in humans -
PT
XX Example 13; Page 95-107; 116pp; English.

PS The invention relates to antisense compounds targeted to a nucleic
XX acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2)
CC that specifically hybridises with and inhibits the expression of Her2.
CC Antisense compounds of the invention are used for treating diseases or
CC conditions associated with Her2 such as hyperproliferative disorders
CC e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary,
CC neural or cardiac cancer. They are also useful prophylactically e.g.
CC to prevent or delay infection, inflammation and tumour formation. The
CC invention is also used in gene therapy. The present sequence is human
CC Her-2 protein.
XX

Sequence 1255 AA;
SQ

Query Match 3.6%; Score 104; DB 23; Length 1255;
Best Local Similarity 22.5%; Pred. No. 6.3;
Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

QY 81 LYREBAGCPITWKGKIEIQPDRLEPYRNNFLEDVPTKEKYKSGNPLDGG--FPLNAYVT 137
DB 256 LHPNHSGLIC-----ELHCPALVYNTDTFESMBN-----DEGRYTFGASCVT 297

QY 138 PSQGRISPPMELLEKNINIKASTDLGRCAEFA-----FKTVAMDKNKATKYRYFVYDS 193
DB 298 AC-----PYNYL-----STDVGSCTLVCPHNOBVAHEDTQRCCKSKCA--- 339

QY 194 KKRLLCH-----ILVYSQWLMGKKYC-----SVKGEPPDLTWYCFKPRK 232
DB 340 --RVCYGAGMEHLEBRAVATSNIOEFAGCKKIFGSLAFLPESFGDPASNTAPLQPRQL 397

QY 233 SVTEHHLLIYGSAVYGENPDAF--ISKCPN-QALRG-----YRGRV-WKKRC 276
DB 398 QVFTELEETIGLYLISAMPDLSPLDSVFNQNTQVIRGRILHNGAVSLTQGLGISWLGURS 457

QY 277 LDYTELDTVLIERVESKAQCWVKTFENDGVASDQ-----PATYPLTSGASNDMPHLQSD 332
DB 458 L-RELGSGLALIHNNTHLCFVHT-----VPMDOLEFRNP-----QLT-----LHTAN 498

QY 333 QPHSGGVARNGFYVDTTGE-----GKCLASDQ-----VPDCLVSDAANSYTAAG 379
DB 499 RPEDECVGEGLACHQLCARGHCWGPPTQCVNCSQFLNGDCEVBCRYLQGLPREYVNA 558

QY 380 SLSEETPNFIIIPSNPSVTPTPTALQCTAD-----K 412
DB 559 HCLPCHPE-CQPOGSGVTCFGE-ADQCVACAHYKDPFCVARGSGVCPDLSTYPIKPF 616

QY 413 PDSFGACDVOACKKQKTSQVGGQIQSTSVDPCTADEONEGSGNTALLIAGLVALLALL 472
DB 617 PDEGAC--QPC---PINCSTSCVDLDDKGCPRQR--ASPLTSLIS--AVVGLLVVVL 667

QY 473 G 473
DB 668 G 668

RESULT 34
AAE20479
ID AAE20479 standard; Protein; 1255 AA.

XX AAE20479;
AC AAE20479;
XX 01-JUL-2002 (first entry)
DT
XX Human Her-2/neu protein.
DE Human Her-2/neu protein.
XX Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
KW human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Region 1021..1030
FT /note="Naturally processed HLA-B44-restricted epitope"
XX

XX WO200214503-A2.
XX 21-FEB-2002.
XX 14-AUG-2001; 2001WO-USA1733.
XX 14-AUG-2000; 2000US-225152P.
XX 28-SEP-2000; 2000US-236428P.
XX 21-FEB-2001; 2001US-270520P.
XX (CORI-) CORIXA CORP.
XX Hand-zimmermann S, Cheever WA, Foy TM, Lodes MJ, Kalos MD;
XX Mcneill PD, Vedvick TS;
XX WPI; 2002-280758/32.
XX N-PSDB; AAD32743.
XX

Novel isolated Her-2/Neu polypeptide composition useful for therapy,
PT prevention and diagnosis of cancer, preferably breast cancer -
PT
XX Disclosure; Page 114-117; 129pp; English.

PS The invention relates to an isolated Her-2/Neu polypeptide composition
XX effective for eliciting an immune response. The invention is useful for
XX eliciting an immune response in a patient, where the patient is human
XX leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.
XX The composition is useful for the therapy and diagnosis of cancer.
XX preferably breast cancer, in pharmaceutical compositions, e.g., vaccine
XX and other compositions for the diagnosis, prevention and treatment of
XX human malignancies, for stimulating and/or expanding T cells specific for
XX Her-2/Neu polypeptide and for inhibiting the development of cancer in a
XX patient. The invention is useful for stimulating a T cell response in a

CC human patient, as probe or primer for nucleic acid hybridisation, to
 CC selectively form duplex molecules with complementary stretches of the
 CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full
 CC length gene from a suitable library, and to direct expression of a
 CC polypeptide in appropriate host cells. The composition is useful in
 CC prophylactic or therapeutic applications and for the treatment of cancer,
 CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-
 CC associated malignancies. The invention is useful in gene therapy. The
 CC present sequence is human Her-2/neu protein.

XX Sequence 1255 AA;

Query Match 3.6%; Score 104; DB 23; Length 1255;

Best Local Similarity 22.5%; Pred. No. 6.3; Mismatches 174; Indels 156; Gaps 27;

Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

QY 81 LVRBPAGLCPIWKGKHEIQOQDRLPYRNNFLDVPTEKEYKOSGNPLPGG---FNLNFT 137
 DB 256 LHPNHSGLC-----ELHCPALVTYNTDTPESMPN-----PEGRTFGASCVT 297
 QY 138 PEGQRISSPPMELLEKNISIKASTDLGRCABFA---FKTVAMDKNNKATKRYRPFYVDS 193
 DB 298 AC-----PYNVL-----STDVGSCTTLCPLHNOEVTADGTQCEKSKPCA--- 339
 QY 194 KKRLLCH-----ILVSMQMEGKKYC-----SVKGEPPDLTWYCFKPRK 232
 DB 340 --RVCTGLGMEHLREVRVAVTSANIQEPAGCKKIFGSLAFPSFGDDPSNTAPLOPBL 397
 QY 233 SVTENHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
 DB 398 QVFETLEITGLYLIASWPDSLPDLISVFONLQVIRGRILHNGAYSLTGLGISMGLRS 457
 QY 277 LVTTEITLTVIERVESKACQWKTENDGVASDQ---PHTYPLTSQASMNWMLPHQSD 332
 DB 458 L--RELGSGLALIHNTLHLCFVHT-----VPMQDLFRNH-----QAL-----LHTEN 498
 QY 333 QHSGSGVGNNGYVYDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAG 379
 DB 499 RREDECEVGGGLACHQLCANHGCKGPPPTQVNCQPLRBOECVEECRVLQGLPREVYNAK 558
 QY 380 SLSEETPNFIIIPSNPSVTPTPTETALQCTAD-----KF 412
 DB 559 HCLPCHRE--CQPNQSVTCEGPE-AQCVCAAHYKDPFCVAPCPSPGVKPDLSYMPIMWF 616
 QY 413 PPSFGACDVQACKRQKTCVGGIOGSTVDCIADBEONEGSGNTALAGLAVGVLLALL 472
 DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKGCAPABOR--ASPLTSIIS--AVVGILLVVL 667
 QY 473 G 473
 DB 668 G 668

RESULT 35

AAMS1143 AAMS1143 standard; Protein; 1255 AA.

XX AC AAMS1143;

XX DT 17-JUN-2002 (first entry)

XX DE Human Her-2/neu oncogene-encoded p185 glycoprotein.

XX KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;

XX KM tyrosine kinase; receptor; C-erbB2; gene therapy.

XX OS Homo sapiens.

XX FH key Location/Qualifiers

FT Domain 1..653 /note= "extracellular domain"

FT Domain 676..1255 /note= "intracellular domain"

FT Domain 990..1255 /note= "phosphorylation domain"

XX WO200212341-A2.

XX 14-FEB-2002.

XX 03-AUG-2001; 2001WO-US24283.

XX 03-AUG-2000; 2000US-0632507.

XX (CORI-) CORIXA CORP.

XX (SMIK) SMITHLINE BECHAM BIOLOGICALS.

XX Cheever MA, Gheysen D;

XX WPI; 2002-241743/29.

XX N-PSDB; ABA92250.

XX Her-2/neu fusion protein for treating or preventing cancer by eliciting

XX or enhancing an immune response to the protein, has Her-2/neu

XX extracellular domain fused to Her-2/neu intracellular or

XX phosphorylation domain

XX Claim 68; Fig 7; 141pp; English.

XX The present sequence is that of human Her-2/neu (p185 glycoprotein

XX or c-erbB2), an oncogenic self-protein and target for anti-cancer

XX vaccines. The Her-2/neu gene is amplified and p185 is overexpressed

XX in a variety of cancers, including breast, ovarian, colon, lung and

XX prostate cancer. Her-2/neu is a member of the tyrosine kinase

XX family of receptor-like glycoproteins. It comprises an extracellular

XX domain with homology to the epidermal growth factor receptor

XX (EGFR), a highly hydrophobic transmembrane domain and a C-terminal

XX intracellular domain that also shows homology to EGFR. Its

XX overexpression correlates with a poor prognosis in breast and

XX ovarian cancers. The invention provides Her-2/neu fusion

XX proteins, nucleic acids encoding them, viral vectors, and vaccines

XX comprising the fusion proteins or nucleic acid molecules. In

XX preferred fusion proteins, the extracellular domain of a Her-2/neu

XX protein is fused to a Her-2/neu intracellular domain or

XX phosphorylation domain (or its DeltaCD fragment). An immune

XX response to Her-2/neu protein is elicited or enhanced by

XX administering the fusion protein in the form of a vaccine, or by

XX transfecting cells of an animal ex vivo with a nucleic acid

XX encoding the fusion protein, and delivering the transfected cells

XX to the animal. The fusion proteins, nucleic acids, and isolated

XX specific T-cells are useful for inhibiting the development of a

XX SQ Sequence 1255 AA;

Query Match 3.6%; Score 104; DB 23; Length 1255;

Best Local Similarity 22.5%; Pred. No. 6.3; Mismatches 174; Indels 156; Gaps 27;

Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

QY 81 LVRBPAGLCPIWKGKHEIQOQDRLPYRNNFLDVPTEKEYKOSGNPLPGG---FNLNFT 137
 DB 256 LHPNHSGLC-----ELHCPALVTYNTDTPESMPN-----PEGRTFGASCVT 297
 QY 138 PEGQRISSPPMELLEKNISIKASTDLGRCABFA---FKTVAMDKNNKATKRYRPFYVDS 193
 DB 298 AC-----PYNVL-----STDVGSCTTLCPLHNOEVTADGTQCEKSKPCA--- 339
 QY 194 KKRLLCH-----ILVSMQMEGKKYC-----SVKGEPPDLTWYCFKPRK 232
 DB 340 --RVCTGLGMEHLREVRVAVTSANIQEPAGCKKIFGSLAFPSFGDDPSNTAPLOPBL 397
 QY 233 SVTENHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276

Db 398 QVPELTLEETGYLYXISAWDSDLPSLPONLOYIRGLIHNGVLSLTGLGISTWGLRS 457

QY 277 LDYBELTDTVIERVESKCAQWKTFFENDVASDQ---PHTYPLTSQASYNNDWPLHQSD 332

Db 458 L--RELGGSLALIHNTHTCFVHT-----VPMQLFRNPH-----QAL-----LHTAN 498

QY 333 QPHSGGVGNNGFYVYDVTGE-----GKCALSDQ-----VPDCLVSDAAVSYTAAG 379

Db 499 RDEDEGVGGGLCAHQLCARGHCMGPPPTQCINCSQFLRGQECYBRCRVLQGLFREYVNAK 558

QY 380 SISETPNFTIPSNPSVTPPTPETAQCTAD-----KF 412

Db 559 HCLPCHPE--CQPNQNGSVTCFGRPE--AQCVACAHYKDPFCVAPCPSGVKEDLSYMPIWK 616

QY 413 PDSFGADVQACRKRQTKSCVGGQIGTSTVDCHTDEONCGSNATLAIAGLAVGVLTLAL 472

Db 617 PRBBGAC--QPC---PINCTHSGVDDDDKDCGRPAQR--ASPLTSITS--AVVGILVVVL 667

QY 473 G 473

Db 668 G 668

RESULT 36

AAU77114 standard; Protein; 1255 AA.
AAU77114;
AAU77114;
05-JUN-2002 (first entry)
Human Her-2/neu polypeptide.
Human; Her-2/neu; cytosolic; haematological malignancy; CML;
acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
Homo sapiens.
MO200213847-A2.
21-FEB-2002.
13-AUG-2001; 2001WO-US25408.
14-AUG-2000; 2000US-0638280.
28-SEP-2000; 2000US-0675904.
(CORI-) CORIXA CORP.
Gaiger A, Cheever MA, Hand-zimmermann S;
WPI; 2002-280741/32.
N-PSDB; ABR10730.
Inhibiting haematological malignancy development by administering
polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide
encoding the polypeptide, or antigen presenting cells expressing the
polypeptide -
Disclosure; Page 71-74; 74pp; English.

Seq	Sequence	1255 AA;	3.6%;	Score 104;	DB 23;	Length 1255;
Query Match	Beat Local Similarity	22.5%;	Pred. No. 6.3;			
Matches 108;	Conservative	43;	Mismatches 174;	Indels 156;	Gaps 27	
QY	81	LYRPAGICLPWIGKHIELOPDRLEPYRNFFLEDPTEKEYKOSGNPLDGG--FLNRYNT	137			
DB	256	LHFNHSIGIC-----ELHCPALTYLNTDTEFSMEN-----PEGRTYFASCVT	297			
QY	138	PSGORISPFMBLEKXSNIKASTDLCRCAPFA-----PKTVAMDKNATKYRYPFYVDL	193			
DB	298	AC-----PYNLY-----SIDVSGCTLYCPLHNOEVTIAEDGTQCEKSKFCA---	339			
QY	194	KKRLLCH-----ILVYSQMLEGKKYC-----SVKGEPPDLTWYCFKPRK	232			
DB	340	--RVCYGIGMEHELEVRVAVTSANIQEFAGCKKIFCSLAFLPESPFGDBASNTAPLQPBQL	397			
QY	223	SVTEHHILYISAYVGENPDAF--ISKPRN-QALRG-----YRGRV-WKKGRG	276			
DB	398	QVFLELEBITLYLVIASMPDPLPDLISVQNIQVIRGILHNGAVSLTLOGIGISWLGURS	457			
QY	277	LDYTELFTVLEIERYSSKQCKWKTFFENDGVASDQ-----PHYTYPLTQASANDMWPLHOSD	332			
DB	458	L--RELSGGLALIHNTILCFVHT-----VEMDOLFRRPH-----QAL-----LHRTAN	498			
QY	333	QPHSGGVGRNYGYFYVDITGE-----GKCALSDQ-----VPDCLVSDSAASYTAAG	379			
DB	499	RPEDECVGEGLACHQLCARGHCMWPGPTQCVCNCSQFLRGQECVECECVLQGLPREYVNAK	558			
QY	380	SLSEETPFIILPSNPSVTPFPPTPEALQCTAD-----KFL	412			
DB	559	HCLPCHPE-COPQNGSVTCFGE--ADQCVAAAHYKDPFCVAKCPGSKVKPDLSTWPIKFL	616			
QY	413	PDFSGACVQACKROKTSYVCGGOIQSTSVSDCTADQNEKSGSNTALLIAGLVGVLLALL	472			
DB	617	PDEBSAC--QC--PINCHTSVCVDLDDKGPABGR--ASPLTISIS--AVGILLVVVL	667			
QY	473	G 473				
DB	668	G 668				

RESULT 37

AAK39568	
ID	AAK39568 standard; Protein; 1433 AA.
XX	
AC	AAK39568;
XX	
DT	25-MAR-2003 (updated)
DT	07-FEB-1994 (first entry)
XX	
DE	Sequence of c-erbB-2 tumour antigen.
XX	
KW	Tumour antigen; c-erbB-2; glycoprotein.
XX	
OS	Homo sapiens.
XX	
PN	W09316185-A2.
XX	
PD	19-AUG-1993.
XX	
PF	05-FEB-1993; 93WO-US01055.
XX	
PR	06-FEB-1992; 92US-0831967.
XX	
PA	(CETU) CETUS ONCOLOGY CORP.
XX	
PI	(CREA-) CREATIVE BIOMOLECULES INC.
XX	
XX	Houston LU, Huston JS, Oppermann H, Ring DB;
DR	WP1; 1993-272889/34.
DR	N-PSDB; AAO46083.

XX New single chain Fv polypeptide binding to C-erbB-2 tumour
 PT antigen - for imaging or treating breast or ovarian cancer etc.
 XX
 XX Disclosure; pages 48-54; 87pp; English.
 PS
 CC c-erbB-2 refers to a protein antigen expressed on the surface of
 CC tumour cells, such as breast and ovarian tumour cells, which is an
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
 CC pt. of about 5.3 (see AA046083, AA839583). X in AA839583 represents
 CC the location of a stop codon in AA046083.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 1433 AA;
 SQ
 Query Match 3.6%; Score 104; DB 14; Length 1433;
 Best Local Similarity 21.3%; Pred. No. 7.8;
 Matches 103; Conservative 47; Mismatches 173; Indels 160; Gaps 26;
 QY 81 LYREFAGLCPIWGKHI ELQPPRLPRNNFLDVPREKYYKSGNPLPGG---FNLNPFY 137
 DB 256 LHFHNSGIC-----ELHCPALVTYNTDTPESMPN-----PEGRTYFGASCVT 297
 QY 138 PEGORISPEPMELLENKSNIKASTDLGRCAEFA---FKTVAMDKNNKATKYRPFVYDS 193
 DB 298 AC-----FNYVL-----STDVGSCTLVCPILHNGSVTAEDGTQREKSKPCA--- 339
 QY 194 KRLDCH-----LLYVSQMLMEGKCYC-----SVKGEPPDLTWYCFKPKK 232
 DB 340 --RVCCGLGMEHLREVRAVTSANIOEFACCKRI FGSIAFLPESFDODPASNAPLOPEHL 397
 QY 233 SVYENHHLIYGSAYVGENDAF--ISKCN--CALRGY-----RFGWKKGRCIDYTELT- 283
 DB 398 QVFETLEOITGYLYISAMPDLSVFNLOVIRKRIIHNGAYSLTGLGISTWGLRS 457
 QY 284 -----DVIYERESKAQCQWVTFFENDGVAADQPTTYPLTSGASWMDWPLHQ 330
 DB 456 LRELSGGLALIHNNHTLSFVHYTP--WDOLFNN-----PH-----QAL-----LHT 496
 QY 331 SDOPHSGGVGRNYGYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTA 377
 DB 497 ANRPEDECVGEGGLACHQLCARGHCWGPPTQCVNCSQFLRGQECVECHVLOGLPREYVN 556
 QY 378 ASSLSEPTNFIIIPNSVSTPPTPTALQCTAD----- 410
 DB 557 ASHCILPCHE--CQPOGSVTCFGE--ADQCVACAHYKPPFCVACRPSGVKDLSTMPWT 614
 QY 411 KPPDSFGACDVQACKRKQTSQVGGQIQSTSVDTADEQNEGCSNTALLIAGLAVGVLLTA 470
 DB 615 KPPDEEGAC--QPC---PINCHTSCVDLDDKGCAPAEQR--ASPLTSIIS--AVVGLIIV 665
 QY 471 LIG 473
 DB 666 VLG 668
 XX
 XX RESULT 38
 XX AAB53307
 XX ID AAB53307 standard; Protein; 365 AA.
 XX
 XX AAB53307;
 XX
 XX 09-MAR-2001 (first entry)
 XX
 XX Human colon cancer antigen protein sequence SEQ ID NO:847.
 XX
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytotoxic; cardioactive; neuroprotective; vulnerary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW neoplastic; anti-infective; antibacterial; gene therapy; wound;
 KW neutral disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.

XX
 OS Homo sapiens.
 XX
 XX WO20005351-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 08-MAR-2000; 2000WO-US05883.
 XX
 XX 12-MAR-1999; 99US-0124270.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Ruben SM;
 XX
 XX WPI, 2000-587534/55;
 XX N-PSDB; AAC98064.
 XX
 XX Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -
 PS Claim 11; Page 1395-1396; 2104pp; English.
 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytoskeletal, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnerary, nephrotoxic, anti-infective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies for the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 365 AA;
 SQ
 Query Match 3.5%; Score 103.5; DB 21; Length 365;
 Best Local Similarity 19.7%; Pred. No. 1;
 Matches 93; Conservative 48; Mismatches 121; Indels 211; Gaps 22;
 QY 101 PDRLEPYNRNFEDVETEKE---YKQGNP-----LFG---GFNLNFTPSGORIS-P 145
 DB 6 FGGCPWVLP.SLPDQTDLDRPGRSRTGRPDAAAMELPGLCGALLGFLCLSGIAVEVK 65
 QY 146 FPMELLEKNKSNIKASTDLGRCAEFAFKTVAMDKNNKATKYRPFVYDSKKLCHILYISM 205
 DB 66 VTEPL-----STPLGKTAELT-----C----- 83
 QY 206 QLMGKKTCSYKGEPPDLTWYCFKPKSVTENHHLIYGSAYVGENDAFISKCPNALRG 265
 DB 84 -----TSTSVGDSFALEMSFGQPKRPISSHPLTYT-----NG 118
 QY 266 YRFGWKKGRCLDYTELDTYIERYESKAQCQWVTFFENDGVAADQPTTYPLTSGASNDW 325
 DB 119 HLVPYSGSKSRVSLQNPPTV-----GVA-----TLKLTLD----- 148
 QY 326 WPLHSDQPHSGGVGRNYGYVDTTGEKCALSDQVDPDCLVSDSAVSYTAAGLSSET 385
 DB 149 --VHPSD-----TGYTLQVNNP--DPYTNGLGLNLTIV----- 179
 QY 386 PNFIFIPSNP-----SVTPPTETALQCTADK-----FPDSFGACDVQACKR 426
 DB 180 --LVPSNPPLCGSQSGQTIVGSGTALRCSSSEGAAPKYVNWRLGFFPPSPGSMWQ----- 233
 QY 427 OKTSCVGGQIQSTSVDTCTAD-----EQNEGCS-----NTALLIAGLAVG--G 465

Db 234 ---DEVSGQLITLNLSTSSGTYRCVATNMQGSASCELTLSTVTEPSQGRVAGALIGVLG 290
Qy 466 VLLIALLGGGCGYFAKRLDRNKGVQAHAHHEHFQSDRGARKRP---SDLMQEA 515
Db 291 VLLLSV-----AAFCVRFQKERKKPKETYGSGDLRADA 325

RESULT 39
AAG75613
ID AAG75613 standard; Protein; 365 AA.
XX
AC AAG75613;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6177.
XX
KM Human; colon cancer; colon cancer antigen; diagnosis; detection;
KM Colorectal carcinoma; chromosome 11.
XX
OS Homo sapiens.
XX
PN MO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR N-PSDB; AAH35018.
XX
PT Nucleic acid encoding 4277 human colon cancer-associated polypeptides,
XX
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 11; Page 7849-7851; 9803PP; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patient's own production of P.
CC Additionally, N may be used to produce the colon cancer-associated P,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 66 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 365 AA;

Query Match 3.5%; Score 103.5; DB 22; Length 365;
Best Local Similarity 19.7%; Pred. No. 1;
Matches 93; Conservative 48; Mismatches 121; Indels 211; Gaps 22;

Qy 101 PDRLPYRNPFLEDPTEKE-----YKSGNP-----LPG-----GFNLNFVTPSGQRIS-P 145
Db 6 PGCGPWLPSLPDTOTDLDRPPGSRGSRPDAAAEPLGPFLLCGLLGLSLAVEVK 65

Qy 146 FPMELLEKNKNIKASTDLGRCAEPAFTVAMDKNKATKYRPPVYDSKKRLCHILYVSM 205
Db 66 VPTPL-----STPLGKTABL-----C----- 83
Qy 206 QLMGKKYCYSVKPEPDLTWCFKPKRSVTENHLLITGSAYVGENPDPAFISKCPNALRG 265
Db 84 -----TYSYTSVGDSPFALEWSFVQPKRPISESHPILYFT-----NG 118
Qy 266 YRFGVWKGRCLDVTDLDTYIERVESKAQCQVWTFENDDGVASDPHTYPLTSGASNDW 325
Db 119 HLTPYTSKSKKVSLLQNPPTV-----GVA-----TLKLT----- 148
Qy 326 WPLHQSDQPHSGGVGRNYGVYVDVTGEGKALSDQVDPDCLVSDAAVSYTAAGSLSEBT 385
Db 149 --VHPSD-----TGYLCQVNP--PDFYTNGLGLNLIV----- 179
Qy 386 PNFIIPSNP-----SVTPPEPTALQCTADK-----PDSFGACVQACKR 426
Db 180 --LVPPSNPLCSOGQTSVGSSTALRCSSSEGAEPYVMVRLGTFPPSPGSMVQ----- 233
Qy 427 QKTSVGGQIQSTSDCTAD-----BQNEGS-----NTALINGLAVG---G 465
Db 234 ---DEVSGQLITLNLSTSSGTYRCVATNMQGSASCELTLSTVTEPSQGRVAGALIGVLG 290
Qy 466 VLLIALLGGGCGYFAKRLDRNKGVQAHAHHEHFQSDRGARKRP---SDLMQEA 515
Db 291 VLLLSV-----AAFCVRFQKERKKPKETYGSGDLRADA 325

RESULT 40
AAU98923
ID AAU98923 standard; Protein; 1223 AA.
XX
AC AAU98923;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human breast cancer antigen, Her2 variant.
XX
KM Human; Her2; cytostatic; antiviral; immunostimulant;
KM cell-mediated immune response; tumour; breast cancer;
KM virus infection; prostate cancer; colorectal cancer; pancreatic cancer;
KM lymphoma; leukaemia; hepatocellular carcinoma; hepatitis; herpesvirus;
KM human immunodeficiency virus; HIV; flavivirus; pestivirus.
XX
OS Homo sapiens.
XX
PN MO200240059-A2.
XX
PD 23-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US45626.
XX
PR 01-NOV-2000; 2000US-0704232.
XX
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
PA (MINC/) MINCHEFF M S.
PA (LOUK/) LOUKINOV D I.
PA (ZOUB/) ZOUBAK S.
XX
PI Mincheff MS, Loukinov DI, Zoubak S;
XX
DR WPI; 2002-527524/56.
DR N-PSDB; ABR66207.
XX
PT Inducing a cell-mediated immune response against a target antigen,
PT reducing undesired cells and stimulating presentation of an antigen by
PT a cell, comprises administering a polynucleotide encoding a variant of
PT an antigen -
XX
PS Claim 21; Page 134-138; 146PP; English.
XX
CC The invention relates to a method of inducing a cell-mediated immune

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OM protein - protein search, using sw model

Run on: October 2, 2003, 16:00:20 ; Search time 43 Seconds
(without alignments)
1209.936 Million cell updates/sec

Title: US-10-039-770a-1

Perfect score: 541
Sequence: 1 MGLVGVQLLVADCTIFA.....EAEENIDGERTHWVEGDY 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	1.7	387	2	B83679
2	9	1.7	401	2	B87354
3	9	1.7	923	2	G90656
4	9	1.7	923	2	G85507
5	8	1.5	130	2	S52116
6	8	1.5	230	2	D70718
7	8	1.5	287	2	A60643
8	8	1.5	383	2	A93503
9	8	1.5	396	2	A91903
10	8	1.5	463	2	AH0189
11	8	1.5	466	2	JO2263
12	8	1.5	480	2	F70785
13	8	1.5	1126	2	T01491
14	8	1.5	1268	2	S52781
15	8	1.5	1348	2	S51656
16	8	1.5	3430	1	GNMVMV
17	8	1.5	3433	1	GNMVMV
18	8	1.5	3434	1	GNMVMV
19	7	1.3	23	2	A60996
20	7	1.3	122	2	T51036
21	7	1.3	133	2	G64863
22	7	1.3	133	2	H90837
23	7	1.3	133	2	A85696
24	7	1.3	141	2	JO1561
25	7	1.3	151	2	AG1972
26	7	1.3	160	2	C70513
27	7	1.3	161	2	F82322
28	7	1.3	169	2	H87591
29	7	1.3	175	2	B83411

30	7	1.3	178	2	AG2369	cytochrome b6/f-co
31	7	1.3	182	2	T16472	hypothetical prote
32	7	1.3	185	2	T36745	probable RNA polym
33	7	1.3	188	2	C81224	conserved hypotnet
34	7	1.3	204	2	D83334	conserved hypotnet
35	7	1.3	206	2	A40305	bilialy glycoprote
36	7	1.3	207	2	C82979	hypothetical prote
37	7	1.3	206	2	F84563	hypothetical prote
38	7	1.3	215	2	JX0244	pyroglutamate1-pepti
39	7	1.3	215	2	S23432	pyroglutamate1-pepti
40	7	1.3	217	2	AG3100	replicative DNA he
41	7	1.3	217	2	A64133	ATP-binding transp
42	7	1.3	218	2	H65023	hypothetical 22.2K
43	7	1.3	218	2	C85891	hydrogenase 4 Fe-S
44	7	1.3	218	2	G91046	hydrogenase 4 Fe-S
45	7	1.3	220	2	D75611	conserved hypotnet
46	7	1.3	220	2	T21730	hypothetical prote
47	7	1.3	224	2	T35897	probable secreted
48	7	1.3	226	2	G70148	ribosomal protein
49	7	1.3	227	2	E25973	pertussis toxin ch
50	7	1.3	234	2	S29000	G protein-coupled
51	7	1.3	234	2	C98186	hypothetical prote
52	7	1.3	235	2	E82106	basal-body rod mod
53	7	1.3	241	2	S53812	BmGAT beta isofor
54	7	1.3	245	2	T15739	hypothetical prote
55	7	1.3	246	2	AF0429	conserved hypotnet
56	7	1.3	247	2	A96932	phosphoserine phos
57	7	1.3	247	2	AC1332	potassium channel
58	7	1.3	247	2	AC1703	potassium channel
59	7	1.3	248	2	T04758	hypothetical prote
60	7	1.3	251	2	T17784	PBCV-1 33kd peptid
61	7	1.3	255	2	AC1293	ABC transporter (A
62	7	1.3	255	2	A11664	ABC transporter (A
63	7	1.3	257	2	S00682	IGF R receptor al
64	7	1.3	258	2	B83044	hypothetical prote
65	7	1.3	264	2	T35056	probable integral
66	7	1.3	267	2	T02616	hypothetical prote
67	7	1.3	269	2	D69996	amino acid ABC tra
68	7	1.3	271	2	F83188	phosphatidate cyti
69	7	1.3	271	2	JC4832	phosphatidate cyti
70	7	1.3	272	2	AD0080	undecaprenol kinas
71	7	1.3	276	1	BVECG	g1g protein - Bsc
72	7	1.3	276	2	C91162	protein of g1p reg
73	7	1.3	276	2	D86008	transcription anti
74	7	1.3	277	2	C97073	transcription anti
75	7	1.3	278	2	A39037	carcinomabryonic a
76	7	1.3	278	2	UC1507	bilialy glycoprote
77	7	1.3	278	2	UC1506	bilialy glycoprote
78	7	1.3	289	2	E69207	conserved hypotnet
79	7	1.3	291	2	AG1170	ABC transporter, p
80	7	1.3	291	2	A11527	ABC transporter, p
81	7	1.3	293	2	B83054	hypothetical prote
82	7	1.3	298	2	G64350	coenzyme F420 hydr
83	7	1.3	305	2	UC4525	nucleic acid-bindi
84	7	1.3	307	2	A36955	translocation prot
85	7	1.3	308	2	D83629	probable permease
86	7	1.3	314	2	F86805	ection transporter
87	7	1.3	315	2	F80165	envelope glycoprot
88	7	1.3	322	2	F84948	NMDH2 dehydrogenas
89	7	1.3	324	2	A44241	clavaminate syntha
90	7	1.3	324	2	S13497	CAMP-binding prote
91	7	1.3	327	2	B69856	oligopeptide trans
92	7	1.3	327	2	S53811	BmGAT beta isofor
93	7	1.3	335	2	S11464	CMBP1 protein - si
94	7	1.3	335	2	A10295	plative vitamin B1
95	7	1.3	338	2	B75285	probable iron ABC
96	7	1.3	341	2	UC1511	bilialy glycoprote
97	7	1.3	341	2	UC1512	bilialy glycoprote
98	7	1.3	344	2	E72173	DDR protein - vari
99	7	1.3	355	2	T52177	root hairless prot
100	7	1.3	372	2	B72579	probable drug resi
101	7	1.3	376	2	S45107	hypothetical prote
102	7	1.3	379	2	T22392	hypothetical prote

103	1.3	387	2	G72506	hypothetical prote	176	1.3	723	1	JN0531	p-aminobenzoic aci
104	1.3	392	2	A82481	probable transcrip	177	1.3	727	1	A38206	procollagen-lysine
105	1.3	399	2	G86872	galactokinase (EC	178	1.3	733	2	D83588	conserved hypotnet
106	1.3	400	2	T45319	hypothetical prote	179	1.3	738	2	T45916	hypothetical prote
107	1.3	401	2	E70646	probable fadE23 pr	180	1.3	741	2	D75500	ATP-dependent ctp
108	1.3	403	2	H69362	succinyl-diaminopi	181	1.3	745	2	T39952	hypothetical prote
109	1.3	405	2	T35370	probable transmemb	182	1.3	755	2	B75346	probable competent
110	1.3	405	2	A12934	chromate transport	183	1.3	773	2	AH2061	hypothetical prote
111	1.3	405	2	B86934	conserved hypotnet	184	1.3	782	2	T48246	ribonuclease II-11
112	1.3	409	2	F98347	probable transport	185	1.3	794	2	E72202	hypothetical prote
113	1.3	412	2	F95394	probable transmemb	186	1.3	800	2	S37387	internalin A precu
114	1.3	417	2	B83357	probable MFS trans	187	1.3	802	1	TVH0P4	conserved hypotnet
115	1.3	417	2	T26295	hypothetical prote	188	1.3	830	2	F83288	hypothetical prote
116	1.3	424	2	S15146	hypothetical prote	189	1.3	839	2	F75518	hypothetical prote
117	1.3	424	2	F83556	hypothetical prote	190	1.3	839	2	T12827	protein-lysine k
118	1.3	426	2	H87507	hypothetical prote	191	1.3	894	1	A41527	hypothetical prote
119	1.3	436	2	G75363	integral membrane	192	1.3	942	2	T19553	outer capsid prote
120	1.3	444	2	D69472	nodulation protein	193	1.3	959	2	B60017	probable coiled co
121	1.3	447	2	T49350	hypothetical prote	194	1.3	968	2	T39908	hypothetical prote
122	1.3	449	2	A1075	inner membrane pro	195	1.3	971	2	T00268	NAD ADP-ribosyltra
123	1.3	449	2	T49125	hypothetical prote	196	1.3	994	2	A47474	hypothetical struc
124	1.3	450	2	G81652	2-amino-4-hydroxy-	197	1.3	1010	2	T41077	hypothetical prote
125	1.3	450	1	MMMSR1	biliary glycoprote	198	1.3	1014	2	T24412	surface antigen B8
126	1.3	458	2	JC1509	biliary glycoprote	199	1.3	1081	2	T31094	glycosidase homolo
127	1.3	459	2	F97937	hypothetical prote	200	1.3	1090	2	AG1749	glycosidase homolo
128	1.3	459	2	H95059	transmembrane prot	201	1.3	1091	2	AF1380	microbial collagen
129	1.3	461	2	A27672	hypothetical gag p	202	1.3	1104	1	A36866	probable pyruvate
130	1.3	462	1	Q0BED4	HHRF4 protein - hu	203	1.3	1174	2	E64888	probable pyruvate
131	1.3	466	2	T07404	probable glucosylt	204	1.3	1174	2	H90878	probable oxidoredu
132	1.3	469	2	D81017	chloride channel p	205	1.3	1174	2	B85740	probable oxidoredu
133	1.3	473	2	A86208	hypothetical prote	206	1.3	1174	2	AH0663	probable pyruvate-
134	1.3	474	2	T36685	probable sodium/pr	207	1.3	1177	2	AG0284	probable pyruvate-
135	1.3	477	2	F87329	hypothetical prote	208	1.3	1187	2	A12044	pyruvate (flavodox
136	1.3	480	2	A82042	xanthine/uracil pe	209	1.3	1191	2	S70963	pyruvate (flavodox
137	1.3	481	2	A26483	bindin precursor -	210	1.3	1197	2	T39613	pyruvate (flavodox
138	1.3	485	2	B40552	NADH2 dehydrogenas	211	1.3	1199	2	S77082	pyruvate-flavodoxi
139	1.3	499	1	DELVN4	multidrug resistanc	212	1.3	1199	2	AD2156	hypothetical prote
140	1.3	503	1	B69532	transcription fact	213	1.3	1202	2	T37867	latent transformin
141	1.3	509	2	A53741	iron (III)-transpo	214	1.3	1251	2	A57293	hypothetical prote
142	1.3	512	2	B83060	NADH dehydrogenase	215	1.3	1526	2	T19473	hypothetical prote
143	1.3	518	2	AG3135	NAD-dependent form	216	1.3	1659	2	H97926	endo-beta-N-acetyl
144	1.3	518	2	E98152	hypothetical prote	217	1.3	1659	2	G95057	complement C3 prec
145	1.3	518	2	F75460	biliary glycoprote	218	1.3	1663	1	C3HU	complement C3 prec
146	1.3	521	2	C15058	biliary glycoprote	219	1.3	1663	1	C3MS	complement C3 prec
147	1.3	521	2	S34338	biliary glycoprote	220	1.3	1663	1	C3RT	complement C3 prec
148	1.3	526	2	UC4101	aspartate ammonia-	221	1.3	1666	1	C3GP	fatty-acid synthas
149	1.3	530	2	D87255	apolipoprotein N-a	222	1.3	1857	1	S01787	probable adhesin h
150	1.3	541	2	D82302	SAR DNA-binding pr	223	1.3	1910	2	AF0394	notch4 - mouse
151	1.3	550	2	T06379	hypothetical prote	224	1.3	1964	2	T09059	probable phosphati
152	1.3	554	2	A11829	protein T7N9.10 (i	225	1.3	2337	2	T40577	tyrocidine synthet
153	1.3	563	2	C86397	cytochrome b6 homo	226	1.3	6486	2	T1076	T-cell receptor al
154	1.3	563	2	S21043	hypothetical prote	227	1.1	12	2	PH1171	T-cell receptor al
155	1.3	570	2	T46911	transport ATP-bind	228	1.1	15	2	S26515	T-cell receptor al
156	1.3	578	2	A13604	nitrate transpor	229	1.1	15	2	PH0806	cytochrome P450 PB
157	1.3	585	2	T51361	nitrate transpor	230	1.1	20	2	A60822	STP5 protein - Str
158	1.3	586	2	PC6006	ecfolding protei	231	1.1	27	2	S42491	intestinal trefol
159	1.3	586	2	UC2407	homothallic switch	232	1.1	28	2	A56356	cytochrome P450mt4
160	1.3	592	2	E70488	cytochrome-c oxida	233	1.1	42	2	A34259	citrate synthase f
161	1.3	600	2	T00759	hypothetical prote	234	1.1	42	2	T46861	hypothetical prote
162	1.3	600	2	G96720	nitrate transpor	235	1.1	44	2	C72270	tm1 protein - mou
163	1.3	600	2	S07638	spore coat protein	236	1.1	44	2	S54144	hypothetical prote
164	1.3	602	2	S71557	pyruvate decarboxy	237	1.1	46	2	C69745	hypothetical prote
165	1.3	606	2	A77429	oligopeptidase ABC	238	1.1	47	2	D81666	hypothetical prote
166	1.3	608	2	S05790	hypothetical prote	239	1.1	48	2	F82414	hypothetical prote
167	1.3	610	2	D83656	auxin response fac	240	1.1	53	2	F84125	hypothetical prote
168	1.3	638	2	T08917	gag polypeptid	241	1.1	54	2	D77342	hypothetical prote
169	1.3	643	1	F0LJLK	hypothetical prote	242	1.1	56	2	B68806	hypothetical prote
170	1.3	647	2	T23814	hypothetical prote	243	1.1	61	2	B61384	Comper's gland muc
171	1.3	658	2	C82512	transketolase (EC	244	1.1	62	2	E84200	hypothetical prote
172	1.3	665	2	E84940	protein W28.1 (Imp	245	1.1	62	2	T23216	hypothetical prote
173	1.3	670	2	S88297	peroxidase (EC 1.1	246	1.1	63	2	F75371	hypothetical prote
174	1.3	690	2	S28222	probable DNA helic	247	1.1	64	2	A47438	lingual epithelial
175	1.3	706	2	S57374		248	1.1	64	2	A56128	lingual antimicrob

249	6	1.1	65	2	A30478	NADH2 dehydrogenas	322	6	1.1	109	2	G64609	hypothetical prote
250	6	1.1	65	2	F89906	hypothetical prote	323	6	1.1	109	2	C83432	conserved hypotnet
251	6	1.1	67	2	S45538	hypothetical prote	324	6	1.1	111	2	S54635	probable membrane
252	6	1.1	71	2	A12988	fibrinase associate	325	6	1.1	111	2	T36386	probable lxr2-like
253	6	1.1	73	2	F70641	hypothetical prote	326	6	1.1	111	2	A13591	hypothetical prote
254	6	1.1	75	2	G69394	H+-transporting At	327	6	1.1	113	2	A57141	ferredoxin 2 (4Fe-4
255	6	1.1	75	2	D82592	hypothetical prote	328	6	1.1	113	2	D84255	hypothetical prote
256	6	1.1	76	2	S61818	M-like protein enn	329	6	1.1	114	2	D83976	cytochrome caa3 ox
257	6	1.1	76	2	A43537	heat-stable antige	330	6	1.1	115	2	T04407	probable phospholi
258	6	1.1	76	2	I53107	CD4 precursor - r	331	6	1.1	115	2	D75434	hypothetical prote
259	6	1.1	77	1	A56903	hypothetical prote	332	6	1.1	116	1	IPAF	insulin precursor
260	6	1.1	79	2	A10052	probable membrane	333	6	1.1	116	2	H83562	conserved hypotnet
261	6	1.1	80	2	S23963	intestinal trefoile	334	6	1.1	117	2	T26752	hypothetical prote
262	6	1.1	80	2	A48996	B cell surface ant	335	6	1.1	117	2	T17315	hypothetical prote
263	6	1.1	81	2	LWSPA	H+-transporting tw	336	6	1.1	118	2	E83556	hypothetical prote
264	6	1.1	81	1	LWRZA	H+-transporting tw	337	6	1.1	119	2	B49905	hypothetical prote
265	6	1.1	81	1	LWZMC	H+-transporting tw	338	6	1.1	119	2	AD0935	protein secretion
266	6	1.1	81	1	LWNTA	H+-transporting tw	339	6	1.1	119	2	T47169	probable membrane
267	6	1.1	81	1	LWMLA	H+-transporting tw	340	6	1.1	120	2	T44554	hypothetical prote
268	6	1.1	81	1	LWPM	H+-transporting tw	341	6	1.1	121	2	AD2578	transcription regu
269	6	1.1	81	2	A29599	H+-transporting tw	342	6	1.1	121	2	C97360	hypothetical prote
270	6	1.1	81	2	A41441	intestinal trefoil	343	6	1.1	122	1	WITAI	alpha-amylase/cryp
271	6	1.1	81	2	S30250	phycocyanin linker	344	6	1.1	122	2	E70764	hypothetical prote
272	6	1.1	82	2	S73167	H+-transporting tw	345	6	1.1	122	2	AE0803	hypothetical prote
273	6	1.1	82	2	S26958	H+-transporting tw	346	6	1.1	122	2	S07364	hypothetical prote
274	6	1.1	82	2	S58349	H+-transporting tw	347	6	1.1	123	2	G72458	seminal vesicle se
275	6	1.1	82	2	T07211	H+-transporting tw	348	6	1.1	124	2	A72629	hypothetical prote
276	6	1.1	82	2	T09628	hypothetical prote	349	6	1.1	126	2	S12988	hypothetical prote
277	6	1.1	83	2	S39516	H+-transporting tw	350	6	1.1	126	2	A55688	brain natriuretic
278	6	1.1	83	2	G70765	hypothetical prote	351	6	1.1	126	2	D95013	natriuretic peptid
279	6	1.1	84	2	E84010	hypothetical prote	352	6	1.1	126	2	E97885	hypothetical prote
280	6	1.1	84	2	S28248	NADH2 dehydrogenas	353	6	1.1	126	2	F81143	hypothetical prote
281	6	1.1	86	2	B96709	hypothetical prote	354	6	1.1	126	2	AD3508	transcription regu
282	6	1.1	86	2	T47355	hypothetical prote	355	6	1.1	127	2	I46269	granulocyte-macrop
283	6	1.1	89	2	C84016	hypothetical prote	356	6	1.1	127	2	E75301	hypothetical prote
284	6	1.1	90	2	UC7395	salmon-type gonado	357	6	1.1	128	2	AB2487	hypothetical prote
285	6	1.1	90	2	AC3735	gonadoliberin prec	358	6	1.1	128	2	S31009	hypothetical prote
286	6	1.1	90	2	I51095	gonadoliberin prec	359	6	1.1	128	2	A81153	gene 64 protein -
287	6	1.1	90	2	G96915	bofa B. subtilis o	360	6	1.1	129	2	H72806	type I restriction
288	6	1.1	91	2	H86701	hypothetical prote	361	6	1.1	129	2	AF0560	probable DNA prima
289	6	1.1	91	2	AC3378	hypothetical prote	362	6	1.1	130	2	AF0560	probable methylate
290	6	1.1	92	1	BVCNP	Sugar fermentation	363	6	1.1	130	2	S31003	gene 58 protein -
291	6	1.1	92	2	C91137	regulatory factor	364	6	1.1	131	2	S46702	hypothetical prote
292	6	1.1	92	2	F85982	Sugar fermentation	365	6	1.1	131	2	S77285	hypothetical prote
293	6	1.1	94	2	S62084	M-like protein ann	366	6	1.1	132	2	F97165	probable vacuolar
294	6	1.1	95	2	A10903	Ner-like regulator	367	6	1.1	133	2	I38653	hypothetical prote
295	6	1.1	96	2	A42799	hypothetical prote	368	6	1.1	133	2	S46688	melanoma antigen M
296	6	1.1	97	1	FETA	ferredoxin [2Fe-2S	369	6	1.1	133	2	AF3232	conjugal transfer
297	6	1.1	97	2	T34765	small hydrophobic	370	6	1.1	133	2	H75386	hypothetical prote
298	6	1.1	98	1	PEFM2	ferredoxin [2Fe-2S	371	6	1.1	133	2	AB2421	glutathione peroxi
299	6	1.1	98	1	PEFM2E	ferredoxin [2Fe-2S	372	6	1.1	134	2	S68899	hypothetical prote
300	6	1.1	98	2	S28199	ferredoxin [2Fe-2S	373	6	1.1	134	2	F97984	hypothetical prote
301	6	1.1	98	2	S28199	dopamine D4 recept	374	6	1.1	135	2	S57892	T cell receptor WI
302	6	1.1	98	2	I54366	glycine-rich prote	375	6	1.1	135	2	A45835	ly6 homolog RK10 p
303	6	1.1	99	2	T03297	lipid transfer pro	376	6	1.1	135	2	F87515	hypothetical prote
304	6	1.1	99	2	A60879	seminal vesicle se	377	6	1.1	136	2	T49378	hypothetical prote
305	6	1.1	99	2	B95115	hypothetical prote	378	6	1.1	137	2	B83234	hypothetical prote
306	6	1.1	101	2	H72211	hypothetical prote	379	6	1.1	138	2	G40605	response regulator
307	6	1.1	102	2	D90203	ATP synthase subun	380	6	1.1	138	2	S24084	envelope protein -
308	6	1.1	102	2	A64845	hypothetical prote	381	6	1.1	138	2	S24073	envelope protein -
309	6	1.1	102	2	H86816	hypothetical prote	382	6	1.1	138	2	S24106	envelope protein -
310	6	1.1	103	2	AF0856	conserved hypotnet	383	6	1.1	138	2	H81258	probable periplasm
311	6	1.1	103	2	S72917	hypothetical prote	384	6	1.1	138	2	C82758	hypothetical prote
312	6	1.1	105	2	C30535	Ig kappa chain v r	385	6	1.1	139	2	A38612	insulin-like growt
313	6	1.1	106	2	P10088	Ig kappa chain v r	386	6	1.1	139	2	H64064	colR protein - Hae
314	6	1.1	106	2	AE1842	multidrug exporter	387	6	1.1	139	2	S43580	C28A5.5 protein -
315	6	1.1	107	2	D82537	ferredoxin XF2601	388	6	1.1	140	2	H71903	hypothetical prote
316	6	1.1	107	2	B83766	hypothetical prote	389	6	1.1	140	2	AH1980	hypothetical prote
317	6	1.1	107	2	P96029	hypothetical prote	390	6	1.1	140	2	AH0085	probable membrane
318	6	1.1	108	2	AB3388	heB protein (limpo	391	6	1.1	141	2	S15145	hypothetical prote
319	6	1.1	109	2	UH0335	T-cell receptor al	392	6	1.1	141	2	E83345	hypothetical prote
320	6	1.1	109	2	C53302	hemf 3'-region hyp	393	6	1.1	141	2	AB3373	hypothetical prote
321	6	1.1	109	2	A10812	probable membrane	394	6	1.1	141	2	I39059	hypothetical prote

395	6	1.1	141	2	S15785	heat-stable antigen
396	1.1	142	2	JT0573	retinoic acid-indu	
397	6	1.1	143	1	FOBOGM	granulocyte-macrop
398	6	1.1	143	2	E30338	DNA transport mach
399	6	1.1	143	2	F84390	hypothetical prote
400	6	1.1	143	2	T36978	probable transpos
401	6	1.1	143	2	AS3045	translocation initia
402	6	1.1	144	1	FOHUGM	granulocyte-macrop
403	6	1.1	144	2	S74059	hypothetical prote
404	6	1.1	144	2	A75369	conserved hypotet
405	6	1.1	144	2	C53045	translocation initia
406	6	1.1	145	2	A32537	T-cell receptor al
407	6	1.1	145	2	F75337	transposase - Dein
408	6	1.1	145	2	D84458	probable translati
409	6	1.1	145	2	T08000	translocation initia
410	6	1.1	146	2	I40443	hypothetical prote
411	6	1.1	147	2	T35696	xylanase A - Strept
412	6	1.1	147	2	B36529	hemoglobin P3 - po
413	6	1.1	147	2	S13157	hypothetical prote
414	6	1.1	147	2	G71282	hypothetical prote
415	6	1.1	147	2	T17958	hypothetical prote
416	6	1.1	150	2	C84371	hypothetical prote
417	6	1.1	150	2	D75347	hypothetical prote
418	6	1.1	152	2	E71645	single-strand bind
419	6	1.1	152	2	G97861	glycine-rich prote
420	6	1.1	152	2	T07858	interleukin-4 prec
421	6	1.1	153	1	A25946	granulocyte-macrop
422	6	1.1	153	1	FQMSGM	hypothetical prote
423	6	1.1	153	2	T09981	tumor related prot
424	6	1.1	154	2	T01983	hypothetical prote
425	6	1.1	154	2	D71071	probable ATPase, c
426	6	1.1	154	2	C71379	probable ATPase, c
427	6	1.1	154	2	F83632	NADH2 dehydrogenas
428	6	1.1	155	2	S59155	hypothetical prote
429	6	1.1	155	2	E97507	conserved hypotet
430	6	1.1	155	2	A12725	hypothetical prote
431	6	1.1	155	2	AEO048	H+-exporting ATPas
432	6	1.1	156	1	JN0456	H+-exporting ATPas
433	6	1.1	156	2	A56680	flagellar protein
434	6	1.1	156	2	AF0222	hypothetical prote
435	6	1.1	156	2	T16066	probable Olfactory
436	6	1.1	157	2	S58020	cholesterol hemolo
437	6	1.1	157	2	AG1312	oleosin 2 - barley
438	6	1.1	158	2	S57779	chemotaxis protein
439	6	1.1	158	2	G87623	hypothetical prote
440	6	1.1	158	2	C71406	probable transcrip
441	6	1.1	158	2	G83438	conserved hypotet
442	6	1.1	158	2	A69178	conserved hypotet
443	6	1.1	158	2	C96005	H+-exporting ATPas
444	6	1.1	159	1	S42878	plastoquinol-plast
445	6	1.1	160	1	A61088	sulfur-rich protei
446	6	1.1	160	2	UC5205	apoptosis inducer
447	6	1.1	160	2	S58214	hypothetical prote
448	6	1.1	160	2	T02151	lacyoylglycathione
449	6	1.1	160	2	AF3517	H+-exporting ATPas
450	6	1.1	161	1	S43893	conserved hypotet
451	6	1.1	161	2	AB3583	Vacuolar ATP synth
452	6	1.1	162	2	T50253	phycocyanin alpha
453	6	1.1	163	2	A29674	phycocyanin alpha
454	6	1.1	163	2	AH1872	probable membrane
455	6	1.1	163	2	S66795	funarate hydratase
456	6	1.1	164	2	B72364	disease resistance
457	6	1.1	164	2	T07759	hypothetical prote
458	6	1.1	164	2	T23249	hypothetical prote
459	6	1.1	164	2	T00891	granulocyte colony
460	6	1.1	165	2	JC2081	pall protein - Pae
461	6	1.1	166	2	S52308	hypothetical prote
462	6	1.1	166	2	T21142	probable integral
463	6	1.1	167	2	T36290	hypothetical prote
464	6	1.1	167	2	AH2173	protein (imported
465	6	1.1	168	2	D95349	transcription regu
466	6	1.1	168	2	A12865	hypothetical prote
467	6	1.1	168	2	G97642	
468	6	1.1	170	2	T03018	glycine-rich prote
469	6	1.1	170	2	E81662	Holliday junction
470	6	1.1	170	2	D71504	crossover junction
471	6	1.1	170	2	C71024	hypothetical prote
472	6	1.1	171	2	G90077	conserved hypotet
473	6	1.1	171	2	AD3400	N utilization subu
474	6	1.1	172	2	T02230	NBS-LRR type resis
475	6	1.1	172	2	AC3176	conserved hypotet
476	6	1.1	173	2	D58893	NADH2 dehydrogenas
477	6	1.1	173	2	E90623	hypothetical prote
478	6	1.1	173	2	D83298	hypothetical prote
479	6	1.1	174	2	F72607	probable heterocys
480	6	1.1	176	2	C82816	limbrial assembly
481	6	1.1	176	2	H75332	alkyrim-related pr
482	6	1.1	176	2	C82792	hypothetical prote
483	6	1.1	176	2	H69156	conserved hypotet
484	6	1.1	178	1	REBBSF	ribosomal protein
485	6	1.1	179	1	REBBSF	hypothetical prote
486	6	1.1	179	2	A64551	hypothetical prote
487	6	1.1	179	2	D71957	protein F2489.22 f
488	6	1.1	180	2	H53334	Tspo Tryptophan ri
489	6	1.1	180	2	H75418	hypothetical prote
490	6	1.1	180	2	H66311	FilA6.4 protein -
491	6	1.1	181	2	B82908	inorganic pyrophos
492	6	1.1	182	2	F83378	nosil protein (limp
493	6	1.1	182	2	T44654	hypothetical prote
494	6	1.1	182	2	A64007	hypothetical prote
495	6	1.1	182	2	E82967	hypothetical prote
496	6	1.1	182	2	C90936	hypothetical prote
497	6	1.1	182	2	G85784	hypothetical prote
498	6	1.1	182	2	A64935	hypothetical prote
499	6	1.1	183	2	S53143	core antigen - hep
500	6	1.1	185	2	JC4085	glycine-rich cutic
501	6	1.1	185	2	T15399	hypothetical prote
502	6	1.1	186	2	AH2898	ATP Synthase delta
503	6	1.1	186	2	T15368	hypothetical prote
504	6	1.1	186	2	T41601	hypothetical prote
505	6	1.1	186	2	H90788	probable major pil
506	6	1.1	186	2	A85649	probable pilin sub
507	6	1.1	187	1	A41654	superoxide dismuta
508	6	1.1	187	1	G69308	probable 2-oxogluc
509	6	1.1	187	2	T30679	probable DNA-direc
510	6	1.1	187	2	F65009	hypothetical prote
511	6	1.1	188	2	A97674	ATP synthase delta
512	6	1.1	188	2	D87705	intracellular sept
513	6	1.1	188	2	AD0525	probable fibrillar
514	6	1.1	189	1	IVB011	interferon alpha-I
515	6	1.1	189	1	IVB01D	interferon alpha-I
516	6	1.1	189	2	AE1316	GTP cyclohydrolyse
517	6	1.1	189	2	G70485	hypothetical prote
518	6	1.1	189	2	E84314	hypothetical prote
519	6	1.1	190	2	S15275	cutis protein - Str
520	6	1.1	190	2	AD3413	hypothetical membr
521	6	1.1	191	2	A75518	guanyl--specific ri
522	6	1.1	191	2	H97364	hypothetical prote
523	6	1.1	192	2	G76506	hypothetical prote
524	6	1.1	192	2	B81911	probable molybdopt
525	6	1.1	193	2	S32992	hypothetical prote
526	6	1.1	193	2	B95340	hypothetical prote
527	6	1.1	194	2	AG1145	limdazoleglycerol-
528	6	1.1	195	2	A43858	alyl hydroperoxid
529	6	1.1	195	2	D82313	2-amino-4-hydroxy-
530	6	1.1	196	2	T01982	tumor related prot
531	6	1.1	197	2	A53126	syndecan-4 precurs
532	6	1.1	198	2	A12622	conserved hypotet
533	6	1.1	198	2	A75270	conserved hypotet
534	6	1.1	198	2	S14456	XA-1 protein preu
535	6	1.1	200	2	H90477	hypothetical prote
536	6	1.1	201	2	S57712	krig protein - hum
537	6	1.1	202	2	D96962	probable metal-dep
538	6	1.1	202	2	H95329	protein (imported
539	6	1.1	203	2	T25222	hypothetical prote
540	6	1.1	204	2	F83306	hypothetical prote

541	6	1.1	205	2	S37804	614	6	1.1	230	2	A75260	hypothetical prote
542	6	1.1	205	2	S55670	615	6	1.1	230	2	AC0888	probable membrane
543	6	1.1	205	2	A48929	616	6	1.1	231	2	S11429	nitrate reductase
544	6	1.1	205	2	B97302	617	6	1.1	231	2	E90887	cryptic nitrate re
545	6	1.1	206	2	T07797	618	6	1.1	231	2	D85730	cryptic nitrate re
546	6	1.1	206	2	S72581	619	6	1.1	231	2	AH0671	respiratory nitrat
547	6	1.1	207	2	D90526	620	6	1.1	231	2	F69977	two-component resp
548	6	1.1	207	2	AG0055	621	6	1.1	231	2	H81698	hypothetical prote
549	6	1.1	207	2	AE0632	622	6	1.1	231	2	E96555	unknown protein [i
550	6	1.1	209	2	C69783	623	6	1.1	231	1	S13625	eosinophil major b
551	6	1.1	210	2	G71685	624	6	1.1	233	1	S71464	ribonuclease (EC 3
552	6	1.1	210	2	D93606	625	6	1.1	233	2	T21494	hypothetical prote
553	6	1.1	211	2	H64961	626	6	1.1	233	2	T00566	hypothetical prote
554	6	1.1	211	2	F90967	627	6	1.1	233	2	A12442	hypothetical prote
555	6	1.1	211	2	E85815	628	6	1.1	234	1	S15102	eosinophil major b
556	6	1.1	211	2	D82600	629	6	1.1	235	1	CTMSP	corticotropin / li
557	6	1.1	212	2	H83305	630	6	1.1	235	1	CTMRP	corticotropin / li
558	6	1.1	213	2	D70972	631	6	1.1	236	2	D72556	hypothetical prote
559	6	1.1	214	2	A87276	632	6	1.1	237	2	A90529	potassium uptake p
560	6	1.1	214	2	T34856	633	6	1.1	237	2	T26660	hypothetical prote
561	6	1.1	214	2	G95391	634	6	1.1	237	2	AG3474	carbamoyl-phosphat
562	6	1.1	215	2	S25358	635	6	1.1	238	2	I52638	neuronal growth-re
563	6	1.1	216	2	A54305	636	6	1.1	238	2	F70107	hypothetical prote
564	6	1.1	216	2	B87342	637	6	1.1	239	1	Q0B8G5	HLF2 protein - hu
565	6	1.1	217	2	A97405	638	6	1.1	240	2	A39842	insulin-like growt
566	6	1.1	217	2	T04580	639	6	1.1	240	2	S75017	hypothetical prote
567	6	1.1	218	2	C86337	640	6	1.1	240	2	B82833	conserved hypotet
568	6	1.1	218	2	G70438	641	6	1.1	241	1	R7H5H5	ribosomal protein
569	6	1.1	218	2	AC3537	642	6	1.1	241	1	RKN218	phosphoprotein p -
570	6	1.1	219	2	AC2036	643	6	1.1	241	1	BE9885	transcription regu
571	6	1.1	219	2	C65074	644	6	1.1	242	2	S60143	cellulase (EC 3.2.
572	6	1.1	219	2	C91100	645	6	1.1	243	2	A25037	afes regulatory pr
573	6	1.1	219	2	G85945	646	6	1.1	244	1	JN0703	carbonyl reductase
574	6	1.1	219	2	AG0872	647	6	1.1	244	1	A28053	phosphoribosylamin
575	6	1.1	219	2	AG2124	648	6	1.1	245	1	AE2089	proteolipid protei
576	6	1.1	220	2	I50588	649	6	1.1	245	2	A12126	hypothetical prote
577	6	1.1	220	2	F83159	650	6	1.1	245	2	A12126	hypothetical prote
578	6	1.1	220	2	F64327	651	6	1.1	245	2	F71887	probable sulfate u
579	6	1.1	220	2	H87695	652	6	1.1	246	2	D83540	probable ABC tra
580	6	1.1	220	2	D84420	653	6	1.1	246	2	B95144	infected-cell prot
581	6	1.1	220	2	A12910	654	6	1.1	246	2	B48350	hypothetical prote
582	6	1.1	220	2	G97685	655	6	1.1	246	2	S23538	probable integral
583	6	1.1	221	2	S51868	656	6	1.1	246	2	T36203	hypothetical prote
584	6	1.1	221	2	T50665	657	6	1.1	246	2	T04765	hypothetical prote
585	6	1.1	221	2	JC7587	658	6	1.1	246	2	H98011	hypothetical prote
586	6	1.1	222	1	JT0085	659	6	1.1	248	2	T14002	aquaporin TIP7 - c
587	6	1.1	222	1	E71024	660	6	1.1	248	2	T14001	aquaporin TIP8 -
588	6	1.1	222	2	B90669	661	6	1.1	248	2	T12632	water channel prot
589	6	1.1	222	2	E85519	662	6	1.1	248	2	T01648	probable tonoplast
590	6	1.1	223	1	KIHUA3	663	6	1.1	248	2	T07819	probable water cha
591	6	1.1	223	2	H83462	664	6	1.1	248	2	T48885	water channel prot
592	6	1.1	223	2	AB0161	665	6	1.1	248	2	C83431	type III export pr
593	6	1.1	223	2	A29770	666	6	1.1	248	2	B90890	hypothetical prote
594	6	1.1	224	2	AB3127	667	6	1.1	248	2	A98235	ferredoxin-NADP re
595	6	1.1	224	2	G98160	668	6	1.1	248	2	A86082	ferredoxin-NADP re
596	6	1.1	225	1	RDECMG	669	6	1.1	248	2	AD3456	phosphoglycolate p
597	6	1.1	225	2	D90845	670	6	1.1	248	2	S40867	ferredoxin-NADP re
598	6	1.1	225	2	C85703	671	6	1.1	249	1	A61087	myelin P0 glycopro
599	6	1.1	225	2	D95016	672	6	1.1	249	1	B64571	probable neuraminy
600	6	1.1	225	2	F97889	673	6	1.1	249	2	E71865	probable neuraminy
601	6	1.1	226	2	T14960	674	6	1.1	250	2	F71442	probable membrane
602	6	1.1	226	2	T49807	675	6	1.1	250	2	J01012	Tob87-18C protein
603	6	1.1	226	2	CA2124	676	6	1.1	250	2	S13719	probable membrane
604	6	1.1	227	1	S68150	677	6	1.1	250	2	S51781	integral membrane
605	6	1.1	227	2	T46456	678	6	1.1	250	2	T48884	membrane channel p
606	6	1.1	228	2	S48116	679	6	1.1	250	2	H96521	protein F2ID18.8 l
607	6	1.1	228	2	D36914	680	6	1.1	251	2	T26010	hypothetical prote
608	6	1.1	228	2	T32259	681	6	1.1	251	2	B83413	molysate-binding
609	6	1.1	229	2	E90058	682	6	1.1	251	2	AP1665	hypothetical prote
610	6	1.1	229	2	T06204	683	6	1.1	251	2	AH1293	hypothetical prote
611	6	1.1	229	2	F97367	684	6	1.1	251	2	D69363	conserved hypotet
612	6	1.1	229	2	AG2585	685	6	1.1	251	2	C83987	ABC transporter (A
613	6	1.1	229	2	F84370	686	6	1.1	252	2	G70967	probable clpx' pro

687	6	1.1	252	2	H72469	hypotheical prote
688	6	1.1	253	2	C72758	probable enoyl-CoA
689	6	1.1	253	2	AH2107	hypotheical prote
690	6	1.1	253	2	C87589	conserved hypotet
691	6	1.1	254	2	A12802	hypotheical prote
692	6	1.1	254	2	B97582	phosphoribosylamin
693	6	1.1	254	2	T33021	hypotheical prote
694	6	1.1	255	2	C95411	probable GntR-fam1
695	6	1.1	256	1	MEMSA	7S nerve growth fa
696	6	1.1	256	1	T11233	H+-transporting tw
697	6	1.1	256	2	A54322	corticotropic / 11
698	6	1.1	256	2	A10267	probable membrane
699	6	1.1	256	2	AB2019	hypotheical prote
700	6	1.1	256	2	C90443	hypotheical prote
701	6	1.1	256	2	D87681	hypotheical prote
702	6	1.1	256	2	G70830	hypotheical prote
703	6	1.1	257	2	AH1865	hypotheical prote
704	6	1.1	257	2	S24812	minor fibrillar pro
705	6	1.1	258	2	I40374	N-acetylglutamate
706	6	1.1	258	2	G83069	probable oxidoredu
707	6	1.1	260	2	T35293	probable cobalamn
708	6	1.1	260	2	T18909	hypotheical prote
709	6	1.1	260	2	D84568	hypotheical prote
710	6	1.1	260	2	F69278	conserved hypotet
711	6	1.1	260	2	T40430	conserved hypotet
712	6	1.1	261	2	A25606	tissue kallikrein
713	6	1.1	261	2	G64373	proeasome alpha s
714	6	1.1	263	2	T28146	class II histocomp
715	6	1.1	263	2	A13629	tautine transport
716	6	1.1	264	1	CTMKP	corticotropic / 11
717	6	1.1	264	1	S22090	catechol O-methyl
718	6	1.1	265	1	CTBOP	corticotropic / 11
719	6	1.1	265	2	S16592	chlorophyll a/b-bi
720	6	1.1	265	2	H71105	hypotheical prote
721	6	1.1	265	2	B95988	hypotheical prote
722	6	1.1	265	2	D69263	conserved hypotet
723	6	1.1	266	2	T03570	carbonate dehydrat
724	6	1.1	266	2	C90257	translation initia
725	6	1.1	266	2	G64022	hypotheical prote
726	6	1.1	267	1	CTHOP	corticotropic / 11
727	6	1.1	267	2	A34078	prolactin-related
728	6	1.1	267	2	T22978	hypotheical prote
729	6	1.1	267	2	F87665	hypotheical prote
730	6	1.1	267	2	H69373	hypotheical prote
731	6	1.1	267	2	AC2493	hypotheical prote
732	6	1.1	268	2	S67583	KM1 protein - yea
733	6	1.1	268	2	C90709	thiol disulfide in
734	6	1.1	268	2	G85559	thiol, disulfide in
735	6	1.1	268	2	B64794	hypotheical prote
736	6	1.1	268	2	AB2498	hypotheical prote
737	6	1.1	269	1	T35532	probable diheme cy
738	6	1.1	269	1	S74490	type IV prepilin p
739	6	1.1	269	2	AD3051	hypotheical prote
740	6	1.1	269	2	B69180	conserved hypotet
741	6	1.1	269	2	E72808	gp65 protein - Myc
742	6	1.1	269	2	G96925	bicin-lacetyl-CoA
743	6	1.1	270	2	C86838	hypotheical prote
744	6	1.1	270	2	B88734	protein F32E10.2 l
745	6	1.1	270	2	G72390	dihydroorotate deh
746	6	1.1	271	2	D82924	conserved hypotet
747	6	1.1	271	2	E81384	prolipoprotein dia
748	6	1.1	271	2	A11102	dihydroorotate sy
749	6	1.1	271	2	G83554	hypotheical prote
750	6	1.1	272	2	I48268	bilary glycoprote
751	6	1.1	272	2	C75137	hypotheical prote
752	6	1.1	272	2	H98234	ferichrome transp
753	6	1.1	273	1	R5EC2	ribosomal protein
754	6	1.1	273	2	B85997	50S ribosomal subu
755	6	1.1	273	2	P91151	50S ribosomal subu
756	6	1.1	273	2	AB1472	probable lipoprote
757	6	1.1	273	2	AF1110	probable lipoprote
758	6	1.1	273	2	AF3210	ABC transporter, m
759	6	1.1	273	2	F86665	ABC transporter pe
760	6	1.1	274	2	C82059	ribosomal protein
761	6	1.1	274	2	UC2474	glutamate-cysteine
762	6	1.1	274	2	S44616	C08C.2 protein -
763	6	1.1	275	2	S77388	nitrate transport
764	6	1.1	275	2	G64368	hypotheical prote
765	6	1.1	277	2	A37416	bloodstream-specif
766	6	1.1	277	2	UC7903	collectin liver 1
767	6	1.1	278	1	S57643	stearyl-CoA 9-des
768	6	1.1	278	2	AF2699	conserved hypotet
769	6	1.1	278	2	P97481	probable integral
770	6	1.1	278	2	D70504	hypotheical prote
771	6	1.1	278	2	D83080	hypotheical prote
772	6	1.1	278	2	T15461	hypotheical prote
773	6	1.1	279	2	S73526	probable lipoprote
774	6	1.1	279	2	T33771	hypotheical prote
775	6	1.1	279	2	D82243	transcription regu
776	6	1.1	280	1	C70784	probable diheme cy
777	6	1.1	280	1	AD1109	B. subtilis ComEC
778	6	1.1	280	2	E89981	hypotheical prote
779	6	1.1	281	2	S37541	H+-transporting tw
780	6	1.1	282	2	G64479	hypotheical prote
781	6	1.1	282	2	B95138	conserved hypotet
782	6	1.1	282	2	B97999	conserved hypotet
783	6	1.1	282	2	H65116	hypotheical prote
784	6	1.1	282	2	T13526	hypotheical prote
785	6	1.1	282	2	D97138	DNA replication pr
786	6	1.1	282	2	AF2672	conserved hypotet
787	6	1.1	282	2	D97454	hypotheical prote
788	6	1.1	283	2	F72476	hypotheical prote
789	6	1.1	284	1	H69355	conserved hypotet
790	6	1.1	284	2	H69277	branched-chain ami
791	6	1.1	284	2	S52003	major intrinsic pr
792	6	1.1	284	2	H68898	undecaprenol kinas
793	6	1.1	284	2	S08385	nodo protein - Rhi
794	6	1.1	284	2	A43721	nodule formation p
795	6	1.1	285	2	H69369	branched-chain ami
796	6	1.1	285	2	S74771	hypotheical prote
797	6	1.1	285	2	H83733	RNA polymerase ECF
798	6	1.1	285	1	QOEC4A	hypotheical 30.9K
799	6	1.1	286	2	T38888	probable oxidoredu
800	6	1.1	286	2	C91103	mechanosensitive c
801	6	1.1	286	2	F85948	probable transport
802	6	1.1	286	2	A10874	probable membrane
803	6	1.1	287	2	A82318	conserved hypotet
804	6	1.1	287	2	AH2519	hypotheical prote
805	6	1.1	287	2	G69766	conserved hypotet
806	6	1.1	288	1	B36961	type IV prepilin p
807	6	1.1	288	2	T31087	probable dTP-L-tn
808	6	1.1	288	2	S75324	aspartoacylase (EC
809	6	1.1	289	2	F65129	phosphoribulokinas
810	6	1.1	289	2	F91154	probable phosphori
811	6	1.1	289	2	C86000	probable phosphori
812	6	1.1	289	2	A11002	phosphoribulokinas
813	6	1.1	289	2	AH0112	probable membrane
814	6	1.1	289	2	T41846	HE65 ori105 - Bomb
815	6	1.1	289	2	AG1353	hypotheical prote
816	6	1.1	289	2	AH1723	hypotheical prote
817	6	1.1	290	2	T03552	malicase transport
818	6	1.1	290	2	A82946	hypotheical prote
819	6	1.1	290	2	H98336	malicase transport
820	6	1.1	290	2	S48301	geranylgeranyl tra
821	6	1.1	291	2	I48602	insulin-like growt
822	6	1.1	291	2	E71491	probable geranyl t
823	6	1.1	291	2	D90491	ABC transporter, A
824	6	1.1	291	2	AB3235	nitriolriacetate
825	6	1.1	291	2	A13092	hypotheical prote
826	6	1.1	292	2	B81650	geranylgeranyl pyr
827	6	1.1	292	2	AB2893	metal dependent be
828	6	1.1	292	2	E97668	hypotheical prote
829	6	1.1	292	2	H82214	conserved hypotet
830	6	1.1	293	2	AE1927	3-ketoacyl-acyl ca
831	6	1.1	293	2	AB3051	hypotheical prote
832	6	1.1	293	2	H82184	glycerol-3-phospha

833	6	1.1	293	2	A87473	Smp-30/Cgr1 family	906	6	1.1	313	2	D85855	probable kinase ye
834	6	1.1	293	2	H70713	hypothetical prote	907	6	1.1	313	2	A75256	conserved hypothet
835	6	1.1	294	2	S72897	pyrroline-5-carbox	908	6	1.1	313	2	A89971	cmp-binding-factor
836	6	1.1	294	2	JCS305	hypothetical prote	909	6	1.1	314	2	C70562	probable DTDP-Gluc
837	6	1.1	294	2	T05028	nodulin-26-like pr	910	6	1.1	314	2	S66274	annexin - pepper
838	6	1.1	294	2	SS2426	s-SNAP protein - 1	911	6	1.1	314	2	T02961	annexin p33 - maize
839	6	1.1	294	2	D87691	ABC transporter, A	912	6	1.1	314	2	AD0482	sugar-binding tran
840	6	1.1	295	2	G70745	probable proc prot	913	6	1.1	315	1	JC5093	ribose-phosphate d
841	6	1.1	295	2	E95200	fructokinase [limp	914	6	1.1	315	2	T06164	peroxidase (EC 1.1
842	6	1.1	295	2	D98067	fructokinase (EC 2	915	6	1.1	315	2	T06172	peroxidase (EC 1.1
843	6	1.1	295	2	D75010	UDP-N-acetylglucos	916	6	1.1	315	2	T29258	hypothetical prote
844	6	1.1	295	2	B66742	amino acid ABC tra	917	6	1.1	315	2	AH3567	permease [imported
845	6	1.1	296	2	B83384	conserved hypothet	918	6	1.1	316	2	T50027	annexin-like prote
846	6	1.1	296	2	C82645	transcription regu	919	6	1.1	316	2	T52464	hypothetical prote
847	6	1.1	296	2	S72444	DNA-binding protei	920	6	1.1	316	2	A80669	probable virulence
848	6	1.1	296	2	A87311	hypothetical prote	921	6	1.1	317	1	E69763	probable ferrichro
849	6	1.1	297	2	WZECN	N-acetylneuraminat	922	6	1.1	317	2	S16916	plastoquinol plast
850	6	1.1	297	2	E85986	N-acetylneuraminat	923	6	1.1	317	2	E83344	probable adhesion
851	6	1.1	297	2	B91141	N-acetylneuraminat	924	6	1.1	318	2	T50026	annexin-like prote
852	6	1.1	297	2	A80908	N-acetylneuraminat	925	6	1.1	318	2	I59301	bone marrow stroma
853	6	1.1	298	2	A87147	methyl mycolic aci	926	6	1.1	318	2	C83062	hypothetical prote
854	6	1.1	298	2	E82157	probable N-acetyl	927	6	1.1	319	2	E89872	hypothetical prote
855	6	1.1	298	2	B64180	arac-like transcri	928	6	1.1	319	2	JC5624	olfactory receptor
856	6	1.1	298	2	AC3617	oligopeptide trans	929	6	1.1	319	2	JC4390	bone marrow stroma
857	6	1.1	299	2	E90573	methyltransferase	930	6	1.1	319	2	G75106	hypothetical prote
858	6	1.1	299	2	B69155	hypothetical prote	931	6	1.1	319	2	G75628	hypothetical prote
859	6	1.1	299	2	H87567	hypothetical prote	932	6	1.1	319	2	T49852	hypothetical prote
860	6	1.1	299	2	AEO461	probable membrane	933	6	1.1	320	2	C87657	alcohol dehydrogen
861	6	1.1	300	1	A69444	thioresoxin-disulf	934	6	1.1	320	2	T31130	hypothetical prote
862	6	1.1	300	2	B98235	fnud protein (Au00	935	6	1.1	320	2	C72862	hypothetical prote
863	6	1.1	300	2	T47460	hypothetical prote	936	6	1.1	321	2	H82240	conserved hypothet
864	6	1.1	300	2	S36430	hypothetical prote	937	6	1.1	321	2	S76551	hypothetical prote
865	6	1.1	300	2	A97329	transcription regu	938	6	1.1	322	2	G72421	hypothetical prote
866	6	1.1	300	2	AEO535	hypothetical prote	939	6	1.1	322	2	AB1851	iron(III) ABC tran
867	6	1.1	301	2	T27648	hypothetical prote	940	6	1.1	322	2	A37759	hypothetical prote
868	6	1.1	302	2	G84053	hypothetical prote	941	6	1.1	323	2	D72289	piv protein - Mora
869	6	1.1	303	2	T29321	hydrid-endo-beta-1	942	6	1.1	323	2	A72508	oligopeptide ABC t
870	6	1.1	303	2	A97383	hypothetical prote	943	6	1.1	323	2	C84961	probable cobalam
871	6	1.1	303	2	AH2600	hypothetical prote	944	6	1.1	323	2	E86935	lipidic acid synthe
872	6	1.1	304	2	C83891	hypothetical prote	945	6	1.1	324	2	E87196	conserved hypothet
873	6	1.1	304	2	T23801	hypothetical prote	946	6	1.1	324	2	G69515	probable hydrolase
874	6	1.1	305	1	H75285	probable phosphos	947	6	1.1	324	2	G90896	transcription regu
875	6	1.1	305	2	B69548	molybdopterin oxid	948	6	1.1	324	2	H90269	probable transcrip
876	6	1.1	305	2	B84413	hypothetical prote	949	6	1.1	325	2	C82251	GDEF family prote
877	6	1.1	305	2	A38422	insulin-like prote	950	6	1.1	325	2	B31595	hypothetical prote
878	6	1.1	306	2	H97007	probable permease	951	6	1.1	325	2	I52998	interferon regulat
879	6	1.1	306	2	T19934	hypothetical prote	952	6	1.1	325	2	A10715	interferon regulat
880	6	1.1	306	2	T52340	cell wall-plasma m	953	6	1.1	326	2	B71681	probable inner mem
881	6	1.1	306	2	T06607	hypothetical prote	954	6	1.1	326	2	T36497	pyruvate dehydroge
882	6	1.1	308	2	A82684	conserved hypothet	955	6	1.1	326	2	D97743	probable branched-
883	6	1.1	309	1	SS1356	olfactory receptor	956	6	1.1	326	2	T08849	hypothetical prote
884	6	1.1	309	2	FOFVF	gas polyporein -	957	6	1.1	326	2	G85727	alternative respir
885	6	1.1	309	2	I51900	carbonic anhydrase	958	6	1.1	326	2	T30166	probable transport
886	6	1.1	309	2	H89832	hypothetical prote	959	6	1.1	326	2	H95984	hypothetical prote
887	6	1.1	310	1	T38493	hypothetical prote	960	6	1.1	327	2	B82918	probable transcrip
888	6	1.1	310	1	VA2031	300K antigen Ag231	961	6	1.1	327	2	T04004	DNA-directed RNA p
889	6	1.1	310	1	B69475	conserved hypothet	962	6	1.1	327	2	T35482	hypothetical prote
890	6	1.1	310	1	A70481	acetoin utilizatio	963	6	1.1	327	2	E69430	hypothetical prote
891	6	1.1	310	2	S67181	hypothetical prote	964	6	1.1	327	2	F71497	hypothetical prote
892	6	1.1	310	2	T55976	conserved hypothet	965	6	1.1	327	2	H85720	hypothetical prote
893	6	1.1	310	2	T37824	hypothetical prote	966	6	1.1	328	2	A95897	probable UDPglucos
894	6	1.1	311	2	JC2541	bone marrow stroma	967	6	1.1	328	2	A13600	UDPglucose 4-epime
895	6	1.1	311	2	C84101	hypothetical prote	968	6	1.1	328	2	AC0750	probable deaminase
896	6	1.1	311	2	D95076	peptide methionine	969	6	1.1	328	2	T07610	WS176 protein - ri
897	6	1.1	312	2	C82356	peptide ABC transp	970	6	1.1	328	2	S32369	gamma-SNAP protein
898	6	1.1	312	2	F81279	enterochelin uptak	971	6	1.1	328	2	A36330	interferon regulat
899	6	1.1	312	2	G69423	branched-chain ami	972	6	1.1	328	2	A13017	enhanced entry pro
900	6	1.1	312	2	H84153	hypothetical prote	973	6	1.1	329	2	A12023	prochlorophyllid
901	6	1.1	312	2	C87562	conserved hypothet	974	6	1.1	329	2	A48715	gal-beta(1-3/1-4)G
902	6	1.1	312	2	A56911	TRAD protein - hu	975	6	1.1	329	2	T17033	lucine rich repea
903	6	1.1	313	2	H95158	probable ABC trans	976	6	1.1	329	2	T22221	hypothetical prote
904	6	1.1	313	2	B64985	hypothetical 33.6K	977	6	1.1	329	2	T44459	arginine metabolis
905	6	1.1	313	2	B91011	probable kinase [1	978	6	1.1	329	2	B41344	lutropin-choriogon

979 6 1.1 329 2 D41344
 980 6 1.1 329 2 A31595
 981 6 1.1 329 2 A27990
 982 6 1.1 329 2 C98293
 983 6 1.1 330 1 C69042
 984 6 1.1 330 2 JQ2262
 985 6 1.1 330 2 AB0225
 986 6 1.1 330 2 T46994
 987 6 1.1 330 2 A10239
 988 6 1.1 330 2 T30238
 989 6 1.1 331 2 C69376
 990 6 1.1 331 2 T51899
 991 6 1.1 331 2 E88991
 992 6 1.1 331 2 C41344
 993 6 1.1 332 2 AC0158
 994 6 1.1 332 2 S75621
 995 6 1.1 332 2 A49879
 996 6 1.1 332 2 T42370
 997 6 1.1 332 2 B95978
 998 6 1.1 333 1 HLHUC
 999 6 1.1 333 2 H87220
 1000 6 1.1 333 2 AB3797

ALIGNMENTS

RESULT 1

E83679
 multidrug-efflux transporter BH0237 [imported] - Bacillus halodurans (strain C-125)
 C.Species: Bacillus halodurans
 C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C/Accession: E83679
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maeni, N.; Fujii, F.; Hirai
 Nucleic Acids Res. 28, 4317-4331, 2000
 A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A.Reference number: A83650, MUID:20512582, PMID:11058132

A/Accession: E83679

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-387 <STO>

A/Cross-references: GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BA803956.1; GSPDB:GN00

A/Experimental source: strain C-125

C/Genetics: BH0237

A/Gene: BH0237

Query Match

Best Local Similarity 1.7%; Score 9; DB 2; Length 387;
 Matches 9; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVLL 469

DB 73 LAVGVLL 81

RESULT 2

G87364
 conserved hypothetical protein CC0931 [imported] - Caulobacter crescentus
 C.Species: Caulobacter crescentus
 C.Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C/Accession: G87364

R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.U.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 N.; J.; Ermolenko, W.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A.Title: Complete Genome Sequence of Caulobacter crescentus.

A/Reference number: A87249; MUID:21173698; PMID:11259647

A/Accession: G87364

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-401 <STO>

A/Cross-references: GB:AE005673; NID:G13422203; PIDN:AAK22915.1; GSPDB:GN00148

C/Genetics:

A/Gene: CC0931

Query Match

Best Local Similarity 1.7%; Score 9; DB 2; Length 401;
 Matches 9; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 TALAGLAV 463

DB 36 TALAGLAV 44

RESULT 3

G90656
 hypothetical protein EC80223 [imported] - Escherichia coli (strain O157:H7, substrain RT.
 C.Species: Escherichia coli
 C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C/Accession: G90656
 R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hatlori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001

A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A/Reference number: A89629; MUID:21156231; PMID:11258796

A/Accession: G90656

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-923 <HAY>

A/Cross-references: GB:BA000007; PIDN:BA833646.1; PID:G13359679; GSPDB:GN00154

A/Experimental source: strain O157:H7, substrain RMD 0509952

C/Genetics:

A/Gene: EC80223

C/Supfamily: endopeptidase Clp ATP-binding chain

Query Match

Best Local Similarity 1.7%; Score 9; DB 2; Length 923;
 Matches 9; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 GGVLLALL 472

DB 114 GGVLLALL 122

RESULT 4

G85507
 probable proteinase 20254 [imported] - Escherichia coli (strain O157:H7, substrain EDL93
 C.Species: Escherichia coli
 C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C/Accession: G85507

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
 Iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamouzis, K.; Apodaca,
 Nature 409, 529-533, 2001

A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: G85507

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-923 <STO>

A/Cross-references: GB:AE005174; NID:G12512960; PIDN:AG54523.1; GSPDB:GN00145; UMGF:202

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: 20254

C/Supfamily: endopeptidase Clp ATP-binding chain

Query Match

Best Local Similarity 1.7%; Score 9; DB 2; Length 923;
 Matches 9; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 GGVLLALL 472

DB 114 GGVLLALL 122

RESULT 5

S52116

transforming protein sk1 - axolotl (fragment)
 N/Alternate names: proto-oncogene sk1
 C/Species: Ambystoma mexicanum (axolotl)
 C/Date: 14-Jul-1995 #sequence_revision 14-Feb-1997 #text_change 20-Jun-2000
 C/Accession: S52116
 R/Ludolph, D.C.; Neff, A.W.; Parker, M.A.; Mescher, A.L.; Smith, R.C.; Malajinski, G.M.
 Biochim. Biophys. Acta 1260, 102-104, 1995
 A/Title: Cloning and expression of the axolotl proto-oncogene sk1.
 A/Reference number: S52116; MUID:95092782; PMID:7999783
 A/Accession: S52116
 A/Molecule type: mRNA
 A/Residues: 1-130 <LUD>
 A/Cross-references: EMBL:D28907; NID:9762853; PIDN:BA18908.1; PID:92160486
 C/Genetics:
 A/Gene: sk1
 C/Superfamily: sk1 transforming protein
 C/Keywords: oncogene; transforming protein

Query Match 1.5%; Score 8; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 ALTAGGCT 477
 |||||
 Db 36 ALTAGGCT 43

RESULT 6

D70718 hypothetical protein RV0966c - Mycobacterium tuberculosis (strain H37RV)

C/Species: Mycobacterium tuberculosis

C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000

C/Accession: D70718

R/Cole, S.T.; Broch, R.; Parkhill, J.; Garner, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: D70718

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-230 <COL>

A/Cross-references: GB:Z79700; GB:AL123456; NID:93261628; PIDN:CAB01985.1; PID:e264092;

C/Genetics:

A/Experimental source: strain H37Rv

C/Accession:

A/Gene: RV0966c

C/Superfamily: Mycobacterium tuberculosis hypothetical protein RV2862c

Query Match 1.5%; Score 8; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 LLLALLGG 474
 |||||
 Db 118 LLLALLGG 125

RESULT 7

A60643 antigen 5401 - Elmeria tenella (fragment)

C/Species: Elmeria tenella

C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 18-Jun-1993

C/Accession: A60643

R/Danforth, H.D.; Augustine, P.C.; Ruff, M.D.; McCandless, R.; Strausberg, R.L.; Likel,

Poult. Sci. 68, 1643-1652, 1989

A/Title: Genetically engineered antigen confers partial protection against avian coccidia

A/Reference number: A60643; MUID:90160107; PMID:2622819

A/Accession: A60643

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-287 <DAN>

F,11-120/Region: 22-residue repeats (A-G-X-X-G-G-S-G-G-X-A-E-E-L-P-G-E-G-G-A-G)
 Query Match 1.5%; Score 8; DB 2; Length 287;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 VGGVLLLA 470
 |||||
 Db 219 VGGVLLLA 226

RESULT 8

AF3503 benzocaine membrane transport protein [imported] - Brucella melitensis (strain 16M)

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C/Accession: AF3503

R/Delvecchio, V.G.; Kapetral, V.; Redkar, R.U.; Patra, G.; Mijer, C.; Los, T.; Ivanova, P.

; Mazur, M.; Goldstein, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesac

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A/Reference number: AD3252; PMID:11756688

A/Accession: AF3503

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-383 <KUR>

A/Cross-references: GB:AE008917; PIDN:AL53193.1; PID:G17984067; GSPDB:GN00190

A/Experimental source: strain 16M

C/Genetics:

A/Gene: BMEI2012

A/Map position: 1

Query Match 1.5%; Score 8; DB 2; Length 383;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 ALTAGLAV 463
 |||||
 Db 364 ALTAGLAV 371

RESULT 9

AF1903 hypothetical protein alr0776 [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C/Accession: AF1903

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AF1903

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-396 <KUR>

A/Cross-references: GB:BA000019; PIDN:BA872733.1; PID:G17130121; GSPDB:GN00179

A/Experimental source: strain PCC 7120

C/Genetics:

A/Gene: alr0776

Query Match 1.5%; Score 8; DB 2; Length 396;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GLSSSTRS 29
 |||||
 Db 266 GLSSSTRS 273

RESULT 10

AH0189

Amino acid permease [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AF0189
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarragga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AF0001; MUID:21470413; PMID:11586360
A:Accession: AF0189
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-463 <KIR>
A:Cross-references: GB:AL590842; PIDN:CA930379.1; PID:G15795598; GSPDB:GN00175
C:Genetic8:
A:Gene: YPO157
C:Superfamily: arginine permease

Query Match 1.5%; Score 8; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 SUSEPTPN 387
|||||||
DB 230 SUSEPTPN 237

RESULT 11
J02263
glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) precursor - soybean
C:Species: Glycine max (soybean)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 24-Nov-1999
C:Accession: J02263
R:Sangwan, I.; O'Brian, M.R.
Plant Physiol. 102, 829-834, 1993
A:Title: Expression of the soybean (Glycine max) glutamate 1-semialdehyde aminotransferase
A:Reference number: J02263; MUID:94105331; PMID:8278535
A:Accession: J02263
A:Molecule type: mRNA
A:Residues: 1-466 <SAN>
A:Cross-references: GB:U12453; NID:G310566; PIDN:AAA33968.1; PID:G310567
C:Comment: This enzyme catalyzes delta-aminolevulinic acid synthesis from glutamate 1-se
C:Function: porphyrin biosynthesis
C:Superfamily: ornithine-oxo-acid aminotransferase
C:Keywords: intramolecular transference; isomerase; phosphoprotein; pyridoxal phosphate
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-466/Product: glutamate 1-semialdehyde aminotransferase #status predicted <MAT>
F:306/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 1.5%; Score 8; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LSSSTRSR 30
|||||||
DB 17 LSSSTRSR 24

RESULT 12
F70785
hypothetical protein RV2205C - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: F70785
R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70785
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-480 <COL>
A:Cross-references: GB:F70283; GB:AL123456; NID:G3261561; PIDN:CAA94248.1; PID:G233581;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV2205C

Query Match 1.5%; Score 8; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 PPTPTAL 405
|||||||
DB 223 PPTPTAL 230

RESULT 13
T01491
ubiquitin-protein ligase homolog F1707.15 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
C:Accession: T01491
R:Vysotskaya, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N. submitted to the EMBL Data Library, June 1998
A:Description: *Arabidopsis thaliana* chromosome 1 BAC F1707 sequence.
A:Reference number: Z14334
A:Accession: T01491
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1126 <VYS>
A:Cross-references: EMBL:AC003671; NID:G2833627; PID:G1176690; GSPDB:GN00059; ATSP:F1707
A:Experimental source: cytovar Columbia
C:Genetics:
A:Gene: ATSP:F1707.15
A:Map position: 1
A:Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2
C:Superfamily: ubiquitin-protein ligase homolog
F:756-1120/Domain: ubiquitin-protein ligase homolog <UBT>

Query Match 1.5%; Score 8; DB 2; Length 1126;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ASGUSST 27
|||||||
DB 492 ASGUSST 499

RESULT 14
S52781
neurocan - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C:Accession: S52781
R:Rauch, U.; Foreberg, N.; Kulbe, G.; Arnold-Ammer, I.; Feeseler, R. submitted to the EMBL Data Library, February 1995
A:Description: Amino acid sequence of mouse neurocan and brevican and their different ex
A:Reference number: S52781
A:Accession: S52781
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1268 <RAU>
A:Cross-references: EMBL:X84727; NID:G758629; PIDN:CAA59226.1; PID:G758630
C:Superfamily: aggregan; C-type lectin homolog; complement factor H repeat homolog; EG
F:1176-253/Domain: link protein repeat homolog <LNK1>
F:274-355/Domain: link protein repeat homolog <LNK2>
F:964-955/Domain: EGF homolog <EGF>
F:1040-1160/Domain: C-type lectin homolog <LCH>
F:1167-1223/Domain: complement factor H repeat homolog <FHD>

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Query Match      1.5%; Score 8; DB 2; Length 1268;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      218 GEPDLTW 225
Db      413 GEPDLTW 420

RESULT 15
SS1656
Vascular endothelial growth factor receptor - Japanese quail
N:Alternate names: quail endothelial kinase 1 (Qek 1); vascular endothelial growth fact
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 07-May-1995 #sequence revision 01-Sep-1995 #text_change 08-Dec-2000
C:Accession: J04953; A56598; I51162; S51656
R:Elchmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996
A:Title: Molecular cloning of Qek 1 and 2, two quail vascular endothelial growth factor
A:Reference number: J04953; MUID:97017121; PMID:8863722
A:Accession: J04953
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1348 <E1C1>
A:Cross-references: EMBL:X83288; NID:G603523; PIDN:CAA58268.1; PID:G603524
A:Note: submitted to the EMBL Data Library, December 1994
R:Elchmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Mech. Dev. 42, 33-48, 1993
A:Title: Two molecules related to the VEGF receptor are expressed in early endothelial c
A:Reference number: A56598; MUID:93378866; PMID:8396413
A:Accession: A56598
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 910-1348 <E1C2>
A:Cross-references: GB:S65205; NID:G410680; PIDN:AAE28127.1; PID:G410681
A:Note: sequence extracted from NCBI backbone (NCBIN:137162; NCBI:P:137163)
R:Marcelle, C.; Elchmann, A.
Oncogene 7, 2479-2487, 1992
A:Title: Molecular cloning of a family of protein kinase genes expressed in the avian en
A:Reference number: I50595; MUID:93096482; PMID:1281306
A:Accession: I51162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1023-1079 <MAR>
A:Cross-references: EMBL:X65994; NID:G395226; PIDN:CAA9364.1; PID:G938278
A:Note: the species is not identified by the authors; the most probable species is shown
C:Comment: This protein is an endothelial-specific receptor and binds vascular endothel
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; embryo; growth factor receptor; transmembrane protein
F:1-19/Domains: signal sequence #status predicted <SIG>
F:20-1138/Product: vascular endothelial growth factor receptor 1 #status predicted <NAT>
F:756-777/Domains: transmembrane #status predicted <TM>
F:833-1160/Domains: protein kinase homology <KIN>
F:831-839/Region: protein kinase ATP-binding motif

Query Match      1.5%; Score 8; DB 2; Length 1348;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      405 LQCTADKF 412
Db      559 LQCTADKF 566

RESULT 16
GNMWV
genome polyprotein - West Nile virus
N:Contains: core protein V2; membrane-associated glycoprotein NV2 precursor; membrane-as
C:Species: West Nile virus
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 19-Jan-2001
C:Accession: A25256

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R:Castle, E.; Leiner, U.; Nowak, T.; Wengler, G.; Wengler, G.
Virology 149, 10-26, 1986
A:Title: Primary structure of the West Nile flavivirus genome region coding for all non
A:Reference number: A25256; MUID:66124703; PMID:3753811
A:Accession: A25256
A:Molecule type: genomic RNA
A:Residues: 1-3430 <CAS>
A:Cross-references: GB:M10103; GB:M12294; NID:G136167; PIDN:AAA48498.1; PID:G136168
A:Note: parts of this sequence, including the amino ends of the mature proteins, were de
C:Superfamily: yellow fever virus genome polyprotein
C:Keywords: ATP; core protein; glycoprotein; membrane-associated protein; nucleotide bin
F:1-92/Product: core protein V2 #status predicted <CV2>
F:105-233/Product: membrane-associated glycoprotein NV2 precursor #status predicted <NV2>
F:105-123/Domains: nonterminal signal sequence #status predicted <SS>
F:124-233/Product: membrane-associated glycoprotein NV2 #status predicted <NV2>
F:216-233/Product: membrane-associated nonglycosylated protein V1 #status predicted <NV1>
F:275-787/Product: membrane-associated glycoprotein V3 precursor #status predicted <NV3>
F:275-280/Domains: nonterminal signal sequence #status predicted <SS>
F:291-787/Product: membrane-associated glycoprotein V3 #status predicted <NV3>
F:788-2109/Product: nonstructural protein NV4 #status predicted <NV4>
F:1695-1702/Region: nucleotide-binding motif A (P-loop)
F:1782-1787/Region: nucleotide-binding motif B
F:1786-1789/Region: DEAH motif
F:2580-3427/Product: nonstructural protein NV5 #status predicted <NV5>
F:138,917,962,994,1289,1659,2336,2459,2489,2573,2739,2759,2864,2902/Binding site: C

Query Match      1.5%; Score 8; DB 1; Length 3430;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      461 LAVGVVL 468
Db      772 LAVGVVL 779

RESULT 17
GNMWV
genome polyprotein - Kunjin virus (strain MRM61C)
N:Contains: capsid protein C; envelope protein E; membrane protein M; nonstructural prot
in NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: Kunjin virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 19-Jan-2001
C:Accession: A28697
R:Coia, G.; Parker, M.D.; Speight, G.; Byrne, M.E.; Westaway, E.G.
J. Gen. Virol. 69, 1-21, 1988
A:Title: Nucleotide and complete amino acid sequences of Kunjin virus: definitive gene o
A:Reference number: A28697; MUID:88089524; PMID:2826559
A:Accession: A28697
A:Molecule type: genomic RNA
A:Residues: 1-3433 <COI>
A:Cross-references: GB:D00246; NID:G221966; PIDN:BA00176.1; PID:G221967
C:Superfamily: yellow fever virus genome polyprotein
C:Keywords: ATP; capsid protein C; envelope protein E; membrane protein; nonstructural prote
C:Keywords: ATP; capsid protein C #status predicted <CPC>
F:124-290/Product: capsid protein C #status predicted <CPC>
F:124-290/Product: membrane protein M precursor #status predicted <MP>
F:124-215/Domains: nonterminal signal sequence #status predicted <SIG>
F:216-280/Product: membrane protein M #status predicted <MP>
F:291-791/Product: envelope protein E #status predicted <EP>
F:792-1143/Product: nonstructural protein NS1 #status predicted <NS1>
F:1144-1374/Product: nonstructural protein NS2a #status predicted <NS2a>
F:1375-1505/Product: nonstructural protein NS2b #status predicted <NS2b>
F:1506-2124/Product: nonstructural protein NS3 #status predicted <NS3>
F:1699-1706/Region: nucleotide-binding motif A (P-loop)
F:1786-1791/Region: nucleotide-binding motif B
F:1790-1793/Region: DEAH motif
F:2125-2273/Product: nonstructural protein NS4a #status predicted <NS4a>
F:2274-2528/Product: nonstructural protein NS4b #status predicted <NS4b>
F:2529-3433/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match      1.5%; Score 8; DB 1; Length 3433;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 461 LAVGSVLL 468
|||||
Db 776 LAVGSVLL 783

RESULT 18

GNMWV
genome polypeptide - Murray Valley encephalitis virus (strain Australia)
N:Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS
a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: Murray Valley encephalitis virus
C:Date: 30-Jun-1988 #sequence_revision 17-Feb-1994 #text_change 19-Jan-2001
C:Accession: A24635; A60288
R:Daigarno, L.; Trent, D.W.; Strauss, J.H.; Rice, C.M.
J. Mol. Biol. 187, 309-323, 1986
A:Title: Partial nucleotide sequence of the Murray Valley encephalitis virus genome: com
A:Reference number: A24635; MUID:86200215; PMID:3009829
A:Accession: A24635
A:Molecule type: genomic RNA
A:Residues: 1-1780 <DAL>
A:Cross-references: GB:X03467; NID:959329; PIDN:CAA27184.1; PID:9755731
R:Lee, E.; Fernon, C.; Simpson, R.; Weir, R.C.; Rice, C.M.; Daigarno, L.
Virus Genes 4, 197-213, 1990
A:Title: Sequence of the 3' half of the Murray Valley encephalitis virus genome and map
A:Reference number: A60288; MUID:91102934; PMID:1702914
A:Accession: A60288
A:Molecule type: genomic RNA
A:Residues: 1504-1778, 'V', 1780-3434 <LEB>
C:Superfamily: yellow fever virus genome polypeptide; glycoprotein; nonstructural protein;
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
F:1126-292/Product: capsid protein #status predicted <CAP>
F:1126-211/Product: membrane protein precursor #status predicted <GLC>
F:1126-211/Product: nonterminal signal sequence #status predicted <SIG>
F:218-292/Product: membrane protein #status predicted <GLM>
F:218-292/Product: transmembrane #status predicted <TM1>
F:293-793/Product: envelope protein #status predicted <ENV>
F:773-791/Product: transmembrane #status predicted <TM2>
F:794-1205/Product: nonstructural protein NS1 #status predicted <NS1>
F:1206-1372/Product: nonstructural protein NS2a #status predicted <NS2a>
F:1373-1503/Product: nonstructural protein NS2b #status predicted <NS2b>
F:1504-2122/Product: nonstructural protein NS3 #status predicted <NS3>
F:1697-1704/Product: nucleotide-binding motif A (P-loop)
F:1768-1789/Product: nucleotide-binding motif B
F:1788-1791/Product: DEAH motif
F:2123-2414/Product: nonstructural protein NS4a #status predicted <NS4a>
F:2415-2529/Product: nonstructural protein NS4b #status predicted <NS4b>
F:2530-3434/Product: nonstructural protein NS5 #status predicted <NS5>
F:73,140,446/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 1.5%; Score 8; DB 1; Length 3434;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 465 GVLLALL 472
|||||
Db 2228 GVLLALL 2235

RESULT 19

A60996
Complement C3 - bovine (fragment)
N:Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 07-Oct-1994
C:Accession: A60996
R:Awat, H.
FEBS Microbiol. Lett. 71, 305-310, 1990
A:Title: Association of a 38 kDa bovine serum protein with the outer membrane of Bordet
A:Reference number: A60996
A:Accession: A60996
A:Molecule type: protein
A:Residues: 1-23 <ANW>
A>Note: this protein was purified from Bordetella pertussis outer membranes after expo

ected after exposure to human serum
C:Comment: Complement C3 contains two chains, formed by removal of four residues and lin
alternative complement pathways, releases the C3a anaphylatoxin from the amino end of t
native-complement-pathway C3/C5 convertase.
C:Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C:Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
C:Comment: The major site of synthesis of this plasma protein is the liver.
C:Superfamily: alpha-2-macroglobulin
C:Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;

Query Match 1.3%; Score 7; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 358 LSDQVPD 364
|||||
Db 6 LSDQVPD 12

RESULT 20

hypothetical protein B15120.60 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000
C:Accession: T51036
R:Schulte, U.; Aign, V.; Hobeisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z55286
A:Accession: T51036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <SCH>
A:Cross-references: EMBL:AL389900; GSPDB:GN00116; NCSP:B15120.60
A:Experimental source: BAC clone B15120; strain OR74A
C:Genetics:
A:Gene: NCSP:B15120.60
A:Map position: 6
C:Superfamily: Neurospora crassa hypothetical protein B15120.60

Query Match 1.3%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 SASISGN 42
|||||
Db 89 SASISGN 95

RESULT 21

YcgK protein precursor - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: G64863
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G64863
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-113 <BLAT>
A:Cross-references: GB:AE000216; GB:U00096; NID:91787417; PIDN:AAC74262.1; PID:91787426;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: YcgK
C:Superfamily: Escherichia coli YcgK protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-133/Product: YcgK protein #status predicted <MAT>
Query Match 1.3%; Score 7; DB 2; Length 133;

Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALL 472
|||
Db 10 VLLALL 16

RESULT 22
H90837
hypothetical protein ECA672 (imported) - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: H90837
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Ganawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A59629; MUID:21156231; PMID:11258796
A:Accession: H90837
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA835095.1; PID:g13361136; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:
A:Gene: ECA672
C:Superfamily: Escherichia coli ycgK protein

Query Match 1.3%; Score 7; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALL 472
|||
Db 10 VLLALL 16

RESULT 23
A85696
hypothetical protein ycgK [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A85696
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, B.J.; Davis, N.W.; Lam, A.; Diallanata, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85696
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <STO>
A:Cross-references: GB:AE005174; NID:g12514875; PIDN:AAG56029.1; GSPDB:GN00145; UWGP:Z18
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ycgK
C:Superfamily: Escherichia coli ycgK protein

Query Match 1.3%; Score 7; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALL 472
|||
Db 10 VLLALL 16

RESULT 24
J01561
hypothetical 15.3k protein - Lymantria dispar nuclear polyhedrosis virus
N:Alternate names: hypothetical protein 5
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Sep-1999
C:Accession: J01561
R:Bjornson, R.M.; Rohmann, G.F.
J. Gen. Virol. 73, 1499-1504, 1992
A:Title: Nucleotide sequence of the polyhedron envelope protein gene region of the Lyman
A:Reference number: F00359; MUID:92300345; PMID:1607868
A:Accession: J01561
A:Molecule type: DNA
A:Residues: 1-141 <BJO>
A:Cross-references: DDBJ:D10836
A:Note: the authors translated the codon TAT for residue 19 as Thr, and TAT for residue
C:Superfamily: Lymantria dispar nuclear polyhedrosis virus hypothetical 15.3k protein

Query Match 1.3%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 376 TAAGSL 382
|||
Db 121 TAAGSL 127

RESULT 25
AG1972
hypothetical protein alr1330 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG1972
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuch
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG1972
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA873287.1; PID:g17130677; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1330

Query Match 1.3%; Score 7; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 384 ETPNFI 390
|||
Db 71 ETPNFI 77

RESULT 26
C70513
hypothetical protein Rv2120c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
C:Accession: C70513
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70513
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-160 <COL>
A:Cross-references: GB:Z97559; GB:AL123456; NID:g3261820; PIDN:CA810716.1; PID:e328401;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv2120c

C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV2120c

Query Match 1.3%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VILLALL 472
DB 6 VILLALL 12

RESULT 27

conserved hypothetical protein VC0439 [imported] - Vibrio cholerae (strain N16961 serog

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: F82322

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gilm, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamshayan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F. 1, R.R.; Mekalanos, J.U.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: F82322

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-161 <HEI>

A:Cross-references: GB:AE004311; GB:AE003852; NID:g9654856; PIDN:AAF93612.1; GSPDB:GN001

A:Experimental source: serogroup O1, strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0439

A:Map position: 1

C:Superfamily: primosomal operon 14K protein

Query Match 1.3%; Score 7; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 IAGLAVG 464
DB 140 IAGLAVG 146

RESULT 28

H87591
hypothetical protein CC2768 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: H87591

R:Heiman, W.C.; Feildbylum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gilm, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: H87591

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-169 <STO>

A:Cross-references: GB:AE005673; NID:g13424364; PIDN:AAK24732.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2768

Query Match 1.3%; Score 7; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VILLALL 472
DB 46 VILLALL 52

RESULT 29

B83411
hypothetical protein PA1867 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: B83411

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Micooguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: B83411

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-175 <STO>

A:Cross-references: GB:AE004613; GB:AE004091; NID:g9947856; PIDN:AG05256.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA1867

Query Match 1.3%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VILLALL 472
DB 37 VILLALL 43

RESULT 30

AG2369
cytochrome b6/f-complex iron-sulfur protein [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AG2369

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi

Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AG2369

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-178 <KDB>

A:Cross-references: GB:BA000019; PIDN:BA876210.1; PID:g17133647; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: petC

C:Superfamily: ubiquinol-cytochrome-c reductase iron-sulfur protein; Rieske [2Fe-2S] hom

Query Match 1.3%; Score 7; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 ALIAGLA 462
DB 78 ALIAGLA 84

RESULT 31

T16472
hypothetical protein F56C9.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16472

R:Du, Z.

submitted to the EMBL Data Library, May 1994

A:Description: The sequence of C. elegans coemid F56C9.

A:Reference number: S46725

A:Accession: T16472

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-182 <DUZ>
A:Cross-references: EMBL:U00063; NID:G488186; PID:G488194; PIDN:AA08717.1; CESP:F56C9.8
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F56C9.8
A:Introns: 19/3; 48/3; 74/2; 93/2

Query Match 1.3%; Score 7; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 464 GCVLLA 470
29 GGVLLA 35

RESULT 32
T36745
Probable RNA polymerase sigma factor - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T36745
R:Saunders, D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajadream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21613
A:Accession: T36745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-185 <SAN>
A:Cross-references: EMBL:AL096849; PIDN:CAB50938.1; GSPDB:GN00070; SCOEDB:SC11.12C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC11.12C
C:Superfamily: transcription initiation factor sigma E

Query Match 1.3%; Score 7; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 LTVLVAD 15
11 LTVLVAD 17

RESULT 33
C81224
conserved hypothetical protein NMB0215 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: C81224
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:2017555; PMID:10710307
A:Accession: C81224
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <TER>
A:Cross-references: GB:AE002379; GB:AE002098; NID:G7225435; PIDN:AAF40671.1; PID:G722543
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0215
C:Superfamily: Escherichia coli conserved hypothetical protein b1821

Query Match 1.3%; Score 7; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 164 GRCAEFA 170
|||||||

Db 161 GRCAEFA 167
|||||||

RESULT 34
D83334
conserved hypothetical protein PA2484 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83334
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: D83334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-204 <STO>
A:Cross-references: GB:AE004676; GB:AE004091; NID:G9948532; PIDN:AA05872.1; GSPDB:GN001.
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2484

Query Match 1.3%; Score 7; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 370 SAAVSAT 376
93 SAAVSAT 99

RESULT 35
A40305
biliary glycoprotein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 23-Jul-1999
C:Accession: A40305
R:Robbins, J.; Robbins, P.F.; Kozak, C.A.; Callahan, R.
Genomics 10, 583-587, 1991
A:Title: The mouse biliary glycoprotein gene (Bgp): partial nucleotide sequence, express
A:Reference number: A40305; MUID:9136364; PMID:1653760
A:Accession: A40305
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <ROB>
A:Cross-references: GB:M61907; GB:M73534; NID:G192197; PIDN:AAA7298.1; PID:G192198
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
F:2-51/Domain: immunoglobulin homology <IMM>
F:87-144/Domain: immunoglobulin homology <IMM>

Query Match 1.3%; Score 7; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 456 ALTAGLA 462
186 ALTAGLA 192

RESULT 36
C82979
hypothetical protein PA5341 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C82979
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: C82979
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <STO>
 A:Cross-references: GB:A8004946; GB:A8004091; NID:g9951650; PIDN:AAG08726.1; GSPDB:GN001
 A:Experimental source: strain P801
 C:Genetics:
 A:Gene: PA5341
 C:Superfamily: hypothetical protein b1798

Query Match 1.3%; Score 7; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 GVLTLAL 471
 |||||
 DB 191 GVLTLAL 197

RESULT 37
 F84563
 hypothetical protein At2g18380 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: F84563
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talion, L.
 eaus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: F84563
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-207 <STO>
 A:Cross-references: GB:A8002093; NID:g4309729; PIDN:AAD15499.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g18380
 A:Map position: 2

Query Match 1.3%; Score 7; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 STSVDC 444
 |||||
 DB 34 STSVDC 40

RESULT 38
 JX0244
 pyroglutamyl-peptidase I (EC 3.4.19.3) - Bacillus amyloliquefaciens
 N:Alternate names: 5-oxopropyl-peptidase; pyroglutamyl aminopeptidase
 C:Species: Bacillus amyloliquefaciens
 C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 18-Aug-2000
 C:Accession: JX0244
 R:Yoshimoto, T.; Shimoda, T.; Kitazono, A.; Kabashima, T.; Ito, K.; Tsuru, D.
 J. Biochem. 113, 67-73, 1993
 A>Title: Pyroglutamyl peptidase gene from Bacillus amyloliquefaciens: Cloning, sequencin
 A:Reference number: JX0244; MUID:93203177; PMID:8095933
 A:Accession: JX0244
 A:Molecule type: DNA
 A:Residues: 1-215 <YOS>
 A:Cross-references: DDBJ:D11035; NID:g216315; PIDN:BA01791.1; PID:g216316
 C:Superfamily: Bacillus subtilis pyroglutamyl-peptidase I pcg
 C:Keywords: hydrolase; omega peptidase

Query Match 1.3%; Score 7; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 AAVSYTA 377

DB 133 AAVSYTA 139
 |||||

RESULT 39
 S23432
 pyroglutamyl-peptidase I (EC 3.4.19.3) pcg - Bacillus subtilis
 N:Alternate names: 5-oxopropyl-peptidase; pyroglutamate carboxylate peptidase pcg
 C:Species: Bacillus subtilis
 C>Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 18-Aug-2000
 C:Accession: S23432 #sequence_revision 20-Feb-1995 #text_change 18-Aug-2000
 R:Awade, A.; Cleuziat, P.; Gonzales, T.; Robert-Baudouy, J.
 FEBS Lett. 305, 67-73, 1992
 A>Title: Characterization of the pcg gene encoding the pyroglutamate carboxyl peptidase of
 A:Reference number: S23432; MUID:9233527; PMID:1353026
 A:Accession: S23432
 A:Molecule type: DNA
 A:Residues: 1-215 <AWA>
 A:Cross-references: EMBL:X66034; NID:g40036; PIDN:CAA6833.1; PID:g40037
 A:Experimental source: strain 168
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bortner
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
 lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holteppel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel
 Y. M.; Ogawa, K.; Ogata, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
 Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpet, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Wintere, P.; Wipat, A.; Yamamoto, H.; Yamano, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zunsstein, E.; Yoshikawa, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9364377
 A:Accession: G69673
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-215 <KUN>
 A:Cross-references: GB:259105; GB:AL009126; NID:g2632457; PIDN:CAB12059.1; PID:g2632551
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: pcg; pcg
 C:Superfamily: Bacillus subtilis pyroglutamyl-peptidase I pcg
 C:Keywords: hydrolase; omega peptidase

Query Match 1.3%; Score 7; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 AAVSYTA 377
 |||||
 DB 133 AAVSYTA 139

RESULT 40
 AG3100
 replicative DNA helicase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AG3100
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: A82577; MUID:21608550; PMID:11743193
 A:Accession: AG3100
 A:Status: preliminary
 A:Molecule type: DNA

Tue Oct 7 10:37:59 2003

A:Residues: 1-217 <KUR>
A:Cross-references: GB:AE008689, PIDN:AAL45221.1, PID:gi7742902, GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4427
A:Map position: linear chromosome

Query Match 1.3% Score 7, DB 2, Length 217;
Best Local Similarity 100.0%; Pred.No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 377 AAGSLSE 383
|||
Db 33 AAGSLSE 39

Search completed: October 2, 2003, 16:06:29
Job time : 63 secs

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OM protein - protein search, using sw model

Run on: October 2, 2003, 15:53:10 / Search time 25 Seconds
(without alignments)
1017.658 Million cell updates/sec

Title: US-10-039-770A-1
Perfect score: 541
Sequence: 1 MGWGVQVLLVTVADCTIFA.....EAEENIQDGETHWVEGDY 541

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 127863 seqs, 47026705 residues
Word size: 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: Swissprot_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.5	200	Y966_MYCTU	P71544 mycobacteri
2	8	1.5	358	YM05_MYCTU	Q10394 mycobacteri
3	8	1.5	466	GSA_SOYBN	P45621 glycine max
4	8	1.5	1268	PCGN_MOUSE	P55066 mus musculu
5	8	1.5	1348	VGR2_COTJA	P55583 coturnix co
6	8	1.5	3430	POLG_MNV	P06935 w genome po
7	8	1.5	3433	POLG_KUNM	P14335 k genome po
8	8	1.3	114	RLA2_PARAR	P41099 parthenium
9	7	1.3	133	YCGK_ECOLI	P76002 escherichia
10	7	1.3	137	GILZ_MOUSE	Q94287 mus musculu
11	7	1.3	205	HYPA_ECOLI	P21481 escherichia
12	7	1.3	215	PCP_BACAM	P46107 bacillus am
13	7	1.3	215	PCP_BACSU	P28618 bacillus su
14	7	1.3	217	CLD9_HUMAN	O95484 homo sapien
15	7	1.3	217	CLD9_MOUSE	Q94087 mus musculu
16	7	1.3	217	YG18_HAEIN	P45275 haemophilus
17	7	1.3	226	RL1_BORRU	O51353 borrelia bu
18	7	1.3	234	GU45_RAT	P35898 rattus norv
19	7	1.3	257	FCEA_HUMAN	P13319 homo sapien
20	7	1.3	263	YOD1_CABEL	Q09262 caenorhabdi
21	7	1.3	271	CD5A_PSEAE	O59640 p phosphati
22	7	1.3	272	UPK_YERPE	O8165 yersinia pe
23	7	1.3	276	GRG_ECOLI	P09391 escherichia
24	7	1.3	284	DAPE_BUCAP	O81901 buchnera ap
25	7	1.3	289	AROK_METH	O26896 methanobact
26	7	1.3	298	Y727_METVA	O58137 methanococc
27	7	1.3	307	YSCQ_YERPE	P47713 yersinia pe
28	7	1.3	307	YSCQ_YERPE	P40296 yersinia ps
29	7	1.3	322	NI0H_HUMAN	P57258 buchnera ap
30	7	1.3	331	PHR4_HUMAN	O94196 homo sapien
31	7	1.3	333	CAP1_DICDI	P19198 dicystostei
32	7	1.3	335	BTUC_YERPE	O84dx4 yersinia pe
33	7	1.3	352	2185_MOUSE	O62394 mus musculu

34	7	1.3	376	YQCB_ERWCA	Q47417 erwina car
35	7	1.3	399	GALI_LACTA	Q9747 lactococcus
36	7	1.3	399	GALI_LACTC	Q9747 lactococcus
37	7	1.3	408	PGK_THKAC	O9195 thermoplasma
38	7	1.3	424	VG46_BPPFI	P5131 bacterioph
39	7	1.3	430	YKJ5_STRCO	O9Kye60 streptomyce
40	7	1.3	431	NMTH_CLOAB	O97nt5 clostridium
41	7	1.3	432	OAT_DROAN	P49724 dirosophila
42	7	1.3	436	NMTH_DEIRA	O97nt5 deinosoccus
43	7	1.3	450	FOKP_CHLMU	P82602 c foliate sy
44	7	1.3	462	US29_HCNVA	P09705 human cytom
45	7	1.3	481	BIND_STREU	P06651 strongyloce
46	7	1.3	485	NM4C_MARPO	P06263 marchantia
47	7	1.3	499	GATE_BOMMO	P52167 bombyx mori
48	7	1.3	508	CEA1_MOUSE	P31809 mus musculu
49	7	1.3	521	ASPA_CONGL	Q99200 corynebacte
50	7	1.3	563	CYB_SULAC	P39480 sulfolobus
51	7	1.3	570	MKKS_HUMAN	Q9npj1 homo sapien
52	7	1.3	589	C49A_DROME	O9513 drosophila
53	7	1.3	600	SP96_DICDI	P14328 dicystostei
54	7	1.3	602	DCP1_ORRSA	P51847 cryza sariv
55	7	1.3	608	UL27_HCNVA	P16763 human cytom
56	7	1.3	643	GAG_SFV3L	P27400 stimian foam
57	7	1.3	665	TKT_BUCAI	P57195 buchnera ap
58	7	1.3	690	PERO_DROME	Q01603 drosophila
59	7	1.3	723	PAB5_STRCO	P32483 streptomyce
60	7	1.3	727	PI01_HUMAN	Q02809 homo sapien
61	7	1.3	738	GCP4_ARATH	Q9m350 arabidopsis
62	7	1.3	739	GCP4_MEDTR	O9c68 medicago tr
63	7	1.3	802	FGR4_HUMAN	P22455 homo sapien
64	7	1.3	887	UFO_HUMAN	P20530 homo sapien
65	7	1.3	959	VP2_BTVAV	O06998 bluetongue
66	7	1.3	994	PROL_DROME	P35875 drosophila
67	7	1.3	1009	M2B2_HUMAN	Q9Y265 synecocyst
68	7	1.3	1093	RNT1_NEUCR	Q9heh1 neurospora
69	7	1.3	1104	COLA_CLOPE	P43153 clostridium
70	7	1.3	1174	NIFU_ECOLI	P52647 escherichia
71	7	1.3	1191	NIFU_RHORI	O53046 rhodospirill
72	7	1.3	1199	NIFU_ANASP	Q06879 anabena sp
73	7	1.3	1199	NIFU_STINY	P52965 synecocyst
74	7	1.3	1202	YE01_SCHPO	O13798 schizosacch
75	7	1.3	1663	CO3_HUMAN	P01024 homo sapien
76	7	1.3	1663	CO3_MOUSE	P01027 mus musculu
77	7	1.3	1663	CO3_RAT	P01027 rattus norv
78	7	1.3	1666	CO3_CAVPO	P12387 cavia porce
79	7	1.3	1857	FAS2_PENPA	P15368 p fatty aci
80	7	1.3	1964	NTC4_MOUSE	P21695 mus musculu
81	7	1.3	2337	TOR2_SCHPO	O97782 schizosacch
82	7	1.3	6486	TYCC_BREPA	O30409 b tyrocidin
83	7	1.3	38	DCH5_MTCSP	P00863 micrococcus
84	6	1.1	62	GBG_CABEL	P54406 caenorhabdi
85	6	1.1	64	LAP_BOVIN	Q28880 bos taurus
86	6	1.1	64	TAP_BOVIN	Q28880 bos taurus
87	6	1.1	67	YPUB_BACSU	P51511 bacillus su
88	6	1.1	69	GRK_BACCE	O94b11 bacillus ce
89	6	1.1	75	YA26_STPAE	O8c893 streptyloloc
90	6	1.1	76	CD24_MOUSE	P24887 mus musculu
91	6	1.1	76	CD24_RAT	Q07490 rattus norv
92	6	1.1	80	CD24_HUMAN	P25063 homo sapien
93	6	1.1	80	COXK_MOUSE	P56392 mus musculu
94	6	1.1	81	ATPH_ARATH	P56760 arabidopsis
95	6	1.1	81	ATPH_TORTA	P12231 lotus japon
96	6	1.1	81	ATPH_MARPO	P06287 marchantia
97	6	1.1	81	ATPH_PEA	P08212 pisum sativ
98	6	1.1	81	ATPH_SPIOI	P08483 spinacia ol
99	6	1.1	81	ATPH_TOBAC	P06286 nicotiana t
100	6	1.1	82	TEF3_RAT	Q03191 rattus norv
101	6	1.1	82	ATPH_ANTSP	O02851 antihumanio
102	6	1.1	82	ATPH_CHLRE	Q37304 chlamydomon
103	6	1.1	82	ATPH_CHLVE	O37304 chlamydomon
104	6	1.1	82	ATPH_CVACA	P56297 cyanidium c
105	6	1.1	82	ATPH_MESVI	Q9muc0 mesocistigma
106	6	1.1	82	ATPH_MESVI	Q9muc0 mesocistigma

107	6	1.1	82	1	ATPH_NBPOL	Q9t114 nephrolejmi	180	1.1	153	1	IL4_CERTO	P46652 cercocebus
108	6	1.1	82	1	ATPH_PORPU	P51246 porphyra pu	181	1.1	153	1	IL4_HUMAN	P05112 homo sapien
109	6	1.1	82	1	ATPH_KLEPN	O48414 klebsiella	182	1.1	153	1	IL4_MACFA	P05139 macaca fasc
110	6	1.1	83	1	ATPH_GALSU	P35013 galdiera s	183	1.1	153	1	IL4_MACMU	P51492 macaca mula
111	6	1.1	83	1	N19M_BOVIN	Q02371 bos taurus	184	1.1	153	1	UD03_MYCLE	P33431 mycobacteri
112	6	1.1	83	1	YK76_MYCTU	O10684 mycobacteri	185	1.1	155	1	NU6M_ALBCO	P48922 albinaria c
113	6	1.1	90	1	GON3_DICLA	O91409 dicentrarchi	186	1.1	156	1	VATL_HELVI	P55277 heliothia v
114	6	1.1	90	1	GON3_HABPU	P45652 haplochromi	187	1.1	156	1	VATL_MANSE	P11403 manduca sex
115	6	1.1	90	1	GON3_PAGMA	P51921 pagrus majo	188	1.1	157	1	VATL_AEDAE	O16110 aedes aegyp
116	6	1.1	90	1	GON3_SPAU	P51923 sparus aua	189	1.1	159	1	VATL_DROME	P23380 drosophila
117	6	1.1	92	1	SFSB_ECOLI	P18837 escherichia	190	1.1	160	1	PEPD_SYNY3	Q13322 homo sapien
118	6	1.1	92	1	YQ18_BACAN	O9m114 bacillus an	191	1.1	161	1	VATL_NEUCR	P27589 syntocyst
119	6	1.1	97	1	FER1_COLES	P00222 coloccasia e	192	1.1	160	1	PEPD_SYNY3	P14141 neurospora
120	6	1.1	98	1	FER2_PHYAM	P00231 phytiolacca	193	1.1	162	1	Y79A_METJA	P13113 methanococc
121	6	1.1	98	1	FER2_PHYES	P81373 phytiolacca	194	1.1	163	1	PHCA_ANASP	P07121 anaheana sp
122	6	1.1	98	1	FERB_ALOMA	P81373 alocasia ma	195	1.1	163	1	SR19_DROME	P49963 drosophila
123	6	1.1	99	1	NL74_ORYSA	Q42976 oryza sativ	196	1.1	165	1	NGK7_HUMAN	Q16617 homo sapien
124	6	1.1	101	1	NU1C_OENHO	O9m110 oenothera h	197	1.1	166	1	PAL_PSEPK	P43036 pseudomonas
125	6	1.1	101	1	INSE_ECOLI	P77681 escherichia	198	1.1	169	1	GSNC_SCHMA	Q00277 schistosoma
126	6	1.1	102	1	INSE_SHITL	P59445 shigella fl	199	1.1	170	1	RUVK_CHLMU	O9p199 chlamydia m
127	6	1.1	102	1	FTSB_SALTY	O8x6p2 salmoneila	200	1.1	171	1	RUVK_CHLTR	O84510 chlamydia t
128	6	1.1	103	1	FTSB_KLEAE	O9eyy3 klebsiella	201	1.1	171	1	NU5B_BRUME	O8y2k1 yersenia b
129	6	1.1	105	1	YPPK_SALTY	O9z4t5 salmoneila	202	1.1	171	1	Y334_RALSO	O03175 lactimeria c
130	6	1.1	109	1	INS_SPEPR	O9z4t5 spermothiliu	203	1.1	173	1	NU6M_LATCH	O8y2k1 yersenia b
131	6	1.1	110	1	INS_SPEPR	O9z4t5 spermothiliu	204	1.1	176	1	VP26_EBV	O8y2k1 yersenia b
132	6	1.1	112	1	FER1_CAUCR	O45972 caulobacter	205	1.1	178	1	YFDR_ECOLI	P14348 epstein-bar
133	6	1.1	115	1	INS_VERMO	O9w1r2 verasper mo	206	1.1	179	1	IL22_HUMAN	O8y2k6 homo sapien
134	6	1.1	116	1	INS_LOPPI	P01441 lophius pis	207	1.1	179	1	RU5_BACST	P08895 bacillus st
135	6	1.1	118	1	VAG2_HUMAN	O95670 homo sapien	208	1.1	181	1	ITPR_UREPA	O8y2k6 ureaplasma
136	6	1.1	119	1	GSPI_AERHY	P31377 aeromonas h	209	1.1	182	1	PERP_MOUSE	O88593 mus musculu
137	6	1.1	122	1	IAAT_ELECO	P01087 eleusine co	210	1.1	182	1	Y391_HAEIN	P33992 haemophilus
138	6	1.1	122	1	YK63_MYCTU	O10674 mycobacteri	211	1.1	182	1	YVJA_ECOLI	P76222 escherichia
139	6	1.1	123	1	SV65_RAT	P04812 rattus norv	212	1.1	187	1	KORC_ARCFU	O29779 archaeoglob
140	6	1.1	124	1	MAG3_HUMAN	P43355 homo sapien	213	1.1	187	1	SODC_HAEIN	P25841 haemophilus
141	6	1.1	126	1	ANFC_BOVIN	P52066 bos taurus	214	1.1	188	1	ISPP_CAUCR	O9a288 caulobacter
142	6	1.1	126	1	ANFC_MOUSE	O61839 mus musculu	215	1.1	189	1	GCHI_LISMO	O8y3k1 listeria mo
143	6	1.1	126	1	ANFC_MOUSE	P52077 rattus norv	216	1.1	189	1	INAI_BOVIN	P07348 bos taurus
144	6	1.1	127	1	CSF2_RAT	O48750 rattus norv	217	1.1	189	1	INAD_BOVIN	P49876 bos taurus
145	6	1.1	128	1	VG64_BPML5	O05377 mycobacteri	218	1.1	189	1	INAF_BOVIN	P49877 bos taurus
146	6	1.1	129	1	VG58_BPMD2	O64449 mycobacteri	219	1.1	189	1	YI64_AOUDE	O67915 aquifex aeo
147	6	1.1	130	1	TAT_HVZKR	Q74124 human immun	220	1.1	189	1	YI64_AOUDE	P19661 bos taurus
148	6	1.1	130	1	VG58_BPML5	O05371 mycobacteri	221	1.1	190	1	BCT7_BOVIN	O91u45 nisseeria m
149	6	1.1	130	1	YHL9_YEAST	P38783 saccharomyc	222	1.1	192	1	MOBA_NEIMA	P56747 nisseeria m
150	6	1.1	131	1	AGSR_MOUSE	P56473 mus musculu	223	1.1	192	1	MOBA_NEIMA	O01151 homo sapien
151	6	1.1	132	1	IL4_HORSE	P42202 equus cabal	224	1.1	194	1	HIS7_LISMO	O8Y992 listeria mo
152	6	1.1	133	1	CTFE_YEAST	P38877 saccharomyc	225	1.1	195	1	BID_MOUSE	P70444 mus musculu
153	6	1.1	133	1	SRP_CHLPS	P28164 chlamydia p	226	1.1	197	1	SDC4_CHICK	P49415 gallus gall
154	6	1.1	134	1	TRBC_AGRUV	P54908 agrobacteri	227	1.1	198	1	XAI_XENLA	P24507 xenopus lae
155	6	1.1	134	1	RRF1_DESVH	P33394 desulfovibr	228	1.1	203	1	LEXA_LEPIN	O81663 leptospira
156	6	1.1	139	1	IGF_MYXGL	P22618 myxine glut	229	1.1	205	1	CB03_HUMAN	O01151 homo sapien
157	6	1.1	139	1	TOLE_HAEIN	P43769 haemophilus	230	1.1	205	1	YK07_YEAST	P36061 saccharomyc
158	6	1.1	140	1	CSF2_CAVPO	O60481 cavia porce	231	1.1	206	1	GPBB_MOUSE	P56400 mus musculu
159	6	1.1	140	1	VE6_HPV24	P50777 human papil	232	1.1	209	1	LPCA_CHLRE	O8kaw3 chlorobium
160	6	1.1	141	1	CSF2_MOUSE	P01587 mus musculu	233	1.1	209	1	YGGI_BACSU	P66707 bacillus su
161	6	1.1	142	1	MK_CHICK	P24052 gallus gall	234	1.1	210	1	YR47_CAUCR	O9a413 caulobacter
162	6	1.1	143	1	CMGD_BACSU	P25566 bacillus su	235	1.1	210	1	Y743_CABEL	Q11071 caenorhabdi
163	6	1.1	143	1	CSF2_BOVIN	P11052 bos taurus	236	1.1	211	1	YEDZ_BCOS7	O8xb73 escherichia
164	6	1.1	143	1	IF1A_WHEAT	P47815 triticum ae	237	1.1	211	1	YEDZ_BCOS7	P76343 escherichia
165	6	1.1	143	1	IF1H_HUMAN	O75642 homo sapien	238	1.1	214	1	AB20_BRUPE	O04041 prunus pers
166	6	1.1	143	1	IF1X_HUMAN	P47813 homo sapien	239	1.1	215	1	WM12_YEAST	P23341 saccharomyc
167	6	1.1	143	1	IF1Y_HUMAN	O14602 homo sapien	240	1.1	216	1	SSPN_MOUSE	O63147 mus musculu
168	6	1.1	143	1	MRAR_ENTFA	O07103 enterococcu	241	1.1	219	1	YQFA_ECOLI	O46827 escherichia
169	6	1.1	143	1	NIRI_PARDE	O51699 paracoccu	242	1.1	220	1	ATPL_METJA	O57674 methanococc
170	6	1.1	144	1	CSF2_HUMAN	P04141 homo sapien	243	1.1	221	1	SGF3_CHICK	P48801 gallus gall
171	6	1.1	144	1	IF1A_ONOVI	P56331 onodrychis	244	1.1	221	1	SDPL_HUMAN	O9pnc8 homo sapien
172	6	1.1	145	1	PA2K_BUNCE	O9df52 bungarus ca	245	1.1	222	1	EMBP_HUMAN	P13727 homo sapien
173	6	1.1	146	1	YTAB_HUMAN	O76095 homo sapien	246	1.1	223	1	CDR1_HUMAN	P51861 homo sapien
174	6	1.1	146	1	YTAB_BACSU	P37523 bacillus su	247	1.1	223	1	EMBP_MOUSE	O61878 mus musculu
175	6	1.1	147	1	GLP3_GLYDI	P21660 glycera dib	248	1.1	223	1	KAD4_HUMAN	P27144 homo sapien
176	6	1.1	147	1	Y782_TREPA	O83761 treponema p	249	1.1	225	1	NARI_ECOLI	P11350 escherichia
177	6	1.1	151	1	Y000_MYCPA	O9K537 mycobacteri	250	1.1	227	1	EMBP_RAT	O63189 rattus norv
178	6	1.1	152	1	GST3_HUMAN	O14880 homo sapien	251	1.1	228	1	MODB_RHOCA	O08382 rhododacter
179	6	1.1	152	1	SSB_RICPR	O9zcc2 rickettsia	252	1.1	231	1	NARW_ECOLI	P19317 escherichia

253	6	1.1	231	1	YRKP_BACSU	P54443	326	6	1.1	279	1	Y43D_MYCPN	P75155	mycoplasma
254	6	1.1	233	1	EMBI_CAVPO	P22032	327	6	1.1	280	1	QCRC_MYCTU	Q10386	mycobacteri
255	6	1.1	234	1	A29B_DROME	O46197	328	6	1.1	281	1	ATP6_STRLI	P50012	streptomyce
256	6	1.1	234	1	EMB2_CAVPO	P35709	329	6	1.1	282	1	AROX_METJA	O58833	methanococ
257	6	1.1	235	1	COLI_MOUSE	P01193	330	6	1.1	282	1	YHDR_ECOLI	P46475	methanococ
258	6	1.1	235	1	COLI_MOUSE	P01194	331	6	1.1	284	1	KDGA_PASHA	P95514	pasteurella
259	6	1.1	238	1	NEUM_HUMAN	P17677	332	6	1.1	284	1	NODO_RHLIV	P55728	rhizobium
260	6	1.1	238	1	SSPN_RABIT	P82352	333	6	1.1	284	1	UPK_IACIL	P15787	lactococcus
261	6	1.1	238	1	Y062_BORBU	O51083	334	6	1.1	285	1	T13B_HUMAN	O92275	homo sapien
262	6	1.1	239	1	US21_HCMVA	P09723	335	6	1.1	286	1	YV8_SCHPO	O10216	schizosacch
263	6	1.1	240	1	IBP6_HUMAN	P24592	336	6	1.1	286	1	YVGB_ECOLI	P11666	escherichia
264	6	1.1	240	1	RIJ2_HALMA	P12736	337	6	1.1	286	1	YVGB_EDWIC	O52401	edwardsiell
265	6	1.1	241	1	KRPP_HRSVL	P24567	338	6	1.1	287	1	YCXE_BACSU	P40420	bacillus su
266	6	1.1	241	1	YMF3_BACSU	O31761	339	6	1.1	288	1	LEP4_PSEPU	P36642	pseudomonas
267	6	1.1	242	1	GUNS_TIRIE	P43317	340	6	1.1	288	1	UBIA_PROST	O53366	providencia
268	6	1.1	242	1	NAGB_MYCPE	O8em7	341	6	1.1	289	1	KRPP_ECOLI	P73307	escherichia
269	6	1.1	243	1	SSPN_HUMAN	Q14714	342	6	1.1	290	1	BET4_YEAST	Q00618	s type 11 p
270	6	1.1	244	1	CBR2_MOUSE	P08074	343	6	1.1	291	1	IBP3_MOUSE	P47878	mus muscullu
271	6	1.1	244	1	CBR2_PIG	Q29529	344	6	1.1	293	1	YF09_MYCTU	P71788	mycobacteri
272	6	1.1	245	1	COMB_ANASP	O8Yc25	345	6	1.1	294	1	PROG_MYCLE	P46725	mycobacteri
273	6	1.1	245	1	DMA_SQUAC	P36963	346	6	1.1	295	1	DUSF_HUMAN	O9H1r2	homo sapien
274	6	1.1	245	1	PUR7_ANASP	O8Yur7	347	6	1.1	295	1	PROC_MYCTU	O11141	mycobacteri
275	6	1.1	246	1	CYS2_PSEAE	Q91595	348	6	1.1	296	1	NAAI_ECOLI	O8d458	escherichia
276	6	1.1	246	1	PRTP_HSV2	P36385	349	6	1.1	296	1	NAAI_ECOLI	P06995	escherichia
277	6	1.1	246	1	YLS4_CORGL	P94338	350	6	1.1	297	1	KHSE_PYRAE	O8azx3	pyrobaculum
278	6	1.1	247	1	FENR_ECOLI	P28861	351	6	1.1	297	1	NANA_SALTY	O8z3f0	salmonella
279	6	1.1	247	1	MPUI_CRIGR	O60441	352	6	1.1	297	1	NANA_SALTY	O8z1f6	salmonella
280	6	1.1	247	1	STCI_HUMAN	P52823	353	6	1.1	298	1	VAS2_HAETN	P45008	hemophilus
281	6	1.1	248	1	DSBG_ECO57	P58320	354	6	1.1	299	1	NRAM_MYCTU	Q8qk75	mycoplasma
282	6	1.1	248	1	DSBG_ECOLI	P77202	355	6	1.1	300	1	DAPA_METJA	Q8uq75	methanopyru
283	6	1.1	249	1	FENR_SHILK	P28901	356	6	1.1	300	1	Y270_BUCAC	P42394	buchnera ap
284	6	1.1	249	1	MYPO_CHICK	P37301	357	6	1.1	301	1	KLF7_MOUSE	O99jbo	mus muscullu
285	6	1.1	250	1	DIP_ANTMA	P33560	358	6	1.1	302	1	KLF7_HUMAN	O75840	mus muscullu
286	6	1.1	250	1	TIP1_TOBAC	P21653	359	6	1.1	305	1	CAH4_MOUSE	O64444	mus muscullu
287	6	1.1	250	1	TIP2_TOBAC	P24422	360	6	1.1	305	1	ILP_ERACL	P22334	branchiost
288	6	1.1	252	1	Y067_MYCTU	P71964	361	6	1.1	305	1	NAA2_ECOLI	Q8Idu7	escherichia
289	6	1.1	254	1	PUR7_AGR75	Q8ueb7	362	6	1.1	305	1	YN45_DEIRA	O9rty7	deinococcus
290	6	1.1	256	1	COLI_CAVPO	P19402	363	6	1.1	309	1	CAH4_RAT	P48284	rattus norv
291	6	1.1	256	1	HYPA_HYPLI	P35587	364	6	1.1	309	1	GAG_FUSIV	O9b100	homo sapien
292	6	1.1	257	1	KLK4_MOUSE	P00757	365	6	1.1	309	1	O7A1_HUMAN	Q9wu72	mus muscullu
293	6	1.1	257	1	PAEJ_ECOLI	P33784	366	6	1.1	309	1	T13B_MOUSE	Q9wu72	mus muscullu
294	6	1.1	258	1	ARGB_BACSU	P36840	367	6	1.1	310	1	FIRA_PLAUF	P69916	plasmodium
295	6	1.1	260	1	Y230_ARCFU	O30009	368	6	1.1	310	1	RFMI_YEAST	Q12192	saccharomyc
296	6	1.1	261	1	KLK1_MOUSE	P15947	369	6	1.1	310	1	YE99_SCHPO	O13771	schizosacch
297	6	1.1	261	1	PSMA_METJA	O60177	370	6	1.1	310	1	YS19_STRCO	Q9zab5	streptomyce
298	6	1.1	264	1	COLI_MACNE	P01201	371	6	1.1	311	1	MAB2_MOUSE	O64277	mus muscullu
299	6	1.1	264	1	COMT_RAT	P22734	372	6	1.1	311	1	MAB2_STRPN	Q97rk3	s peptide m
300	6	1.1	264	1	PUR7_RHILIO	Q98nm8	373	6	1.1	312	1	CAH4_BOVIN	O95323	bos taurus
301	6	1.1	265	1	CB23_PEA	P27520	374	6	1.1	312	1	CELF_PRYVA	O85230	pseudorabie
302	6	1.1	265	1	COLI_BOVIN	P01190	375	6	1.1	312	1	TRAD_HUMAN	O15628	homo sapien
303	6	1.1	265	1	CYSH_RHIME	P56891	376	6	1.1	313	1	YEIC_ECOLI	P30235	escherichia
304	6	1.1	265	1	KXHI_CANGA	O74684	377	6	1.1	314	1	TEST_HUMAN	Q9y6m0	homo sapien
305	6	1.1	265	1	Y108_ARCFU	O30128	378	6	1.1	315	1	KERS_BACCL	P42816	bacillus ca
306	6	1.1	266	1	IT2A_SULSO	Q97z79	379	6	1.1	315	1	PERI_HORVU	P27337	hordium vul
307	6	1.1	266	1	YC41_HAEIN	P44133	380	6	1.1	317	1	CYF_CHLRE	P23377	chlamydomon
308	6	1.1	267	1	COLI_HUMAN	P01189	381	6	1.1	318	1	BSTI_HUMAN	O10588	homo sapien
309	6	1.1	267	1	PRR2_BOVIN	P12401	382	6	1.1	319	1	BSTI_RAT	O63072	rattus norv
310	6	1.1	267	1	Y5R4_CAEEL	Q09952	383	6	1.1	319	1	O7A5_HUMAN	Q15622	homo sapien
311	6	1.1	268	1	KXHI_YEAST	P50112	384	6	1.1	319	1	Y597_CAEEL	O09966	caenorhabdi
312	6	1.1	269	1	LEP4_SYNY3	P76640	385	6	1.1	320	1	KITH_PRYVA	P27363	pseudorabie
313	6	1.1	269	1	V669_BPMD2	O64262	386	6	1.1	320	1	Y098_NPVAC	P24745	autographa
314	6	1.1	270	1	PNK1_UREPA	Q9PqW6	387	6	1.1	321	1	RLPA_SYNY3	O55755	synhechoyct
315	6	1.1	270	1	PYRD_THEMEA	Q9Yqg8	388	6	1.1	322	1	PLV_MORBO	P20665	mayoraxella b
316	6	1.1	270	1	REP8_HUMAN	O00124	389	6	1.1	322	1	PLV_MORLA	P19257	mayoraxella l
317	6	1.1	272	1	RIJ2_ECOLI	P03387	390	6	1.1	323	1	COBD_AERPE	Q9yaa0	aeropyrum p
318	6	1.1	273	1	GFR4_RAT	Q9ep12	391	6	1.1	323	1	LIPA_BUCAL	P57357	buchnera ap
319	6	1.1	274	1	GSNO_HUMAN	P48507	392	6	1.1	323	1	Y0C5_MYCLE	O69518	mycobacteri
320	6	1.1	274	1	GSNO_MOUSE	O09172	393	6	1.1	324	1	PHT2_PSEPU	O05182	pseudomonas
321	6	1.1	275	1	YKX2_CAEEL	P34324	394	6	1.1	325	1	IRF1_HUMAN	P10914	rana catesb
322	6	1.1	275	1	NRTB_SYNY3	P73451	395	6	1.1	325	1	NIUM_RANCA	P16672	gyna max
323	6	1.1	275	1	Y5S1_METJA	O57971	396	6	1.1	326	1	KOX3_SOYBN	O03376	glycine max
324	6	1.1	278	1	UPK2_AGR75	P58741	397	6	1.1	326	1	ODPB_RICPR	Q9zbc7	rickettsia
325	6	1.1	278	1	YNP1_CAEEL	Q99q60	398	6	1.1	327	1	DCYD_ECO57	Q8zbc7	escherichia

399	1.1	327	1	DCYD_BCOL6	P59329	472	1.1	372	1	GDF1_HUMAN	P27539
400	1.1	327	1	DCYD_ECOLI	P76316	473	1.1	372	1	LIG6_PHACH	P50622
401	1.1	327	1	DCYD_SALTI	O85589	474	1.1	375	1	BAPE_BACSU	P45943
402	1.1	327	1	DCYD_SALTY	O85287	475	1.1	375	1	YCDO_ECOLI	P75902
403	1.1	327	1	DCYD_SHIFL	P59330	476	1.1	376	1	AROC_THEMEA	O9wy12
404	1.1	327	1	RPOA_UREPA	O9pqn4	477	1.1	376	1	GBAS_LYMET	P30684
405	1.1	327	1	Y8A6_ARCFU	O28826	478	1.1	377	1	Y392_CHLTR	P64272
406	1.1	328	1	IRP1_RAT	P23570	479	1.1	378	1	CARA_RALSO	P64272
407	1.1	329	1	HEM1_FUSNN	O84687	480	1.1	378	1	CYB_ELEMA	O47885
408	1.1	329	1	IRP1_MOUSE	P15314	481	1.1	378	1	CYB_LOXAP	P24958
409	1.1	330	1	DCYD_YERPE	O84f73	482	1.1	378	1	CYB_WAMPR	P22658
410	1.1	330	1	PGIP_PYRCO	O05091	483	1.1	378	1	RAVA_BACSU	P00828
411	1.1	331	1	LDHD_LEUMC	P51011	484	1.1	378	1	SLGI_YEAST	P4867
412	1.1	333	1	CDIC_HUMAN	P29017	485	1.1	379	1	P2X6_MOUSE	O54803
413	1.1	333	1	STAC_HUMAN	O11206	486	1.1	379	1	P2X6_MOUSE	P1579
414	1.1	336	1	VG27_BPM2	O64221	487	1.1	380	1	CAIA_ECOLI	P1579
415	1.1	336	1	VG27_BPM5	O05534	488	1.1	380	1	CAIA_PROSL	O89b20
416	1.1	340	1	YDDR_ECOLI	P77308	489	1.1	380	1	CAIA_SALTY	O82912
417	1.1	344	1	DCUP_BACHD	O9kd10	490	1.1	380	1	CAIA_SALTY	O82912
418	1.1	344	1	DFPB_MOUSE	O54788	491	1.1	380	1	CYB_VERRU	O82912
419	1.1	344	1	RL3_AERPE	O9yfm2	492	1.1	381	1	CYB_PARP	O82912
420	1.1	344	1	SPI2_VARY	P33830	493	1.1	382	1	NUSA_BACHD	O82912
421	1.1	345	1	GAG1_HUMAN	P54826	494	1.1	384	1	GALI_ACTPL	O82912
422	1.1	345	1	HIOM_BOVIN	P10950	495	1.1	384	1	GALI_HABIN	O82912
423	1.1	345	1	RECA_AQUAE	O67905	496	1.1	385	1	TPST_DROME	O82912
424	1.1	345	1	SPI2_RABPU	P42926	497	1.1	385	1	LMPI_EBV	O82912
425	1.1	346	1	NRL1_ARATH	P32861	498	1.1	386	1	LMPI_EBV	O82912
426	1.1	346	1	YR24_CAEEL	O09341	499	1.1	387	1	DADR_MOUSE	O82912
427	1.1	348	1	FEN_METKA	O8rxu4	500	1.1	387	1	DADR_MOUSE	O82912
428	1.1	348	1	RECA_AQUPY	P33542	501	1.1	387	1	RU3A_SCHPO	P40372
429	1.1	348	1	Y567_HELPY	O25591	502	1.1	387	1	RU3B_SCHPO	P40372
430	1.1	348	1	Y735_STRFR	P20186	503	1.1	387	1	SGCA_RABIT	P26584
431	1.1	349	1	AOX1_SAUOU	P22185	504	1.1	387	1	YG49_METUA	P26584
432	1.1	349	1	CTGF_BOVIN	O18739	505	1.1	388	1	GALI_LACHE	O00052
433	1.1	349	1	CTGF_PIG	O19113	506	1.1	388	1	GALI_STRTR	O00052
434	1.1	349	1	Y567_HELPY	O921r4	507	1.1	389	1	GALI_CIOAB	O00052
435	1.1	350	1	ACCO_PESH	P32021	508	1.1	389	1	RU3B_ARATH	P22738
436	1.1	350	1	HYPE_RHIV	P40599	509	1.1	389	1	YD22_DEIRA	O9uru0
437	1.1	350	1	PL6_MOUSE	O9wuh1	510	1.1	390	1	SH1B_RABIT	P49144
438	1.1	351	1	IBHC_RAT	O9wuh1	511	1.1	390	1	GALI_STRMU	P49144
439	1.1	351	1	PL6_HUMAN	O12893	512	1.1	390	1	YV18_SCHPO	O09895
440	1.1	351	1	PLNC_PENCI	P47189	513	1.1	390	1	YV13_ARCFU	O09895
441	1.1	352	1	IBHC_MOUSE	P55104	514	1.1	391	1	TRBL_RHISN	O09895
442	1.1	352	1	R8S1_ARATH	O9e888	515	1.1	392	1	CARA_THEMEA	O5w228
443	1.1	353	1	EDG7_HUMAN	O9ubys	516	1.1	393	1	HIS2_LISMO	O8y9f9
444	1.1	354	1	EDG7_MOUSE	O9e3j1	517	1.1	393	1	SETB_ECOLI	P33026
445	1.1	354	1	EDG7_RAT	O8K5e0	518	1.1	393	1	SETB_SALTY	P33027
446	1.1	354	1	YCDH_HUMAN	P00480	519	1.1	396	1	CATE_HUMAN	P40911
447	1.1	354	1	MLTC_HAEIN	O34538	520	1.1	396	1	DH11_XENLA	O91610
448	1.1	357	1	MCAL_CRIGR	P34649	521	1.1	396	1	PAS_XENLA	P37233
449	1.1	359	1	FIXB_AZOVI	O54873	522	1.1	396	1	S1BL_HUMAN	O75177
450	1.1	360	1	MTSB_IACLC	P34878	523	1.1	398	1	CATE_RAT	P16228
451	1.1	360	1	Y503_CAEEL	O09358	524	1.1	398	1	DH12_XENLA	O91611
452	1.1	361	1	SERC_WIGBR	O84668	525	1.1	398	1	GCST_PYRAB	O9wz8p
453	1.1	362	1	ALBU_HORVU	O84668	526	1.1	399	1	TRMU_AGRYS	O8u9m5
454	1.1	362	1	LEU3_PICAN	P05167	527	1.1	399	1	CHS2_HORVU	O96562
455	1.1	362	1	YEL1_ECOLI	P34733	528	1.1	399	1	CK05_MOUSE	O96562
456	1.1	362	1	YEL1_ECOLI	P33020	529	1.1	399	1	PRSW_BUCHI	P53131
457	1.1	362	1	GALI_CAEEL	P96910	530	1.1	399	1	YV11_STRCL	P18834
458	1.1	363	1	GALI_MYCTV	P21875	531	1.1	400	1	CYH2_HUMAN	O99414
459	1.1	364	1	VM21_BORHE	P25066	532	1.1	400	1	CYH2_MOUSE	P97695
460	1.1	365	1	P43_XENBO	P25066	533	1.1	400	1	MOAI_XENLA	P10667
461	1.1	365	1	P43_XENLA	P25066	534	1.1	400	1	PKGY_TOBAC	O42962
462	1.1	365	1	VSX1_BOVIN	O9gma3	535	1.1	401	1	PKRY_WHEAT	P12783
463	1.1	366	1	BCPA_PROAB	P11741	536	1.1	402	1	KLFC_HUMAN	O94744
464	1.1	368	1	CHEB_PYRAB	O9uyf3	537	1.1	402	1	KLFC_MOUSE	O35738
465	1.1	368	1	CHEB_PYRHO	O58192	538	1.1	402	1	OXAI_YEAST	P33952
466	1.1	368	1	ID12_SULSO	P95997	539	1.1	403	1	ARGD_VIBVU	P59323
467	1.1	368	1	YBX5_SCHPO	O10203	540	1.1	403	1	THIT_LISIN	P29266
468	1.1	369	1	RADA_CERST	O93748	541	1.1	404	1	LMPI_EBVC	O92362
469	1.1	370	1	YG26_YEAST	P53249	542	1.1	404	1	OMI_HUMAN	P51810
470	1.1	371	1	NUIM_NEUCR	P08774	543	1.1	405	1	AK_HELPY	O95j27
471	1.1	371	1	TGT_NEIMB	O9K096	544	1.1	405	1	AK_HELPY	O25827

545	6	1.1	405	1	OA1_MOUSE	P70259	mus musculus	618	6	1.1	461	1	YCUJ_ECOLI	P76037	escherichia
546	6	1.1	405	1	S3AE_BACSU	P49782	bacillus su	619	6	1.1	462	1	GIPR_MESAU	P43028	mesocricetu
547	6	1.1	408	1	ARGD_XANAC	O8h31	xanthomonas	620	6	1.1	462	1	PO22_MOUSE	O00196	mus musculus
548	6	1.1	408	1	ARGD_XANCP	O8554	xanthomonas	621	6	1.1	462	1	SELA_YERPE	O82971	yersinia pe
549	6	1.1	410	1	ARPI_MOUSE	P70295	mus musculus	622	6	1.1	462	1	TPH4_HUMAN	O92759	homo sapien
550	6	1.1	411	1	ARGD_XYLFA	O9d42	xyella fas	623	6	1.1	463	1	TFH4_MOUSE	O70422	mus musculus
551	6	1.1	411	1	NORB_HAEIN	O05011	haemophilus	624	6	1.1	464	1	SRPX_RAT	O03769	rattus norv
552	6	1.1	411	1	PGK_METTH	O27121	metanobact	625	6	1.1	466	1	ANX7_HUMAN	P20073	homo sapien
553	6	1.1	414	1	CUTS_STRCO	O03757	streptomyce	626	6	1.1	466	1	GIPR_HUMAN	P48546	homo sapien
554	6	1.1	416	1	CHRA_PSEAE	P14285	streptomoc	627	6	1.1	466	1	IMP2_DROME	P21614	drosophila
555	6	1.1	417	1	PKGB_LEIME	O27684	leishmania	628	6	1.1	467	1	D4DR_BOVIN	P21917	homo sapien
556	6	1.1	417	1	TKNS_MOUSE	O91w90	mus musculus	629	6	1.1	468	1	PIBB_HUMAN	P02676	bos taurus
557	6	1.1	418	1	CINA_STRPN	P5184	streptococ	630	6	1.1	468	1	MURD_XANCP	O9b775	xanthomonas
558	6	1.1	418	1	Y285_HELPY	O9mf0	helicobacte	631	6	1.1	468	1	MURD_XYLFA	O9b30	xyella fas
559	6	1.1	418	1	Y285_HELPY	P56130	helicobacte	632	6	1.1	469	1	NORM_XYLFA	O9p34	xyella fas
560	6	1.1	419	1	AROA_METTH	O26860	metanobact	633	6	1.1	470	1	CEBK_MOUSE	O63397	mus musculus
561	6	1.1	419	1	CHSD_PETRY	P22925	petunia hyb	634	6	1.1	470	1	XNIF_XENLA	P35617	xenopus lae
562	6	1.1	419	1	KDAF_MOUSE	O09043	mus musculus	635	6	1.1	471	1	HIDA_BACST	O45515	baeilus st
563	6	1.1	420	1	YHAP_BACSU	O07523	bacillus su	636	6	1.1	471	1	NORM_CAUCR	P38163	caulobacter
564	6	1.1	420	1	ALAU_HUMAN	P20848	homo sapien	637	6	1.1	472	1	VTDB_MOUSE	P21614	mus musculus
565	6	1.1	421	1	SHT2_APLCA	O16951	aplysia cal	638	6	1.1	473	1	GLNA_SYNP2	P28605	synecococ
566	6	1.1	421	1	CCG8_RAT	O8wh5	rattus norv	639	6	1.1	473	1	PHDK_NOCSK	O24723	nocardioid
567	6	1.1	421	1	HMDH_AERPE	O9as4	aetopyrum p	640	6	1.1	474	1	Y068_MYCCE	P47314	mycoplasma
568	6	1.1	423	1	CCG8_MOUSE	O8vhw2	mus musculus	641	6	1.1	476	1	VTDB_RAT	P04276	rattus norv
569	6	1.1	423	1	GATM_MOUSE	O96964	mus musculus	642	6	1.1	477	1	XYNA_STRLI	P26514	streptomyce
570	6	1.1	423	1	GATM_RAT	P50442	rattus norv	643	6	1.1	478	1	PEKH_ARATH	P50318	arabidopsis
571	6	1.1	423	1	NSMA_HUMAN	O60906	homo sapien	644	6	1.1	478	1	PO22_HUMAN	P09086	homo sapien
572	6	1.1	424	1	ZP3_GALSO	P53786	callithrix	645	6	1.1	478	1	PO22_PIG	O29013	sus scrofa
573	6	1.1	425	1	CCG8_HUMAN	O8vxs	homo sapien	646	6	1.1	479	1	CBSA_SURSO	P58029	sulfolobus
574	6	1.1	425	1	ESC_DROME	O24338	drosophila	647	6	1.1	479	1	PEKC_LEIME	O27685	leishmania
575	6	1.1	425	1	SECY_ODOSI	P49461	odonteila s	648	6	1.1	480	1	HOGT_ARATH	O9m156	arabidopsis
576	6	1.1	425	1	YTR1_EBV	P30119	epstein-bar	649	6	1.1	480	1	YNAO_BACSU	P35356	bacillus su
577	6	1.1	426	1	APEB_MYCLE	O50022	mycobacteri	650	6	1.1	481	1	PEKH_TOBAC	O42991	nicotiana t
578	6	1.1	428	1	SVH_BUCAP	O8r9p3	buchnera ap	651	6	1.1	483	1	BIAR_MELGA	P07700	meleagris g
579	6	1.1	430	1	DR41_RHIME	O9zqm8	rhizobium m	652	6	1.1	485	1	ZDH1_HUMAN	O8vtx9	homo sapien
580	6	1.1	431	1	ACRO_RABIT	P48038	oryctolagus	653	6	1.1	485	1	ZDH1_MOUSE	O8vtn5	mus musculus
581	6	1.1	431	1	H1X1_ANASP	O8vwm8	anabaena sp	654	6	1.1	487	1	SECY_HALMA	P28542	haloarcula
582	6	1.1	431	1	MENF_PASMU	O9cpi5	pasteurella	655	6	1.1	488	1	SECY_HALVO	O977v3	halobacteri
583	6	1.1	431	1	NOOE_THETH	O56229	thermus the	656	6	1.1	491	1	CPBI_RAT	P00176	rattus norv
584	6	1.1	431	1	P2X6_HUMAN	O15547	homo sapien	657	6	1.1	491	1	CPB2_RAT	P04167	rattus norv
585	6	1.1	432	1	KCTP_ECOLI	P17448	escherichia	658	6	1.1	492	1	DEP2_HUMAN	O9uh14	homo sapien
586	6	1.1	432	1	ORC4_XENLA	O93479	xenopus lae	659	6	1.1	493	1	FBL3_HUMAN	O12805	homo sapien
587	6	1.1	433	1	GP22_HUMAN	O99680	homo sapien	660	6	1.1	493	1	FBL3_RAT	O35568	rattus norv
588	6	1.1	433	1	PGKH_SPIOL	P29409	epinacia ol	661	6	1.1	494	1	CPBB_CANFA	P44660	canis famli
589	6	1.1	436	1	UR32_HSVSA	O01040	herpesviru	662	6	1.1	495	1	EXOT_RHIME	P33699	rhizobium m
590	6	1.1	443	1	CAR4_DICDI	O8vxs3	dictyostei	663	6	1.1	495	1	DHAL_ECOLI	P32883	escherichia
591	6	1.1	443	1	HXA3_MOUSE	P02831	mus musculus	664	6	1.1	495	1	YBFI_YEAST	P32622	seccitomye
592	6	1.1	446	1	YD85_PYRHO	O50093	pyrococcus	665	6	1.1	496	1	GALI_ARATH	O9sees	arabidopsis
593	6	1.1	447	1	YPEB_BACHD	O9rc82	bacillus ha	666	6	1.1	496	1	GLK2_THEVA	O9x1e4	thermotoga
594	6	1.1	448	1	VAP1_CHICK	P46936	gallus gall	667	6	1.1	496	1	GLPK_THERO	O9vxs3	thermus agu
595	6	1.1	449	1	C13A_MYCTU	O08447	mycobacteri	668	6	1.1	496	1	GLPK_THERO	O66133	thermus the
596	6	1.1	449	1	COMB_STRPN	P36498	streptococ	669	6	1.1	497	1	SGK3_MOUSE	O9vde8	mus musculus
597	6	1.1	449	1	COMB_STRPN	P36498	streptococ	670	6	1.1	497	1	GLPK_BACHD	O9vde8	mus musculus
598	6	1.1	450	1	GNUT_PSEAE	O9z1j1	pseudomonas	671	6	1.1	497	1	GLPK_FUSIN	O8vtn2	fusobacteri
599	6	1.1	451	1	GPID_CHLMU	O46437	chlamydia m	672	6	1.1	497	1	GLPK_LISIN	O92bhe	listeria in
600	6	1.1	452	1	NORM_BACSU	O31855	bacillus su	673	6	1.1	497	1	GLPK_LISIN	O8v622	listeria mo
601	6	1.1	453	1	SHT1_APLCA	O16950	aplysia cal	674	6	1.1	498	1	GLPK_THETN	O8v8r1	thermaaer
602	6	1.1	453	1	ALN_ECOLI	P77671	escherichia	675	6	1.1	498	1	GLPK_CLOB	O97f94	clostridium
603	6	1.1	454	1	IMDH_PNECA	O12658	pneumocysti	676	6	1.1	498	1	GLPK_LACTA	O9eg64	lactococcus
604	6	1.1	454	1	RNAA_CHLYR	O84300	chlamydia t	677	6	1.1	498	1	GLPK_STAM	O9vuh3	staphylococ
605	6	1.1	454	1	TNNA_RHOCA	O30971	rhodobacter	678	6	1.1	498	1	GLPK_STAM	O8vhw2	staphylococ
606	6	1.1	455	1	AROA_AGRSP	O9r4e4	agrobacteri	679	6	1.1	499	1	GLCD_ECOLI	P52075	escherichia
607	6	1.1	455	1	AROA_RHIME	O926v5	rhizobium m	680	6	1.1	500	1	CPBA_MOUSE	P12791	mus musculus
608	6	1.1	455	1	GIPR_RAT	P43219	rattus norv	681	6	1.1	500	1	GLPK_ANASP	O8vwm5	anabaena sp
609	6	1.1	455	1	PHR_STRGR	P12768	streptomyce	682	6	1.1	500	1	GLPK_CLOPE	O8vwm5	anabaena sp
610	6	1.1	456	1	YMSB_ANASP	O52750	anabaena sp	683	6	1.1	500	1	GLPK_ENTFA	O34154	enterococcu
611	6	1.1	457	1	MMBI_METAC	P58865	methanosarc	684	6	1.1	500	1	GLPK_SALTI	O82y6	salmonella
612	6	1.1	458	1	BFJA_ASHCO	P41752	asbhyia goe	685	6	1.1	500	1	PCLI_ARATH	P57681	arabidopsis
613	6	1.1	458	1	BFJA_YEAST	P02994	saccharomyc	686	6	1.1	501	1	GLPK_DEIRA	O9vtn3	deinococcus
614	6	1.1	458	1	GAL2_HUMAN	O01415	homo sapien	687	6	1.1	501	1	GLPK_SALTY	O9vtn3	deinococcus
615	6	1.1	460	1	BNV_FV123	P13491	human immun	688	6	1.1	501	1	GLPK_SALTY	O9vtn3	deinococcus
616	6	1.1	461	1	CSBC_BACSU	P46333	bacillus su	689	6	1.1	501	1	KPEL_DROME	O05652	drosophila
617	6	1.1	461	1	SILC_SALTY	O9zhd2	salmonella	690	6	1.1	501	1	KN57_CORGL	P46584	corynebacte

691	1.1	502	1	G6P1_XYLPA	O909r6 xyliella fas	764	552	1	K2C6 MOUSE	P50446 mus musculus
692	1.1	502	1	G6P1_XYLPT	O87av7 xyliella fas	765	554	1	G6P1_PSEPK	O881w9 pseudomonas
693	1.1	503	1	YE10_YEAST	P39941 saccharomyc	766	554	1	G6P2_PSEPK	O88d47 pseudomonas
694	1.1	502	1	PUR8_STRLP	P42670 streptomyce	767	554	1	G6P1_PSSSM	O888q7 pseudomonas
695	1.1	504	1	C341_MOUSE	O9jma7 mus musculus	768	557	1	G6P1_MOUSE	P66745 mus musculus
696	1.1	504	1	YBLH_SCHPO	O10341 schizosacch	769	557	1	G6P1_PIG	P80859 sus scrofa
697	1.1	505	1	GLPK_ENTCA	O34153 streptococc	770	557	1	MCP5_ENTAE	P21822 enterobacte
698	1.1	505	1	GLPK_VIBCH	O9k1j9 vibrio chol	771	558	1	G6P1_CRIGR	P50309 cricetulus
699	1.1	505	1	GLPK_VIBPA	O87m72 vibrio para	772	558	1	G6P1_HUMAN	P66744 homo sapien
700	1.1	505	1	GLPK_VIBVU	O88dm6 vibrio vuln	773	560	1	N4C2_ANASP	O8y8e6 haemaphysa sp
701	1.1	505	1	ICAI_PANTR	O28806 pan troglod	774	562	1	ATKA_ALIAC	OQxe11 alicyclobac
702	1.1	505	1	KIR3_RAT	P80203 rattus norv	775	564	1	ATKA_PSEAE	O75398 pseudoonas
703	1.1	507	1	GLPK_MYCPU	O98qy9 mycoplasma	776	566	1	MBHM_ECOLI	O75398 homo sapien
704	1.1	507	1	NRR4_WOLST	O9at85 wolfinella s	777	565	1	DEAF_PANTR	O77562 pan troglod
705	1.1	508	1	CPT7_CHICK	P12394 gallus gall	778	565	1	DEAF_RAT	O88450 rattus norv
706	1.1	508	1	GLPK_MYCLE	O9c881 mycobacteri	779	565	1	VPD4_ECOLI	P76523 escherichia
707	1.1	508	1	GLPK_STRP3	O8K665 streptococc	780	566	1	DEAF_MOUSE	OQ21c5 mus musculus
708	1.1	508	1	GLPK_STRP8	O8mzw9 streptococc	781	566	1	CYDC_BACSU	P37181 escherichia
709	1.1	508	1	GLPK_STRP9	O99y17 streptococc	782	567	1	GSPE_XANCP	P34366 bacillus su
710	1.1	509	1	PA23_HUMAN	O9mz20 homo sapien	783	567	1	VE1G_SCHPO	P31742 xanthomonas
711	1.1	510	1	GLPK_HALNT	O9m85 halobacteri	784	568	1	VE54_YEAST	O33880 schizosacch
712	1.1	510	1	IAI_HUMAN	O01101 homo sapien	785	568	1	Y654_YEAST	P53309 saccharomyc
713	1.1	512	1	AWY1_DEBOC	P19269 debaryomyce	786	569	1	AAKH_HUMAN	OQugj0 homo sapien
714	1.1	512	1	G6PD_CHLPN	O92a86 chlamydia p	787	570	1	LKH1_SCHPO	OQj170 mus musculus
715	1.1	512	1	GLK1_STRCO	O9ada7 streptomyce	788	575	1	LEKH1_SCHPO	O30156 schizosacch
716	1.1	512	1	LNT_ECOLI	P23330 escherichia	789	577	1	YGSU_YEAST	P53333 saccharomyc
717	1.1	512	1	LNT_SALTY	O87576 salmonella	790	579	1	YD49_MYCTU	O11019 mycobacteri
718	1.1	513	1	PDI_HORVU	P80284 hordeum vul	791	580	1	SMTD_BOOMI	P52307 boophilus m
719	1.1	513	1	PDI_MAI2E	P52588 zea mays (m	792	581	1	Z319_MOUSE	OQe8r8 mus musculus
720	1.1	513	1	VLI_HPV48	P50817 human papil	793	582	1	ATKA_HALNT	P57684 halobacteri
721	1.1	515	1	PDI_MHEAT	P52589 triticum ae	794	582	1	Z319_HUMAN	OQp219 homo sapien
722	1.1	515	1	TLCT_CHLPN	O928j2 chlamydia p	795	585	1	RS01_LEPIN	P59117 leptospira
723	1.1	516	1	RSF3_CHLRE	P12359 chlamydomon	796	585	1	YH09_YEAST	P38818 saccharomyc
724	1.1	516	1	Y107_YEAST	P40492 saccharomyc	797	586	1	HO_YEAST	P09932 saccharomyc
725	1.1	520	1	GLPK_MYCTU	O69664 mycobacteri	798	587	1	STD_STREN	OQ7nd6 streptococc
726	1.1	520	1	APH2_YEAST	P38207 saccharomyc	799	590	1	ATY1_MOUSE	OQc9c6 mus musculus
727	1.1	520	1	PHO_DROME	O8s883 drosophila	800	590	1	DS01_PSEAE	O01456 ascaris suu
728	1.1	521	1	SVN_UREPA	O9pcu6 ureaplasma	801	591	1	FLGE_CAUCR	O9nuh5 pseudomonas
729	1.1	521	1	Z286_HUMAN	O9nuc8 homo sapien	802	591	1	PAXI_HUMAN	P35806 caulobacter
730	1.1	523	1	MP11_HUMAN	P33004 homo sapien	803	591	1	ABP1_YEAST	P49023 homo sapien
731	1.1	524	1	HUTH_DEIRA	O92r06 deinococcus	804	592	1	PRTR_HUMAN	P15891 saccharomyc
732	1.1	524	1	PEBT_BOVIN	P09487 bos taurus	805	593	1	Y267_ARCFU	OQ0431 homo sapien
733	1.1	527	1	GALI_YEAST	P04385 saccharomyc	806	597	1	IR2P_METKA	O29972 archaeoglyb
734	1.1	527	1	RBRT_CANAL	O00312 candida alb	807	598	1	TREZ_ARTSO	O8rv06 methanopyru
735	1.1	528	1	ICAI_CANPA	P33729 canis famli	808	598	1	MG02_HUMAN	O44316 arthroacte
736	1.1	528	1	TLCT_CHLTR	O84068 chlamydia t	809	606	1	DNAK_LACIA	O9unf1 homo sapien
737	1.1	529	1	Y632_CHLTR	O9pkx5 chlamydia t	810	607	1	DPOL_BPM02	P42368 lactococcus
738	1.1	529	1	Y632_CHLTR	O84637 chlamydia t	811	612	1	B1R2_MOUSE	O64235 mycobacteri
739	1.1	530	1	Y921_CHLMU	O99jbl chlamydia m	812	612	1	YVW8_YEAST	O62210 mus musculus
740	1.1	530	1	Y921_CHLMU	O09788 schizosacch	813	613	1	ADAS_TRYAB	O03153 saccharomyc
741	1.1	530	1	Y921_CHLMU	O09788 schizosacch	814	613	1	ADAS_TRYAB	O97157 trypanosoma
742	1.1	531	1	CHUB_NEPOL	O9t467 neptrolelmi	815	613	1	DEAD_HAETN	P44586 haemophilus
743	1.1	531	1	PI11_MOUSE	O8i526 mus musculus	816	617	1	DNAK_PROAC	O91791 pneumonibac
744	1.1	532	1	ACMS_VACMU	P28750 macaca mula	817	619	1	DP2S_PYRAB	O92123 pyrococcus
745	1.1	532	1	EXU_DROME	O09460 anaerobioap	818	626	1	PM17_MOUSE	O6b6m6 mus musculus
746	1.1	532	1	PPCK_ANASU	P38745 saccharomyc	819	627	1	GIDA_AGR75	O86090 agrobacteri
747	1.1	532	1	YH87_YEAST	O95132 bos taurus	820	629	1	KH18_MOUSE	P593280 mus musculus
748	1.1	535	1	ICAI_BOVIN	O95132 bos taurus	821	629	1	RA21_XENLA	O93310 xenopus lae
749	1.1	535	1	PPCK_BACTN	O8a414 bacteroides	822	631	1	FRSH_GUTHA	O78516 guillierdia
750	1.1	536	1	ARP_ARATH	P45951 arabidopsias	823	631	1	TAC3_MOUSE	OQj111 mus musculus
751	1.1	536	1	YEN1_SCHPO	O13695 schizosacch	824	633	1	N0UL_MYCTU	O86350 mycobacteri
752	1.1	537	1	AREH_SCHRO	O10269 schizosacch	825	633	1	SE6A9_MOUSE	P28572 mus musculus
753	1.1	539	1	PCCB_HUMAN	P05166 homo sapien	826	633	1	SE6A9_MOUSE	P28572 rattus norv
754	1.1	539	1	PCCB_PIG	P79384 sus scrofa	827	637	1	TETO_CAMBE	P10952 campylobact
755	1.1	540	1	TLIC2_CHLTR	O84502 chlamydia t	828	638	1	OKA1_LYNST	O77408 lymanaea sta
756	1.1	540	1	YTDK_CAEEL	P07633 rattus norv	829	638	1	PD44_MOUSE	P08003 mus musculus
757	1.1	543	1	PCCB_RAT	O97633 rattus norv	830	639	1	SE6A9_BOVIN	O28039 bos taurus
758	1.1	543	1	TLIC2_CHLMU	O99jdp6 chlamydia m	831	639	1	TENO_CAMCO	P23835 campylobact
759	1.1	545	1	ICAI_RAT	O00238 rattus norv	832	639	1	TENO_STRPN	P20174 streptococc
760	1.1	547	1	GSPP_AERHY	P45754 aeromonas h	833	639	1	PRIM_MYCLE	P72533 streptococc
761	1.1	550	1	USHA_SALPU	O9r137 salmonella	834	642	1	TENO_STRPN	O9c8g2 mycobacteri
762	1.1	551	1	PODX_RABIT	O28645 oryctolagus	835	643	1	PD44_RAT	P38659 rattus norv
763	1.1	551	1	Y275_HAEIN	P43375 haemophilus	836	643	1	SL55_HUMAN	O92911 homo sapien

837	6	1.1	647	1	MAOC_FLAPR	P36444	flaveria pr	910	6	1.1	725	1	SP3_MOUSE	O70494	mus musculus
838	6	1.1	649	1	VE1_HPV6A	Q84293	human papil	911	6	1.1	727	1	BR01_DROME	Q01295	drosophila
839	6	1.1	651	1	CSP6_HUMAN	Q9nvc6	h cofactor	912	6	1.1	730	1	MM06_MOUSE	P41245	mus musculus
840	6	1.1	652	1	FAS1_DROME	P10674	drosophila	913	6	1.1	736	1	PRX1_CHICK	Q91018	gallus gall
841	6	1.1	652	1	GR78_CHICK	Q90593	gallus gall	914	6	1.1	736	1	PRX1_HUMAN	Q92786	homo sapien
842	6	1.1	653	1	PEP1_HUMAN	O14829	homo sapien	915	6	1.1	737	1	PRX1_MOUSE	P48437	mus musculus
843	6	1.1	654	1	HS70_HYDRA	Q05944	hydra magni	916	6	1.1	739	1	AD18_HUMAN	Q9Y3q7	homo sapien
844	6	1.1	654	1	PSTA_MYCGE	P47651	mycoplasma	917	6	1.1	741	1	CUL5_CAEEL	Q33639	caenorhabdi
845	6	1.1	656	1	ACSA_RHOCA	O68040	rhodobacter	918	6	1.1	742	1	ZFA_MOUSE	P33607	mus musculus
846	6	1.1	656	1	PER_DROSI	Q03355	drosophila	919	6	1.1	743	1	ANAG_HUMAN	P54802	homo sapien
847	6	1.1	657	1	GRAD_TREPA	O83062	treponema p	920	6	1.1	748	1	PA24_MOUSE	P47713	mus musculus
848	6	1.1	659	1	NRTC_SYNP7	P38045	synectococc	921	6	1.1	749	1	PA24_HORSE	O77793	equus caball
849	6	1.1	660	1	PHUB_ECOLI	P06972	escherichia	922	6	1.1	749	1	PA24_HUMAN	P47712	homo sapien
850	6	1.1	661	1	PER_DROSE	Q03354	drosophila	923	6	1.1	752	1	DRS1_YEAST	P32892	saccharomyc
851	6	1.1	661	1	UAS3_HUMAN	P57075	homo sapien	924	6	1.1	752	1	PA24_RAT	P03093	rattus norv
852	6	1.1	662	1	GARP_HUMAN	O14392	homo sapien	925	6	1.1	753	1	PPE2_HUMAN	O14830	homo sapien
853	6	1.1	662	1	INVI_MAIZE	P49175	zea mays (m	926	6	1.1	754	1	PURL_MYCLE	O60023	homo sapien
854	6	1.1	670	1	PRCK_CUCSA	P42066	cucumis sat	927	6	1.1	754	1	PURL_MYCTU	P54876	mycobacteri
855	6	1.1	671	1	PECK_ARATH	Q94074	arabidopsis	928	6	1.1	755	1	PPAX_CAEEL	Q94876	mycobacteri
856	6	1.1	673	1	FLID_TREMA	O94707	treponema m	929	6	1.1	757	1	MUS2_THEMEA	Q9105	thermotoga
857	6	1.1	673	1	YMS2_HUMAN	O60299	homo sapien	930	6	1.1	757	1	PPE2_MOUSE	O35385	mus musculus
858	6	1.1	673	1	YMS5_YEAST	P53918	saccharomyc	931	6	1.1	758	1	CLPA_ECOLI	P15716	escherichia
859	6	1.1	674	1	GLSK_RAT	P13264	rattus norv	932	6	1.1	759	1	HYPF_RHIV	P28155	rhizobium 1
860	6	1.1	674	1	YL10_VIBCH	Q94991	vibrio chol	933	6	1.1	763	1	TSHR_BOVIN	Q27987	bos taurus
861	6	1.1	675	1	NNOG_RICPR	Q94074	arabidopsis	934	6	1.1	764	1	TSHR_CANFA	P14763	canis famli
862	6	1.1	676	1	NNOG_RICCN	Q94992	ricicetia	935	6	1.1	764	1	TSHR_HUMAN	P47750	homo sapien
863	6	1.1	676	1	PER_DROMA	Q03353	drosophila	936	6	1.1	764	1	TSHR_MOUSE	P47750	mus musculus
864	6	1.1	682	1	ATKB_XANAC	O8ppc9	xanthomonas	937	6	1.1	767	1	TSHR_SHEEP	P66495	ovis aries
865	6	1.1	682	1	VG50_BPM15	Q05262	mycobacteri	938	6	1.1	767	1	ACES_CHICK	P26186	gallus gall
866	6	1.1	683	1	CNG1_RAT	Q062927	r cgmpr-gate	939	6	1.1	768	1	LEB3_MOUSE	Q01102	mus musculus
867	6	1.1	684	1	CNG1_MOUSE	P22974	m cgmpr-gate	940	6	1.1	768	1	LEM3_RAT	P8106	rattus norv
868	6	1.1	686	1	PWA_ARATH	Q94716	arabidopsis	941	6	1.1	768	1	SC23_YEAST	P31303	saccharomyc
869	6	1.1	686	1	SYGB_FUSNN	O8444	fuobacteri	942	6	1.1	769	1	TMEB_MOUSE	Q02208	mus musculus
870	6	1.1	687	1	CICK_RAT	O06393	rattus norv	943	6	1.1	771	1	XYKO_YEAST	Q02208	mus musculus
871	6	1.1	692	1	SE69_HUMAN	P48067	homo sapien	944	6	1.1	772	1	EMAL_DROME	Q9vul3	drosophila
872	6	1.1	692	1	YFB3_YEAST	P43579	saccharomyc	945	6	1.1	772	1	PMIP_YEAST	P35999	saccharomyc
873	6	1.1	694	1	PRK_CAMCO	O33350	campylobact	946	6	1.1	775	1	YTX1_XENTIA	P43380	xenopus lae
874	6	1.1	694	1	PRK_CAMJE	Q9pmu0	campylobact	947	6	1.1	776	1	YOK5_CAEEL	Q11177	caenorhabdi
875	6	1.1	696	1	LSHR_PIG	P16582	sus scrofa	948	6	1.1	780	1	PRTP_HSV1F	P06490	herpes simp
876	6	1.1	698	1	EBF_VIBCH	O9kuz7	vibrio chol	949	6	1.1	781	1	SP3_HUMAN	O02447	homo sapien
877	6	1.1	698	1	VANT_ENTGA	Q9x3p3	enterococcu	950	6	1.1	783	1	NOO3_THETH	Q06223	thermus the
878	6	1.1	699	1	EBF_TAEIN	P43925	haemophilus	951	6	1.1	785	1	K6P1_ASFOR	Q9hg21	aspergillus
879	6	1.1	699	1	EBF_VIBPA	Q87145	vibrio para	952	6	1.1	785	1	PRTP_HSV1A	P10212	herpes simp
880	6	1.1	699	1	EBF_VIBVU	Q8dcq8	vibrio vuln	953	6	1.1	785	1	PRTP_HSV1A	P12835	herpes simp
881	6	1.1	700	1	EBG2_RALSO	O8xm7	ralstonia s	954	6	1.1	790	1	U84A_MOUSE	Q0666	mus musculus
882	6	1.1	700	1	EBG_PASMU	P57938	pasteurella	955	6	1.1	794	1	ZFY1_XENTIA	O01611	xenopus lae
883	6	1.1	701	1	LSHR_BOVIN	Q28005	bos taurus	956	6	1.1	799	1	ZFX1_MOUSE	P17011	mus musculus
884	6	1.1	701	1	TBX2_MOUSE	Q60707	mus musculus	957	6	1.1	800	1	ARNT_RAT	P41739	rattus norv
885	6	1.1	702	1	EBG_BUCAP	P57593	buchnera ap	958	6	1.1	800	1	ZFX_BOVIN	O62836	bos taurus
886	6	1.1	702	1	EBG_BUCAP	O84948	buchnera ap	959	6	1.1	801	1	CADR_HUMAN	P98048	homo sapien
887	6	1.1	702	1	EBG_THICU	O50565	thiobacillu	960	6	1.1	801	1	ZFY_HUMAN	O17392	caenorhabdi
888	6	1.1	702	1	EBG_YERPE	O8xjb3	yersinia pe	961	6	1.1	803	1	CUL4_CAEEL	Q17392	caenorhabdi
889	6	1.1	702	1	TBX2_HUMAN	Q13207	homo sapien	962	6	1.1	805	1	ZFX_HUMAN	P17010	mus musculus
890	6	1.1	703	1	EBG_ECOLI	P02996	escherichia	963	6	1.1	808	1	FGR4_MOUSE	Q03144	mus musculus
891	6	1.1	703	1	EBG_SALTY	P26229	salmonella	964	6	1.1	813	1	FGR2_XENTIA	Q13444	homo sapien
892	6	1.1	704	1	FB1L_CHICK	O73775	gallus gall	965	6	1.1	814	1	AD15_HUMAN	Q03444	homo sapien
893	6	1.1	704	1	LCRD_YEREN	P21210	yersinia en	966	6	1.1	819	1	LON_CHLTR	O84348	chlamydia t
894	6	1.1	704	1	LCRD_YERPE	P31487	yersinia pe	967	6	1.1	820	1	SYFB_DEIRA	Q9rx55	deinococcus
895	6	1.1	704	1	NEUL_RABIT	P42675	oryctolagus	968	6	1.1	821	1	RBL1_ARATH	O04053	arabidopsis
896	6	1.1	704	1	NEUL_RAT	P42676	rattus norv	969	6	1.1	822	1	CAD3_MOUSE	P10287	mus musculus
897	6	1.1	705	1	EBG_XANAC	O8pnc6	xanthomonas	970	6	1.1	824	1	JIP2_HUMAN	Q13347	homo sapien
898	6	1.1	705	1	EBG_XANAC	O8pnc5	xanthomonas	971	6	1.1	824	1	MULTI_HUMAN	Q9udr8	homo sapien
899	6	1.1	705	1	EBG_XYLPF	O9pna9	xyella fas	972	6	1.1	825	1	PBPA_VIBCH	O9kuz7	vibrio chol
900	6	1.1	706	1	FRZ4_DROME	Q9dbw1	drosophila	973	6	1.1	834	1	IF2C_SCHPO	O74957	schizosacch
901	6	1.1	706	1	TRPE_HORSE	P27425	equus caball	974	6	1.1	837	1	MYT5_YEAST	P39016	saccharomyc
902	6	1.1	708	1	NICA_MOUSE	P57716	mus musculus	975	6	1.1	837	1	XYNZ_CLOTM	P10478	clostridium
903	6	1.1	710	1	NICA_HUMAN	Q92542	homo sapien	976	6	1.1	839	1	ZFX2_MOUSE	P17012	mus musculus
904	6	1.1	710	1	EBG_BUCBP	P59451	buchnera ap	977	6	1.1	840	1	YA02_HUMAN	Q92K5	homo sapien
905	6	1.1	711	1	PRE2_YEAST	P36033	saccharomyc	978	6	1.1	842	1	LPFC_SALTY	P33662	salmonella
906	6	1.1	711	1	PRE2_YEAST	O08905	saccharomyc	979	6	1.1	847	1	CD22_HUMAN	P20273	homo sapien
907	6	1.1	717	1	CU4B_HUMAN	Q13620	homo sapien	980	6	1.1	858	1	ALR2_YEAST	P43553	saccharomyc
908	6	1.1	719	1	CI1C_BACTU	O87404	bacillus th	981	6	1.1	860	1	CH12_COCPO	P49197	coccidioidide
909	6	1.1	723	1	S21C_RAT	O99n01	rattus norv	982	6	1.1	861	1	GLND_SHEON	O9eg18	shevanelia

983	6	1.1	863	1	AD17_DROME	O9vac6 drosophila
984	6	1.1	867	1	VI96_IRV1	P22856 tlpula irid
985	6	1.1	872	1	STA_STRE	O97q48 streptococ
986	6	1.1	873	1	FAS2_DROME	P24082 drosophila
987	6	1.1	873	1	VG1B_ILTV6	O02409 infectious
988	6	1.1	876	1	AREA_EMENT	P17429 emericella
989	6	1.1	877	1	PWMT1_CANAL	O74189 candida alb
990	6	1.1	878	1	OSB2_HUMAN	O06992 homo sapien
991	6	1.1	879	1	PRP_HUMAN	O062b2 homo sapien
992	6	1.1	879	1	PRP_MOUSE	O9wv91 mus musculu
993	6	1.1	879	1	PRP_RAT	O62786 ratius norv
994	6	1.1	879	1	MYSP_ONCVO	O02171 onchocerca
995	6	1.1	882	1	AREA_ASPNG	O13412 aspergillus
996	6	1.1	883	1	VG1B_ILTV5	P27415 infectious
997	6	1.1	883	1	VG1B_ILTV7	P24904 infectious
998	6	1.1	889	1	RSC2_YEAST	O06488 saccharomyc
999	6	1.1	893	1	BOSS_DROVI	O24738 drosophila
1000	6	1.1	895	1	DAG1_RABIT	O26685 oryctolagus

ALIGNMENTS

RESULT 1

ID	Y966_MYCTU	STANDARD	PRT	200 AA
AC	P71544			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Hypothetical protein RV0966C			
GN	RV0966C OR MT0994 OR MTCY1D7.08			
OS	Mycobacterium tuberculosis			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.			
OX	NCBI_TaxID=1773;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=H37RV;			
RC	MEDLINE=98295987; PubMed=9634230;			
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,			
RA	Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,			
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,			
RA	Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,			
RA	Hornby T., Jagels K., Krogan A., McLean J., Moule S., Murphy L.,			
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,			
RA	Rutler S., Seeger K., Skelton S., Squares S., Squares R.,			
RA	Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;			
RT	"Deciphering the biology of Mycobacterium tuberculosis from the			
RT	complete genome sequence."			
RT	Nature 393:537-544(1998).			
RL	(2)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC 1551 / Oshkosh;			
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,			
RA	Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,			
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,			
RA	Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,			
RA	Bisnai W.;			
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and			
RT	laboratory strains."			
RT	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; 279700; CAB01985.1; ALT_INIT.			
DR	EMBL; AE00684; AK45243.1; ALT_INIT.			

DR TIGR; MT0994; -

DR Tuberculist; RV0966C; -

KW Hypothetical protein; Complete proteome.

FT CONFLICT 175 175 V > A (IN REF. 2).

SO SEQUENCE 200 AA; 22210 MW; 752F8CFB9B3C02 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 200;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 LLLALLGG 474

Db 88 LLLALLGG 95

RESULT 2

ID	YM05_MYCTU	STANDARD	PRT	358 AA
AC	O10394			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Hypothetical protein RV2205C			
GN	RV2205C OR MT261 OR MTCY190.16C			
OS	Mycobacterium tuberculosis			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.			
OX	NCBI_TaxID=1773;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=H37RV;			
RC	MEDLINE=98295987; PubMed=9634230;			
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,			
RA	Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,			
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,			
RA	Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,			
RA	Hornby T., Jagels K., Krogan A., McLean J., Moule S., Murphy L.,			
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,			
RA	Rutler S., Seeger K., Skelton S., Squares S., Squares R.,			
RA	Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;			
RT	"Deciphering the biology of Mycobacterium tuberculosis from the			
RT	complete genome sequence."			
RT	Nature 393:537-544(1998).			
RL	(2)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC 1551 / Oshkosh;			
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,			
RA	Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,			
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,			
RA	Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,			
RA	Bisnai W.;			
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and			
RT	laboratory strains."			
RT	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.			
CC	-----			
CC	-I- SIMILARITY: BELONGS TO THE GLYCERATE KINASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; 270283; CA94248.1; ALT_INIT.			
DR	EMBL; AE007072; AK46547.1; ALT_INIT.			
DR	TIGR; MT261; -			
DR	Tuberculist; RV2205C; -			
DR	InterPro: IPR004381; Cons_hypoth45.			
DR	Pfam; PF02595; Gly_kinase; 1.			
DR	TIGRFAms; TIGR00045; TIGR00045; 1.			
DR	Hypothetical protein; Transferrase; Kinase; Complete proteome.			
SO	SEQUENCE 358 AA; 35592 MW; ACTEDCSBFB8E41544 CRC64;			

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Query Match      1.5%; Score 8; DB 1; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      398 PPTPPTAL 405
Db      101 PPTPPTAL 108

RESULT 3
GSA_SOYBN
ID_GSA_SOYBN      STANDARD;      PRT;      466 AA.
AC      P43621;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor
      (EC 5.4.3.8) (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-
      AT).
GN      GSA1 OR GSA.
OS      Glycine max (Soybean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eucotsids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX      NCBI_TaxID=3847;
      (1)
RP      SEQUENCE FROM N.A.
RC      TISSUE=Root nodules;
      MEDLINE=94105331; PubMed=8278535;
RA      Sangwan I., O'Brian M.R.;
      "Expression of the soybean (Glycine max) glutamate 1-semialdehyde
      aminotransferase gene in symbiotic root nodules.";
      Plant Physiol. 102:829-834(1993).
      (2)
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Essex;
      MEDLINE=95221396; PubMed=7706283;
RA      Frustaci J.M., Sangwan I., O'Brian M.R.;
      "gsl1 is a universal tetrahydropyridine synthesis gene in soybean and is
      regulated by a GAGA element.";
      J. Biol. Chem. 270:7387-7393(1995).
      (1)
CC      -1- CATALYTIC ACTIVITY: (S)-4-amino-5-oxopentanoate = 5-
      aminolevulinic acid.
CC      -1- COFACTOR: Pyridoxal phosphate.
CC      -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway; second step.
CC      -1- INVOLVED in chlorophyll biosynthesis.
CC      -1- SUBUNIT: Homodimer (by similarity).
CC      -1- SUBCELLULAR LOCATION: Chloroplast.
CC      -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LEAVES OF ETIOLATED
      PLANTLETS INDEPENDENTLY OF LIGHT TREATMENT AND, TO A MUCH LESSER
      EXTENT, IN LEAVES OF MATURE PLANTS.
CC      -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
      aminotransferases.
CC      -----
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      or send an email to license@isb-sib.ch).
      -----
CC      EMBL: L12453; AAA33968.1; -.
CC      EMBL: U20260; AAC48996.1; -.
CC      PIR: J02263; J02263.
CC      HSSP: P24630; ZGSA.
CC      InterPro: IPR005814; Aminoctrans_3.
CC      InterPro: IPR004639; HemL.
CC      Pfam: PF00202; aminoctrans_3; 1.
CC      TIGRFAMs: TIGR00713; hemL; 1.
CC      PROSITE: PS00600; AA TRANSFER CLASS 3; 1.
CC      Porphyrylin biosynthesis; Chlorophyll biosynthesis; Isomerase;
KW

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Query Match      1.5%; Score 8; DB 1; Length 466;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 LSSSTRSR 30
Db      17 LSSSTRSR 24

RESULT 4
PCGN_MOUSE
ID_PCGN_MOUSE      STANDARD;      PRT;      1268 AA.
AC      P55066;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
GN      CSF3 OR NCAN.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c; TISSUE=Brain;
      MEDLINE=96039250; PubMed=7490074;
RA      Rauch U., Grilme B., Kulbe G., Arnold-Ammer I., Beter D.,
      Faessler R.;
      "Structure and chromosomal localization of the mouse neurocan gene.";
      Genomics 28:405-410(1995).
      (1)
CC      -1- FUNCTION: May modulate neuronal adhesion and neurite growth during
      development by binding to neural cell adhesion molecules (NC-CAM
      and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
      acid.
CC      -1- TISSUE SPECIFICITY: BRAIN.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC      -1- SIMILARITY: Contains 2 EGF-like domains.
CC      -1- SIMILARITY: Contains 2 Igk domains.
CC      -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC      -1- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC      -1- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
CC      -----
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      or send an email to license@isb-sib.ch).
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CC      EMBL: X84227; CA59216.1; -.
CC      PIR: S52781; S52781.
CC      HSSP: P00740; IEDM.
CC      MGD: MGI:104694; Cgpg3.
CC      InterPro: IPR002353; Antifreeze2.1.
CC      InterPro: IPR000152; Asx hydroxyl.
CC      InterPro: IPR000742; EGF_2.
CC      InterPro: IPR001881; EGF_Ca.
CC      InterPro: IPR006209; EGF-like.
CC      InterPro: IPR007110; Ig-Ilike.
CC      InterPro: IPR003599; Ig.
CC      InterPro: IPR003006; Ig_MHC.
CC      InterPro: IPR001304; Lectin_C.
CC      InterPro: IPR000538; Link.
CC      InterPro: IPR000436; Sushi_SCR_CCP.
CC      Pfam: PF00008; EGF; 2.
CC      Pfam: PF00047; Ig; 1.
KW

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DR Pfam: PF00059; lectin_c; 1.
DR Pfam: PF00084; sushi; 1.
DR Pfam: PF00193; xlink; 2.
DR PRINTS; PR01265; LINKMODULE.
DR PRINTS; PR00356; ANTIFREZEELI.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCEC; 1.
DR SMART; SM00034; CCEC; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS00186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
DR Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
EGF-like domain; Calcium; Repeat; Sushi; Signal.
KW SIGNAL.
FT CHAIN 1 22
FT FT 1 2268
FT FT 37 157
FT FT 158 253
FT FT 259 355
FT FT 960 1034
FT FT 1036 1165
FT FT 1166 1224
FT FT 58 139
FT FT 181 252
FT FT 205 226
FT FT 279 354
FT FT 303 324
FT FT 964 975
FT FT 964 984
FT FT 984 995
FT FT 1040 1051
FT FT 1068 1160
FT FT 1136 1152
FT FT 1167 1210
FT FT 1196 1223
FT FT 121 121
FT FT 339 339
FT FT 742 742
FT FT 978 978
FT FT 1175 1175
FT FT 1268 AA; 137200 MW; 3014EBE202A2FAEC CRC64;
SQ SEQUENCE

Query Match 1.5%; Score 8; DB 1; Length 1268;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97017121; PubMed=8863722;
RA Eichmann A., Marcelle C., Breant C., Le Douarin N.M.;
RT "Molecular cloning of Quek 1 and 2, two quail vascular endothelial
RL growth factor (VEGF) receptor-like molecules.";
RL Gene 174:3-8(1996).
RN [2]
RP SEQUENCE OF 910-1348 FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=93378866; PubMed=8396413;
RA Eichmann A., Marcelle C., Breant C., Le Douarin N.M.;
RT "Two molecules related to the VEGF receptor are expressed in early
RL endothelial cells during avian embryonic development.";
RL Mech. Dev. 42:33-48(1993).
RN [3]
RP SEQUENCE OF 764-880 FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Embryo;
RX MEDLINE=95301109; PubMed=7781909;
RA Flame I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (Flk-1)
RT are expressed during vasculogenesis and vascular differentiation in
RL the quail embryo.";
RL Dev. Biol. 169:699-712(1995).
CC -1- FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN
CC KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM
CC PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF
CC VASCULAR PERMEABILITY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: IN ALL ENDOTHELIAL TISSUES DURING ONSET OF
CC VASCULARIZATION. IN LATER DEVELOPMENT, PRESENT IN LUNG, HEART,
CC INTESTINE AND SKIN.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE MESODERM AT ONSET OF
CC GASTRULATION. FROM DAY 2, CONFINED TO ENDOTHELIAL TISSUES AND
CC EXPRESSION CONTINUES TO BE WIDESPREAD THROUGHOUT VASCULARIZATION
CC UNTIL E9 WHERE IT BECOMES RESTRICTED TO SPECIFIC REGIONS SUCH AS
CC THE SPINAL CHORD AND HEART VALVES.
CC -1- INDUCTION: IN VITRO, VEGF IS INDUCED BY BASIC FIBROBLAST GROWTH
CC FACTOR (bFGF), UNIQUELY IN THE FIRST 24 H OF CELL CULTURE.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X83288; CAA58268.1; -
DR EMBL; S65205; AAB28127.1; -
DR EMBL; S78345; AAB34594.1; -
DR PIR; JC4953; S51656.
DR HSP; P13362; 1FGK.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RTKinaseII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 6.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2_1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
 KW Angiogenesis; Signal; Transferrin; Tyrosine-protein kinase; Receptor;
 KW Transmembrane; Glycoprotein; Phosphorylation; ATP-binding;
 KW Immunoglobulin domain; Repeat.
 FT CHAIN 1 1348
 FT SIGNAL 1 20
 FT DOMAIN 21 756
 FT TRANSMEM 757 777
 FT DOMAIN 778 1348
 FT DOMAIN 138 106
 FT DOMAIN 138 202
 FT DOMAIN 202 312
 FT DOMAIN 312 405
 FT DOMAIN 405 412
 FT DOMAIN 412 540
 FT DOMAIN 540 651
 FT DOMAIN 651 744
 FT DOMAIN 744 825
 FT NP_BIND 825 839
 FT BINDING 839 859
 FT ACT_SITE 1021 1021
 FT CARBOHYD 43 43
 FT CARBOHYD 47 47
 FT CARBOHYD 63 63
 FT CARBOHYD 93 93
 FT CARBOHYD 138 138
 FT CARBOHYD 153 153
 FT CARBOHYD 201 201
 FT CARBOHYD 240 240
 FT CARBOHYD 290 290
 FT CARBOHYD 310 310
 FT CARBOHYD 355 355
 FT CARBOHYD 386 386
 FT CARBOHYD 513 513
 FT CARBOHYD 556 556
 FT CARBOHYD 603 603
 FT CARBOHYD 613 613
 FT CARBOHYD 622 622
 FT CARBOHYD 666 666
 FT CARBOHYD 688 688
 FT CARBOHYD 710 710
 FT CONFLICT 865 865
 FT SEQUENCE 1348 AA; 150305 MW; ASE4194A76DF5FB3 CRC64;
 Query March 1.5%; Score 8; DB 1; Length 1348;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 405 LOCTADKF 412
 DB 559 LOCTADKF 566
 RESULT 6
 POLG_MNV STANDARD; PRT; 3430 AA.
 AC P06935;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Genome polypeptide (Contains: Capsid protein C (Core protein); Matrix
 DE protein (Envelope protein M); Major envelope protein E; Nonstructural
 DE proteins NS1, NS2A, NS2B, NS4A and NS4B. Protease/helicase
 DE (EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
 DE (NS5)).
 OS West Nile virus (WNV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OX NCBI_TaxId=11082;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=86124703; PubMed=3753811;
 RA Castle E., Leidner U., Nowak T., Wengler G.;
 RT "Primary structure of the West Nile flavivirus genome coding
 RT for all nonstructural proteins";
 RL Virology 149:10-26(1986).
 RN [2]
 RP SEQUENCE OF 1-291 FROM N.A.
 RX MEDLINE=85274372; PubMed=2992152;
 RA Castle E., Nowak T., Leidner U., Wengler G.;
 RT "Sequence analysis of the viral core protein and the
 RT membrane-associated proteins V1 and V2 of the flavivirus West Nile
 RT virus and of the genome sequence for these proteins";
 RL Virology 145:227-236(1985).
 RN [3]
 RP SEQUENCE OF 255-854 FROM N.A.
 RX MEDLINE=86072082; PubMed=3855247;
 RA Wengler G., Castle E., Leidner U., Nowak T., Wengler G.;
 RT "Sequence analysis of the membrane protein V3 of the flavivirus West
 RT Nile virus and of its gene";
 RL Virology 147:264-274(1985).
 RN [4]
 RP DISULFIDE BONDS IN E PROTEIN.
 RX MEDLINE=87122143; PubMed=3811228;
 RA Nowak T., Wengler G.;
 RT "Analysis of disulfides present in the membrane proteins of the West
 RT Nile flavivirus";
 RL Virology 156:127-137(1987).
 CC -1- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
 CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
 CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
 CC precursor polypeptide, commonly with Asp or Glu in the P6
 CC position. Cys or Thr in P1 and Ser or Ala in P1'.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC [RNA] (N).
 CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
 CC PROTEIN C AND MRNA.
 CC
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 CC
 CC EMBL; M12294; AAA48498.1; -.
 DR PIR; A25256; GNMVWV.
 DR HSSP; P14336; ISVB.
 DR MEROPS; S07.001; -.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001122; Flavi_capsidC.
 DR InterPro; IPR000336; Flavi_glycoprote.
 DR InterPro; IPR001850; Flavi_helicase.
 DR InterPro; IPR000068; Flavi_M.
 DR InterPro; IPR001157; Flavi_NS1.
 DR InterPro; IPR000752; Flavi_NS2A.
 DR InterPro; IPR000487; Flavi_NS2B.
 DR InterPro; IPR000404; Flavi_NS4A.
 DR InterPro; IPR001528; Flavi_NS4B.
 DR InterPro; IPR000208; Flavi_NS5.
 DR InterPro; IPR002535; Flavi_propep.
 DR InterPro; IPR002877; Ftsu.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR Pfam; PF01003; Flavi_capsid_1.
 DR Pfam; PF02832; Flavi_glycop_C_1.
 DR Pfam; PF00869; Flavi_glycoprot_1.
 DR Pfam; PF00949; Flavi_helicase_1.
 DR Pfam; PF01004; Flavi_M_1.

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DR PFam; PF00948; Flavi_N51; 1.
DR PFam; PF01005; Flavi_N52A; 1.
DR PFam; PF01002; Flavi_N52B; 1.
DR PFam; PF01350; Flavi_N54A; 1.
DR PFam; PF01349; Flavi_N54B; 1.
DR PFam; PF00972; Flavi_N55; 1.
DR PFam; PF01570; Flavi_propep; 1.
DR PFam; PF01728; FesJ; 1.
DR PFam; PF00271; helicase_C; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
DR SMART; SM00496; Flavi_N51; 1.
DR SMART; SM00490; HELIC_C; 1.
DR PolyProtein; Glycoprotein; Transferrase; RNA-directed RNA polymerase;
DR Core protein; Coat protein; Envelope protein; Hydrolyase; Helicase;
DR ATP-binding; Transmembrane; Nonstructural protein.
DR INIT_MER 1
FT CHAIN 1 123
FT PROPEP 124 215
FT CHAIN 216 290
FT CHAIN 291 787
FT CHAIN 788 1139
FT CHAIN 1140 1370
FT CHAIN 1371 1501
FT CHAIN 1502 2120
FT CHAIN 2121 2269
FT CHAIN 2270 2525
FT CHAIN 2526 3430
FT DOMAIN 388 401
FT NP_BIND 1695 1702
FT SITE 1786 1789
FT DISULFID 293 320
FT DISULFID 350 406
FT DISULFID 364 395
FT DISULFID 382 411
FT DISULFID 476 574
FT DISULFID 591 622
FT CARBOHYD 138 138
FT CARBOHYD 917 917
FT CARBOHYD 962 962
FT CARBOHYD 994 994
FT CARBOHYD 1289 1289
FT CARBOHYD 2336 2336
FT CARBOHYD 2489 2489
SQ SEQUENCE 3430 AA; 379624 MW; 12EAA7E81F01CBEE CRC64;

Query Match 1.5%; Score 8; DB 1; Length 3430;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVLL 468
Db 772 LAVGVLL 779

RESULT 7
POLG_KUNJM STANDARD; PRT; 3433 AA.
ID POLG_KUNJM STANDARD; PRT; 3433 AA.
AC P1435; 082983;
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contants: Capsid protein C (core protein); Matrix
DE protein (Envelope protein M); Major envelope protein E; Nonstructural
DE proteins NS1, NS2, NS4A and NS4B; Protease/helicase (EC 3.4.21.98)
DE (NS3); RNA-directed RNA polymerase (EC 2.7.7.48) (NS5)].
OS Kunjin virus (strain MR61C)
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OC NCBI_TaxID=11078;
OX [1]
RN SEQUENCE FROM N.A.

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RX MEDLINE=88089524; PubMed=2826659;
RA Coia G., Parker M.D., Speight G., Byrne M.E., Westaway E.G.;
RT "Nucleotide and complete amino acid sequences of Kunjin virus:
RT definitive gene order and characteristics of the virus-specified
RT proteins."
RL J. Gen. Virol. 69:1-21(1988).
CC -1- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
CC precursor polyprotein, commonly with Asp or Glu in the P6
CC position, Cys or Thr in P1 and Ser or Ala in P1'.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate +
CC {RNA} (N).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND MNA.
CC PROTEIN C AND MNA.
CC -----
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CC -----
CC EMBL; D00246; BA00176.1; -.
CC PIR; A28697; GNMVAV.
DR HSP; P14336; 1SVB.
DR MEROPS; S07.001; -.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR001850; Flavi_helicase.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR001157; Flavi_N51.
DR InterPro; IPR000752; Flavi_N52A.
DR InterPro; IPR000487; Flavi_N52B.
DR InterPro; IPR000404; Flavi_N54A.
DR InterPro; IPR001528; Flavi_N54B.
DR InterPro; IPR002080; Flavi_N55.
DR InterPro; IPR002535; Flavi_propep.
DR InterPro; IPR002877; FesJ.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVit.
DR PFam; PF01003; Flavi_capsid; 1.
DR PFam; PF02832; Flavi_glycoprote; 1.
DR PFam; PF00869; Flavi_glycoprote; 1.
DR PFam; PF00949; Flavi_helicase; 1.
DR PFam; PF01004; Flavi_M; 1.
DR PFam; PF00948; Flavi_N51; 1.
DR PFam; PF01005; Flavi_N52A; 1.
DR PFam; PF01002; Flavi_N52B; 1.
DR PFam; PF01350; Flavi_N54A; 1.
DR PFam; PF01349; Flavi_N54B; 1.
DR PFam; PF00972; Flavi_N55; 1.
DR PFam; PF01570; Flavi_propep; 1.
DR PFam; PF01728; FesJ; 1.
DR PFam; PF00271; helicase_C; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
DR ProDom; PD001496; Flavi_N51; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC_C; 1.
DR PolyProtein; Glycoprotein; Transferrase; RNA-directed RNA polymerase;
DR Core protein; Coat protein; Envelope protein; Hydrolyase; Helicase;
DR ATP-binding; Transmembrane; Nonstructural protein.
DR INIT_MER 1
FT CHAIN 1 123
FT PROPEP 124 215
FT CHAIN 216 290
MEMBRANE PROTEIN M.

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FT CHAIN 291 791 MAJOR ENVELOPE PROTEIN E.
FT CHAIN 792 1143 NONSTRUCTURAL PROTEIN NS1.
FT CHAIN 1144 1374 NONSTRUCTURAL PROTEIN NS2.
FT CHAIN 1375 1505 NONSTRUCTURAL PROTEIN NS2B.
FT CHAIN 1506 2124 PROTEASE/HELICASE (NS3).
FT CHAIN 2125 2273 NONSTRUCTURAL PROTEIN NS4.
FT CHAIN 2274 2528 NONSTRUCTURAL PROTEIN NS4B.
FT CHAIN 2529 3433 RNA-DIRECTED RNA POLYMERASE (NS5).
FT DOMAIN 388 401 INVOLVED IN FUSION.
FT NP BIND 1639 1706 ATP (POTENTIAL).
FT SITE 1790 1793 DEAD BOX.
FT DISULFID 293 320 BY SIMILARITY.
FT DISULFID 350 406 BY SIMILARITY.
FT DISULFID 364 395 BY SIMILARITY.
FT DISULFID 382 411 BY SIMILARITY.
FT DISULFID 480 578 BY SIMILARITY.
FT DISULFID 595 626 BY SIMILARITY.
FT CARBOHYD 921 921 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 921 921 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 966 966 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 998 998 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 3433 AA; 381363 MW; EE4B888A7D040B99 CRC64;

Query Match 1.3%; Score 8; DB 1; Length 3433;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVLL 468
|||||
DB 776 LAVGVLL 783

RESULT 8
RLA2_PPAR STANDARD; PRT; 114 AA.

AC P41059;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60S acidic ribosomal protein P2.
OS Parthenium argentatum (Guayule, rubber plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Parthenium.
OX NCBI_Taxid=35935;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Line 11591; TISSUE=stem bark;
RA MEDLINE=95062745; PubMed=7972523;
RA Bachhaus R.A., Kunz M., Camara B., Bouvier F., Pan Z.;
RT "Nucleotide sequence of a cDNA for a P2 60S acidic ribosomal protein
from Parthenium argentatum";
RL Plant Physiol. 106:395-395(1994).
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
CC PROTEIN SYNTHESIS.
CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
CC SUBUNIT.
CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL: X78213; CAA55047.1; -;
CC InterPro: IPR001813; 60S_ribosomal.
CC Pfam: PF00428; 60S_ribosomal; 1.
KW Ribosomal protein; Phosphorylation.

SQ SEQUENCE 114 AA; 11502 MW; 4C850AAD572D1A0B CRC64;
Query Match 1.3%; Score 7; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 LIALIGG 474
|||||
DB 8 LIALIGG 14

RESULT 9

YCGK_ECOLI STANDARD; PRT; 133 AA.
ID YCGK_ECOLI
AC P76002;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein ycgK precursor.
GN YCGK OR B1178.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Samped G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map";
RL DNA Res. 3:137-155(1996).

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CC -----

CC EMBL: AE000216; AAC74262.1; -;
CC EMBL: D90751; BAA36012.1; -;
CC EMBL: D90752; BAA36025.1; -;
CC PIR: G64863; G64863.
CC DR SWISS-2DPAGE; P76002; COLI.
CC DR EcoGene; EG13892; YCGK.
CC KW Signal; Complete proteome.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT CHAIN 23 133 PROTEIN YCGK.
SQ SEQUENCE 133 AA; 14906 MW; 54997548219541P1 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALL 472
|||||


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FT METAL 158 158 IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).
FT METAL 162 162 IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 205 AA; 22154 MW; C06ED8F80617B468 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 205;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 CPNOALR 264
Db 162 CPNOALR 168

RESULT 12
PCP_BACAM STANDARD; PRT; 215 AA.
ID PCP_BACAM STANDARD; PRT; 215 AA.
AC P6107;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyrolydione-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-
peptidase) (Pyroglutamyl-peptidase I) (PGP-I) (Pyrase).
GN PCP.
OS Bacillus amyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1390;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-68 AND CYS-144.
RX MEDLINE=93203177; PubMed=8095933;
RA Yoshimoto T., Shimoda T., Kitazono A., Kabashima T., Ito K.,
RA Tezuru D.;
RT "Pyroglutamyl peptidase gene from Bacillus amyloliquefaciens:
RT cloning, sequencing, expression, and crystallization of the expressed
RT enzyme.";
RL J. Biochem. 113:67-73(1993).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99216536; PubMed=10196127;
RA Odagaki Y., Hayaishi A., Okada K., Hirotsu K., Kabashima T., Ito K.,
RA Yoshimoto T., Tezuru D., Sato M., Clardy J.;
RT "The crystal structure of pyroglutamyl peptidase I from Bacillus
RT amyloliquefaciens reveals a new structure for a cysteine protease.";
RL Structure 7:399-411(1999).
CC -1- FUNCTION: REMOVES 5-OXOPROLINE FROM VARIOUS PENULTIMATE AMINO ACID
CC RESIDUES EXCEPT L-PROLINE.
CC -1- CATALYTIC ACTIVITY: 5-oxoprolyl-peptide + H(2)O = 5-oxoproline +
CC peptide.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: MOST ACTIVE AT PH 6.5 AND STABLE AT PH 7.0-9.0.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C15.
CC
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CC -----
CC EMBL; D11035; BAA01791.1; -
CC PIR; JX0244; JX0244.
CC PDB; 1AUG; 23-MAR-99.
CC MEROPS; C15.001; -
CC HAVAP; MF_00417; -
CC InterPro; IPR000816; Peptidase_C15.
CC Pfam; PF01470; Peptidase_C15; 1.
CC ProDom; PD008480; Peptidase_C15; 1.
CC TIGRFAMs; TIGR00504; pyro_pdae; 1.
CC PROSITE; PS01333; PYRASE_GLU; 1.
CC PROSITE; PS01334; PYRASE_CYS; 1.
CC Hydrolase; Thiol peptidase; 3D-structure.
FT ACT_SITE 81

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FT ACT_SITE 144 144
FT ACT_SITE 168 168
FT MUTAGEN 68 68 C->S: NO LOSS OF ACTIVITY.
FT MUTAGEN 144 144 C->S: LOSS OF ACTIVITY.
FT STRAND 3 10
FT HELIX 20 26
FT TURN 27 30
FT STRAND 32 33
FT TURN 34 35
FT STRAND 36 43
FT TURN 47 48
FT HELIX 49 61
FT STRAND 65 71
FT TURN 73 74
FT STRAND 78 81
FT STRAND 83 85
FT STRAND 88 88
FT TURN 95 96
FT STRAND 103 103
FT TURN 107 108
FT STRAND 112 114
FT HELIX 119 128
FT TURN 129 130
FT STRAND 133 133
FT STRAND 136 136
FT HELIX 143 158
FT TURN 160 161
FT STRAND 163 169
FT STRAND 173 175
FT HELIX 186 202
SQ SEQUENCE 215 AA; 23286 MW; 731A9F80733E807C CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 215;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 371 AAASYTA 377
Db 133 AAASYTA 139

RESULT 13
PCP_BACSU STANDARD; PRT; 215 AA.
ID PCP_BACSU STANDARD; PRT; 215 AA.
AC P28618;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyrolydione-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-
peptidase) (Pyroglutamyl-peptidase I) (PGP-I) (Pyrase).
GN PCP.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RX MEDLINE=92339527; PubMed=1353026;
RA Awde A., Cleuziat P., Gonzales T., Robert-Baudouy J.;
RT "Characterization of the pcg gene encoding the pyrolydione carboxyl
RT peptidase of Bacillus subtilis.";
RL FEBS Lett. 305:67-73(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RX MEDLINE=95219079; PubMed=7704254;
RX Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
RT "Determination of a 21548 bp nucleotide sequence around the 24 degrees
RT region of the Bacillus subtilis chromosome.";
RL Microbiology 141:269-275(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=168;

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RX MEDLINE=98044033; PubMed=9384377;
RA Kunat F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertolo M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Bourlier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Broutin S., Bruns C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codan J.J., Comercon I.F., Cummings N.J., Daniel R.A.,
RA Denzov F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabre C., Ferrati E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Jorja B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koester P., Koningsfeld G., Krog S., Kumano M.,
RA Kurita K., Lapides A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maul C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portelle D., Porwolik S., Prescott A.M.,
RA Priesen E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sedate I.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scifone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpeira P., Tognoni A.,
RA Toesato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viati A., Wamut R., Wedler E., Wedler H., Melzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RT Nature 390:249-256(1997).
[4]
RN MEDLINE=93139164; PubMed=1362573;
RP Gonales T., Awade A., Besson C., Robert-Baudouy J.;
RA "Purification and characterization of recombinant pyrrolidone carboxyl
RT peptidase of Bacillus subtilis".
RT J. Chromatogr. A 584:101-107(1992).
CC -1- FUNCTION: REMOVES 5-OXOPROLINE FROM VARIOUS PENULTIMATE AMINO ACID
CC RESIDUES EXCEPT L-PROLINE.
CC -1- CATALYTIC ACTIVITY: 5-oxopropyl-L-peptide + H(2)O = 5-oxoproline +
CC peptide.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C15.
CC -----
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CC -----
DR EMBL: X66034; CAA46833.1; -
DR EMBL: D30808; BAA06485.1; -
DR EMBL: A25847; CAA0177.1; -
DR EMBL: Z99105; CAA12059.1; -
DR PIR: S23432; S23432.
DR HSSP: P46107; LAUG.
DR MEROPS: C15.001; -
DR Subtilisin, BG10873; pcp.
DR HAMAP: MF_00417; -; 1.
DR InterPro: IPR000816; Peptidase_C15.
DR Pfam: PF01470; Peptidase_C15; 1.
DR ProDom: PD008480; Peptidase_C15; 1.
DR TIGRfam: TIGR00504; pyro_pbase; 1.
DR PROSITE: PS01333; PYRASE_GLU; 1.
DR PROSITE: PS01334; PYRASE_CYS; 1.
KW Hydrolase; Thiol protease; Complete proteome.
FT ACT_SITE 81
FT ACT_SITE 144
FT ACT_SITE 144 BY SIMILARITY.

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FT ACT_SITE 168 168 BY SIMILARITY.
SQ SEQUENCE 215 AA; 23774 MW; A8804117BCCFE24 CRC64;
Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 215;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 371 AAVSYTA 377
DB 133 AAVSYTA 139
RESULT 14
CLD9 HUMAN STANDARD; PRT; 217 AA.
AC 095484;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Claudin-9.
GN CLDN9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Keen T.J., Inglehearn C.F.; EMBL/GenBank/DBJ databases.
RL Submitted (NOV-1998) TO THE EMBL/GenBank/DBJ STRANDS.
CC -1- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the claudin family.
CC -----
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CC -----
DR EMBL: AJ130941; CAA10254.1; -
DR Genew; HGNC:2051; CLDN9.
DR InterPro: IPR006187; Claudin.
DR InterPro: IPR006188; Claudin sup.
DR InterPro: IPR004031; PMP22_Claudin.
DR Pfam: PF00822; PMP22_Claudin; 1.
DR PRINTS: PR01077; CLAUDIN.
DR PROSITE: PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 8 28
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
SQ SEQUENCE 217 AA; 22848 MW; 0B49C5B5CB3AAC9C CRC64;
Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 217;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 467 LLLALNG 473
DB 88 LLLALNG 94
RESULT 15
CLD9 MOUSE STANDARD; PRT; 217 AA.
AC 092057;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Claudin-9.

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GN CLDN9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RA SEQUENCE FROM N.A.
RA Morita K., Furuse M., Tsukita S.
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the claudin family.
CC -----
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CC -----
DR EMBL; AF124424; AAD17319.1; -
DR MGD; MGI:1913100; Cldn9.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin_sup.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
DR TIGR; TIGR01077; Claudin.
KM Tight junction; Transmembrane.
FT TRANSMEM 13 33
FT TRANSMEM 82 102
FT TRANSMEM 117 137
FT TRANSMEM 160 180
FT TRANSMEM 217 229;
SQ SEQUENCE 217 AA; 22984 MW; 2B46C7C43A87EFDS CRC64;

Query Match 1.3%; Score 7; DB 1; Length 217;
Best Local Similarity 100.0%; Pred.No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 LLLALLG 473
Db 88 LLLALLG 94

RESULT 16
XG18 HARIN STANDARD; PRT; 217 AA.
ID YG18 HARIN
AC P45275;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein H1618.
GN H1618.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
RN [1]
RA SEQUENCE FROM N.A.
RA STRAIN: Rd / Km20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kitzness E.F.,
RA Kerkavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spirigos T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,
RA Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Frazer C.W., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RA Rd.";
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RL Science 269:496-512(1995).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -----
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CC -----
DR EMBL; U32835; AAC23266.1; -
DR PIR; A64133; A64133.
DR TIGR; H1618; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR Hypothetical protein; ATP-binding; Transport; Complete proteome.
KM NE_BIND 46 53
FT NE_BIND 217 AA; 24079 MW; 8C0675189A65012B CRC64;
SQ SEQUENCE 217 AA; 24079 MW; 8C0675189A65012B CRC64;

Query Match 1.3%; Score 7; DB 1; Length 217;
Best Local Similarity 100.0%; Pred.No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 LLLALLG 473
Db 55 LLLALLG 61

RESULT 17
RL1 BORBU STANDARD; PRT; 226 AA.
ID RL1 BORBU
AC O51353;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L1.
GN RPLA OR BB0392.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
RN [1]
RA SEQUENCE FROM N.A.
RA STRAIN: ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerkavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uterback T., Matthey L., McDonald L., Artlach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RA "Genomic sequence of a Lyme disease spirochete, Borrelia
RA burgdorferi."
RL Nature 390:580-586(1997).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
CC LOCATED IN THE NEIGHBORHOOD OF THE SITE WHERE ELONGATION FACTOR TU
CC IS BOUND TO THE RIBOSOME.
CC -1- SIMILARITY: BELONGS TO THE L1P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL, AE001145; AAC66773.1; -.
DR PIR, G70148; G70148.
DR HSSP, P27150; 1AD2.
DR TIGR, BB0392; -.
DR InterPro; IPR005878; L1_bact_ch1.
DR InterPro; IPR002143; Ribosomal_L1.
DR Pfam; PF00687; Ribosomal_L1; 1.
DR ProDom; PD001114; Ribosomal_L1; 1.
DR TIGRfam; TIGR01169; rplA_bact; 1.
DR PROSITE; PS01199; RIBOSOMAL_L1; 1.
DR Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 226 AA; 25668 MW; 980CC2BE949B02D CRC64;

Query Match 1.3%; Score 7; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 KKRPDDL 511
Db 195 KKRPDDL 201

RESULT 18
G145 RAT STANDARD; PRT; 234 AA.
AC P35898;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Possible gustatory receptor clone PTE45 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN= Fischer; TISSUE=Lingual epithelium;
RX MEDLINE=93138133; PubMed=8380780;
RA Abe K., Kusakabe Y., Yamemura K., Emori Y., Arai S.;
RT "Multiple genes for G protein-coupled receptors and their expression
in lingual epithelia."
RL FEBS Lett. 316:253-256(1993).
CC -1- FUNCTION: POSSIBLE TASTE RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: TONGUE-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR PIR; S29000; S29000.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT TRANSMEM 1 1
FT NON TER 1
FT DOMAIN <1 11 2 (POTENTIAL).
FT TRANSMEM 12 42 3 (POTENTIAL).
FT TRANSMEM 63 62 3 (POTENTIAL).
FT TRANSMEM 84 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 105 4 (POTENTIAL).
FT TRANSMEM 106 138 5 (POTENTIAL).
FT TRANSMEM 139 160 5 (POTENTIAL).
FT TRANSMEM 161 182 6 (POTENTIAL).
FT TRANSMEM 183 202 6 (POTENTIAL).
FT TRANSMEM 203 212 7 (POTENTIAL).
FT TRANSMEM 213 234 7 (POTENTIAL).
FT DISULFID 39 121 BY SIMILARITY.
FT NON TER 234 234
SQ SEQUENCE 234 AA; 25993 MW; BDA1186448F257D9 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 470 ALLGGCC 476
Db 146 ALLGGCC 152

RESULT 19
FCEA HUMAN STANDARD; PRT; 257 AA.
ID FCEA_HUMAN
AC P12319;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
(FcERI) (Ige Fc receptor, alpha-subunit) (Fc-epsilon RI-alpha).
DE FcERI OR FcRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88233953; PubMed=2967464;
RA Kochan J., Petrine L.F., Hakimi J., Kishi K., Kinet J.-P.;
RT "Isolation of the gene coding for the alpha subunit of the human high
affinity IGE receptor."
RL Nucleic Acids Res. 16:3584-3584(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE= Mast cells;
RX MEDLINE=8815102; PubMed=2964640;
RA Shinitzu A., Tepler I., Bentley P.N., Berenstein E.H., Siraganian R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
RN [3]
RP 3D-STRUCTURE MODELLING OF 26-197.
RX MEDLINE=93113350; PubMed=1472946;
RA Padlan E.A., Helm B.A.;
RT "A modeling study of the alpha-subunit of human high-affinity
RT receptor for immunoglobulin-E."
RL Receptor 2:129-144(1992).
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYPHOKINES.
CC -1- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC DISULFIDE LINKED GAMMA CHAINS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC -----
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CC -----
DR EMBL, X06948; CAA30025.1; -.
DR EMBL, J03605; AAA36204.1; -.
DR EMBL, A21606; CAA01564.1; -.
DR PIR, S00682; S00682.
DR PDB; 1ALS; 27-FEB-95.
DR PDB; 1F2Q; 08-JUN-00.
DR PDB; 1F2Q; 08-JUN-00.
DR PDB; 1J86; 29-AUG-01.
DR PDB; 1J87; 29-AUG-01.
DR PDB; 1J88; 29-AUG-01.
DR PDB; 1J89; 05-SEP-01.
DR Genew; HGNC:3609; FcER1A.

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DR MM: 147140; C: integral to plasma membrane; TAG.
DR GO: 0005887; C: integral to plasma membrane; TAG.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_2.
DR SMART: SM00408; IGC2_1.
DR PROSITE: PS00835; IG_LIKE; 2.
KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; 3D-structure.
FT SIGNAL 1 25
FT CHAIN 26 257 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT DOMAIN 26 205 RECEPTOR ALPHA-SUBUNIT.
FT TRANSSEM 206 224 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 225 257 POTENTIAL.
FT DOMAIN 30 110 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 111 193 IG-LIKE 1.
FT DISULFID 51 93 IG-LIKE 2.
FT DISULFID 132 176 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT STRAND 31 35
FT HELIX 39 42
FT TURN 43 43
FT STRAND 48 54
FT STRAND 61 66
FT TURN 67 68
FT STRAND 69 71
FT STRAND 74 74
FT TURN 75 76
FT STRAND 77 79
FT HELIX 82 87
FT STRAND 91 96
FT HELIX 98 100
FT TURN 101 101
FT STRAND 104 107
FT STRAND 114 116
FT HELIX 120 124
FT STRAND 128 133
FT STRAND 143 145
FT HELIX 146 148
FT TURN 149 149
FT STRAND 150 150
FT TURN 152 153
FT STRAND 154 155
FT TURN 156 159
FT STRAND 160 163
FT HELIX 165 170
FT STRAND 175 178
FT STRAND 181 182
FT TURN 183 185
FT STRAND 186 187
FT STRAND 190 193
SQ SEQUENCE 257 AA; 29596 MW; F183BB2357DDAD58 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C32D5.1 in chromosome II.
GN C32D5.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N.;
RN Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RP REVISIONS.
RA Waterston R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U23511; AAC46789.2; -
DR Wormpep; C32D5.1; CB29207.
KW Hypothetical protein.
SQ SEQUENCE 263 AA; 30461 MW; 374D139E822304BB CRC64;

Query Match 1.3%; Score 7; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 20
YOD1 CAEEL STANDARD; PRT; 263 AA.
AC 009262;

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RESULT 21
CDS_PSEAE STANDARD; PRT; 271 AA.
ID 059640;
AC 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidate cytidyltransferase (EC 2.7.7.41) (CDP-diglyceride
DE synthetase) (CDP-diglyceride pyrophosphorylase) (CDP-diglycerol
DE synthase) (CDP-phosphatidate cytidyltransferase) (CDP-DAG
DE synthase) (CDP-DG synthetase).
GN CDSR OR CDS OR PA3651.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=96257274; PubMed=8654980;
RA Taguchi K., Fukutomi H., Kuroda A., Kato J., Ohtake H.;
RT "Cloning of the Pseudomonas aeruginosa gene encoding CDP-diglyceride
RT synthetase."
RL Gene 172:165-166 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey W.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Golty L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

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RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- CATALYTIC ACTIVITY: CTP + phosphatidate = diphosphate + CDP-
CC dicylglycerol.
CC -1- PATHWAY: Phospholipid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CDS FAMILY.
CC -----
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CC -----
DR EMBL, D50811; BAA09437.1; -
DR EMBL, AE004785; AAG07039.1; -.
DR PIR, F83188; F83188.
DR PIR, JC4832; JC4832.
DR InterPro: IPR000374; PCtransf.
DR Pfam: PF01148; CTP_transf_1; 1.
DR PROSITE, PS01315; CDS_1_1; 1.
KW TRANSFERASE; Nucleotidyltransferase; Phospholipid biosynthesis;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 12 32 POTENTIAL.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 75 95 POTENTIAL.
FT TRANSMEM 111 131 POTENTIAL.
FT TRANSMEM 136 156 POTENTIAL.
FT TRANSMEM 174 194 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 251 271 POTENTIAL.
FT TRANSMEM 131 133 WPL -> VAA (IN REF. 1).
FT CONFLICT 131 133
SQ SEQUENCE 271 AA; 28856 MW; 5025059C3F1A64C7 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 LLLALLG 473
Db 202 LLLALLG 208

RESULT 22
UPK_YERPE STANDARD; PRT; 272 AA.
ID UPK_YERPE
AC Q82165;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative undecaprenol kinase (EC 2.7.1.66) (Bactitracin resistance
DE protein).
GN UPK OR BACA OR YPO0649 OR YJ3530.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_Taxid=632;
RA SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaitia M., James K.D., Churcher C., Wungali K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holtroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

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RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=KIM5 / Biovar Medievalis;
RC MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Peterson J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Strelley S.C., McOmough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611(2002).
CC -1- FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl
CC phosphate. Confers resistance to bacitracin (by similarity).
CC -1- CATALYTIC ACTIVITY: ATP + undecaprenol = ADP + undecaprenyl
CC phosphate.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- MISCELLANEOUS: Bacitracin is thought to be involved in inhibition
CC of peptidoglycan synthesis by sequestering undecaprenyl
CC diphosphate reducing the pool of lipid carrier available.
CC -1- SIMILARITY: BELONGS TO THE UPK FAMILY.
CC -----
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CC -----
DR EMBL, AJ414144; CAC89503.1; -
DR EMBL, AE013956; AAM87078.1; -.
DR PIR, AD0080; AD0080.
DR PIR, AD0080; AD0080.
DR HAMAP, MF_01006; -; 1.
DR InterPro: IPR003824; BACA.
DR Pfam, PF02673; BACA_1.
DR TIGRFAMs: TIGR00753; undec_kin_baca_1.
KW TRANSFERASE; Kinase; Antibiotic resistance; Transmembrane;
KW Complete proteome.
FT TRANSMEM 4 26 POTENTIAL.
FT TRANSMEM 47 69 POTENTIAL.
FT TRANSMEM 89 108 POTENTIAL.
FT TRANSMEM 121 138 POTENTIAL.
FT TRANSMEM 153 172 POTENTIAL.
FT TRANSMEM 184 206 POTENTIAL.
FT TRANSMEM 226 248 POTENTIAL.
FT TRANSMEM 253 271 POTENTIAL.
SQ SEQUENCE 272 AA; 29483 MW; 164FC644788F2189 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 464 GGVLLLA 470
Db 128 GGVLLLA 134

RESULT 23
GLPG_ECOLI STANDARD; PRT; 276 AA.
ID GLPG_ECOLI
AC P09351; P76691;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein GLPG.
GN GLPG OR B3424.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RA [1]

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RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
RC STRAIN=K12;
RX MEDLINE=97113527; PubMed=8955387;
RA Zeng G., Ye S., Larson T.J.;
RT "Repressor for the sn-glycerol 3-phosphate regulon of Escherichia
RT coli K-12: primary structure and identification of the DNA-binding
RT domain."
RL J. Bacteriol. 178:7080-7089(1996).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=88319970; PubMed=3045764;
RA Choi Y.-L., Kawase S., Nishida T., Sakai H., Komano T., Kawamukai M.,
RA Uetani R., Kohara Y., Akiyama K.;
RT "Nucleotide sequence of the glpR gene encoding the repressor for the
RT glycerol-3-phosphate regulon of Escherichia coli K12."
RL Nucleic Acids Res. 16:7732-7732(1988).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=9742617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN
RP SEQUENCE FROM N.A.
CC -1- FUNCTION: NOT YET KNOWN.
CC
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CC
CC -----
CC DR EMBL; M54940; AAA23890.1; -.
CC DR EMBL; M96795; AAC28166.1; -.
CC DR EMBL; X07520; CAA30398.1; -.
CC DR EMBL; U18997; AAB58222.1; ALT. INTT.
CC DR EMBL; AE000418; AAC76449.1; -.
CC DR PIR; C65138; BVECGG.
CC DR EcGene; EG10397; glpG.
CC DR InterPro; IPR002610; Rhomboid.
CC DR Pfam; PF01694; Rhomboid.1.
CC KM Glycerol metabolism; DNA-binding; Complete proteome.
CC FT DNA_BIND 190 209 H-T-H MOTIF (BY SIMILARITY).
CC FT CONFLICT 47 47 R -> H (IN REF. 1).
CC FT CONFLICT 178 179 RS -> TL (IN REF. 3).
CC FT CONFLICT 193 193 S -> T (IN REF. 2).
CC SQ SEQUENCE 276 AA; 31307 MW; B55AFB345B07A7E CRC64;

Query Match 1.3%; Score 7; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 IAGIANG 464
DB 255 IAGIANG 261

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OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamai I., Klassen L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Anderson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria."
RL Science 296:2376-2379(2002)
RN
CC -1- CATALYTIC ACTIVITY: L1-2,6-diaminohexanedioate = meso-
CC diaminopentanedioate.
CC -1- PATHWAY: Biosynthesis of lysine from aspartate semialdehyde; sixth
CC step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the diaminopimelate epimerase family.
CC
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CC
CC -----
CC DR EMBL; AE014130; AAM68104.1; -.
CC DR HAMAP; MF_00197; -.
CC DR InterPro; IPR001653; DAP_epimerase.
CC DR Pfam; PF01678; DAP_epimerase; 2.
CC DR TIGRFAMs; TIGR00652; DapF_1.
CC DR PROSITE; PS01326; DAP_EPIPERASE; FALSE NEG.
CC KM Isomerase; lysine biosynthesis; Complete proteome.
CC FT ACT_SITE 83 83 BY SIMILARITY.
CC FT ACT_SITE 227 227 BY SIMILARITY.
CC SQ SEQUENCE 284 AA; 32024 MW; EB37B370320A0089 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 ELLEKXS 155
DB 187 ELLEKXS 193

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RESULT 25.
AROK METTH STANDARD; PRT; 289 AA.
AC 026896;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Shikimate kinase (EC 2.7.1.71) (SK).
OS AROK OR MTH805.
GN Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanobacter.
OX NCBI_TaxID=187420;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A.;
RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pochter B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;

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CC      fifth step.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. ARCHAEAL
CC      SHIKIMATE KINASE SUBFAMILY.
CC      -----
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CC      -----
CC      EMBL, AB000858; AAB85305.1; -.
CC      PIR, E69207; E69207.
CC      HAMAP, MF_00370; -.
CC      InterPro: IPR006204; GHMP_kinase.
CC      InterPro: IPR006203; GHMP_kinase_ATP.
CC      InterPro: IPR000670; Homoser_Kin.
CC      Pfam, PF00288; GHMP_kinase_1.
CC      PRINTS, PR00958; HOMSERKINASE.
CC      PROSITE, PS00627; GHMP_KINASES_ATP, 1.
CC      Aromatic amino acid biosynthesis; Transferase; Kinase; ATP-binding;
CC      Complete proteome.
CC      NP_BIND, 84, 94, ATP (POTENTIAL).
CC      FT, NP_BIND, 289 AA; 30474 MW; 8BE9CC2042AED3FD8 CRC64;
CC      SQ, SEQUENCE, 289 AA; 30474 MW; 8BE9CC2042AED3FD8 CRC64;

Query Match      1.3%; Score 7; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      20 ASGLSSS 26
DB      86 ASGLSSS 92

RESULT 26
Y727_METJA      STANDARD; PRT; 298 AA.
ID      Y727_METJA
AC      Q58137;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein MJ0727.
GN      MJ0727.
OS      Methanococcus jannaschii.
OC      Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC      Methanocaldococcaceae; Methanocaldococcus.
OX      NCBI_TaxID=2190;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX      MEDLINE=96337999; PubMed=8688087;
RA      Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA      Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA      Kierulff A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA      Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA      Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA      Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA      Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA      Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT      "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT      jannaschii."
RL      Science 273:1058-1073 (1996).
CC      -1- SIMILARITY: SOME, TO COENZYME F420 HYDROGENASE ALPHA SUBUNIT.
CC      -----
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CC      EMBL, U67519; AAB98723.1; -.
CC      PIR, G64390; G64390.
CC      DR, TIGR, MJ0727; -.
CC      DR, InterPro: IPR001501; Nt_hdl.
CC      Pfam, PF00374; NtPse_Hases; 1.
CC      KW Hypothetical protein; Complete proteome.
CC      SQ SEQUENCE, 298 AA; 33519 MW; 4DAAD534096A680D CRC64;

Query Match      1.3%; Score 7; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      461 LAVGVL 467
DB      100 LAVGVL 106

RESULT 27
YSCQ_YERPE      STANDARD; PRT; 307 AA.
ID      YSCQ_YERPE
AC      P42713;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Yop proteins translocation protein O.
DE      YSCQ OR YPCD1.43 OR Y5035 OR Y0038.
GN      Yersinia pestis.
OS      Yersinia pestis.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Yersinia.
OX      NCBI_TaxID=632;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=KIM5 / Biovar Mediaevalis;
RX      MEDLINE=94131934; PubMed=8300512;
RA      Fields K.A., Plano G.V., Straley S.C.;
RT      "A low-Ca2+ response (LCR) secretion (ysc) locus lies within the lcrB
RT      region of the LCR plasmid in Yersinia pestis."
RL      J. Bacteriol. 176:569-579 (1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=KIM5 / Biovar Mediaevalis;
RX      MEDLINE=98427122; PubMed=9746557;
RA      Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA      Blatner F.R.;
RT      "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
RT      Yersinia pestis KIM5."
RL      Infect. Immun. 66:4611-4623 (1998).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=KIM5 / Biovar Mediaevalis;
RX      MEDLINE=98422474; PubMed=9748454;
RA      Hu P., Elliott J., McCreedy P., Skowronski E., Garnea J.,
RA      Kobayashi A., Brubaker R.R., Garcia E.;
RT      "Structural organization of virulence-associated plasmids of Yersinia
RT      pestis."
RL      J. Bacteriol. 180:5192-5202 (1998).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CO-92 / Biovar Orientalis;
RX      MEDLINE=21470413; PubMed=11586360;
RA      Parkhill J., Wren B.W., Thomson N.R.,
RA      Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA      Baker S., Baeham D., Bentley S.D., Brooks K., Cereno-Terraza A.M.,
RA      Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA      Felwell T., Hamlin N., Holtroyd S., Jagsis K., Karlyshev A.V.,
RA      Leather S., Mule S., Oyston P.C.F., Quail M., Rutherford K.,
RA      Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT      "Genome sequence of Yersinia pestis, the causative agent of plague."
RL      Nature 413:523-527 (2001).
CC      -1- FUNCTION: COMPONENT OF THE YOP SECRETION MACHINERY.
CC      -1- SIMILARITY: BELONGS TO THE FLIN/MOPA/SPAO FAMILY.

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CC -----
DR EMBL; AF020214; AAB72200.1; -
DR EMBL; AF074612; AAC69788.1; -
DR EMBL; AF053946; AAC62561.1; -
DR EMBL; AL117189; CAB84920.1; -
DR PIR; A36955; A36955.
DR InterPro; IPR001172; Flagellar Flin.
DR InterPro; IPR003283; SecYIOMPO.
DR InterPro; IPR001543; Spoa.
DR Pfam; PF01052; Spoa_1.
DR PRINTS; PR00956; FLGMOTORFLIN.
DR PRINTS; PR01319; TYPE3OMOPROT.
DR ProDom; PD001777; Spoa; 1.
KW Transport; Protein transport; Plasmid; Virulence; Complete proteome.
SQ SEQUENCE 307 AA; 34418 MW; A936083FAE1CC6C4 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 AYGGENP 251
DB 196 AYGGENP 202

RESULT 28
YSCC YERPS STANDARD; PRT; 307 AA.
AC P40296;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE YOP proteins translocation protein Q.
GN YSCC.
OS Yersinia pseudotuberculosis.
OG Plasmid pIB1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YPIII;
RX MEDLINE=94222840; PubMed=8169210;
RA Bergman T., Erickson K., Galyov E., Persson C., Wolf-Watz H.;
RT "The YopN (YopN/D) gene cluster of Yersinia pseudotuberculosis is
RT involved in Yop secretion and shows high homology to the spa gene
RT clusters of Shigella flexneri and Salmonella typhimurium.";
RL J. Bacteriol. 176:2619-2626(1994).
CC -1- FUNCTION: COMPONENT OF THE YOP SECRETION MACHINERY.
CC -1- SIMILARITY: BELONGS TO THE FLIN/MOP/SPPO FAMILY.
CC -----
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CC -----
DR EMBL; L25667; AAA27677.1; -
DR InterPro; IPR001172; Flagellar Flin.
DR InterPro; IPR003283; SecYIOMPO.
DR InterPro; IPR001543; Spoa.
DR Pfam; PF01052; Spoa_1.
DR PRINTS; PR00956; FLGMOTORFLIN.

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DR PRINTS; PR01339; TYPE3OMOPROT.
DR ProDom; PD001777; Spoa; 1.
KW Transport; Protein transport; Plasmid; Virulence.
SQ SEQUENCE 307 AA; 34419 MW; AC360E39C397941F CRC64;

Query Match 1.3%; Score 7; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 AYGGENP 251
DB 196 AYGGENP 202

RESULT 29
NIOH BUCAI STANDARD; PRT; 322 AA.
AC P57258;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NADH-quinone oxidoreductase chain H (EC 1.6.99.5) (NADH dehydrogenase
DE I, chain H) (NDH-1, chain H).
GN NIOH OR BUI60.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. Aps.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain.
CC Couples the redox reaction to proton translocation (for every two
CC electrons transferred, four hydrogen ions are translocated across
CC the cytoplasmic membrane), and thus conserves the redox energy in
CC a proton gradient (By similarity).
CC -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC -1- SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS. SUBUNITS NIOA, H, J,
CC K, L, M, N CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
CC -----
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CC -----
DR EMBL; AP001118; BAB12878.1; -
DR InterPro; IPR001694; Resp_NADH_dh1.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_NDI_1; FALSE NEG.
DR PROSITE; PS00668; COMPLEX1_NDI_2; FALSE NEG.
KW Oxidoreductase; NAD; Quinone; Transmembrane; Complete proteome.
FT TRANSMEM 15
FT TRANSMEM 81
FT TRANSMEM 101
FT TRANSMEM 114
FT TRANSMEM 114
FT TRANSMEM 149
FT TRANSMEM 169
FT TRANSMEM 186
FT TRANSMEM 206
FT TRANSMEM 237
FT TRANSMEM 257
FT TRANSMEM 265
FT TRANSMEM 285
FT TRANSMEM 302
FT TRANSMEM 322
FT SEQUENCE 322 AA; 36972 MW; P251144B9A6A6B52 CRC64;

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Query Match 1.3%; Score 7; DB 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 457 LINGLAV 463
 200 LINGLAV 206

Db

RESULT 30
 FHR4 HUMAN STANDARD; PRT; 331 AA.
 AC 092456; O9UJY6;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Complement factor H-related protein 4 precursor (FHR-4).
 FHR4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=97190290; PubMed=9038172; Tilhorn A., Buck F., Marti T.,
 RA Skerka C., Hellwege J., Weber W., Zipfel P.F.,
 RA Kampen E., Beisiegel U., Zipfel P.F.;
 RT "The human factor H-related protein 4 (FHR-4). A novel short consensus
 RT repeat-containing protein is associated with human triglyceride-rich
 RT lipoproteins.";
 RL J Biol. Chem. 272:5627-5634(1997).
 [2]
 SEQUENCE OF 1-19 FROM N.A.
 RA Male D.A., Ormsby R.J., Giannakis E., Gordon D.L.;
 RT "Promoter region of complement factor H-related 4 (FHR-4) gene.";
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 [3]
 CHARACTERIZATION.
 RX MEDLINE=98136603; PubMed=9476126;
 RA Hellwege J., Skerka C., Zipfel P.F.;
 RT "Biochemical and functional characterization of the factor-H-related
 RT protein 4 (FHR-4).";
 RL Immunopharmacology 38:149-157(1997).
 CC -1- FUNCTION: INVOLVED IN COMPLEMENT REGULATION. CAN ASSOCIATE WITH
 CC LIPOPROTEINS AND MAY PLAY A ROLE IN LIPID METABOLISM.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
 CC -1- PTM: GLYCOSYLATED.
 CC -1- SIMILARITY: Contains 5 Sushi (SCR) domains.
 CC -1- SIMILARITY: STRONG, TO FACTOR H.
 CC -----
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 CC -----
 CC EMBL: X88337; CAA66980.1; -;
 CC EMBL: AF190816; AAF05951.1; -;
 CC HSP; P10998; IVD.
 CC MIM: 605337; -;
 CC GO: GO:0005320; F:apolipoprotein; TAS.
 CC GO: GO:0005209; F:plasma protein; TAS.
 CC InterPro: IPR000436; Sushi_SCR_CCP.
 CC Pfam: PF00084; sushi; 5.
 CC SMART: SM00032; CCP; 4.
 CC DR SMART; Glycoprotein; Sushi; Signal.
 CC KW SIGNAL; 19 POTENTIAL.

FT CHAIN 20 331 COMPLEMENT FACTOR H-RELATED PROTEIN 4.
 FT DOMAIN 23 85 SUSHI 1.
 FT DOMAIN 87 146 SUSHI 2.
 FT DOMAIN 148 205 SUSHI 3.
 FT DOMAIN 210 266 SUSHI 4.
 FT DOMAIN 268 331 SUSHI 5.
 FT DISULFID 24 73 BY SIMILARITY.
 FT DISULFID 56 84 BY SIMILARITY.
 FT DISULFID 88 134 BY SIMILARITY.
 FT DISULFID 117 145 BY SIMILARITY.
 FT DISULFID 149 193 BY SIMILARITY.
 FT DISULFID 176 204 BY SIMILARITY.
 FT DISULFID 211 254 BY SIMILARITY.
 FT DISULFID 240 265 BY SIMILARITY.
 FT DISULFID 269 320 BY SIMILARITY.
 FT DISULFID 303 330 BY SIMILARITY.
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 331 AA; 37325 MW; 5A0D04AB4B841424 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 331;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 NPVTPSG 140
 59 NPVTPSG 65

Db

RESULT 31
 CAP1 DICDI STANDARD; PRT; 333 AA.
 AC P19198;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE CAMP binding protein CABP1A/CABP1B (CABP1 protein).
 GN CAPA OR CABP1.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 NCBI_TaxID=44689;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=AX2;
 RX MEDLINE=91016829; PubMed=2216719;
 RA Grant C.E., Bain G., Tsang A.;
 RT "The molecular basis for alternative splicing of the CABP1
 RT transcripts in Dictyostelium discoideum.";
 RL Nucleic Acids Res. 18:5457-5463(1990).
 [2]
 SEQUENCE FROM N.A.
 RP STRAIN=AX3;
 RX MEDLINE=9109678; PubMed=2176639;
 RA Grant C., Tsang A.;
 RT "Cloning and characterization of cDNAs encoding a novel cyclic AMP-
 RT binding protein in Dictyostelium discoideum.";
 RL Gene 96:213-218(1990).
 [3]
 SEQUENCE FROM N.A.
 RC STRAIN=V12M2;
 RX MEDLINE=91113722; PubMed=1989693;
 RA Bonfils C., Hebert J., Tsang A.;
 RT "A 27-bp deletion is responsible for the expression of a variant
 RT CABP1, a cyclic AMP-binding protein of Dictyostelium discoideum.";
 RL Biochim. Biophys. Acta 1088:145-146(1991).
 CC -1- SUBUNIT: HETERODIMER OF CABP1A AND CABP1B. CABP1A/CABP1B COULD
 CC ALSO ASSOCIATE WITH P31/P34 TO FORM AN ACTIVE COMPLEX.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=CABP1A;
 CC IsoId=P19198-1; Sequence=Displayed;

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CC Name=2; Synonyms=CABP1B;
CC IsoId=P19198-2; Sequence=VSP 000758;
CC -1 SIMILARITY: BELONGS TO THE CAPAB / TERDEX2 FAMILY.
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CC -----
DR EMBL; X52688; CAA36913.1; -
DR EMBL; X52688; CAA38633.1; -
DR EMBL; M36176; AAA33173.1; -
DR EMBL; X55975; CAA39445.1; -
DR PIR; S11484; S11484.
DR PIR; S13497; S13497.
DR Dictydb; DD02019; capa.
DR InterPro; IPR003325; TERD.
DR InterPro; IPR006031; XYPPX.
DR Pfam; PF02342; Terd; 1.
DR Pfam; PF02162; XYPPX; 4.
KM CAMP-binding; Repeat; Alternative splicing.
FT DOMAIN 48 83 3 X 5 AA REPEATS OF MOTIF A.
FT REPEAT 48 52 A-1.
FT REPEAT 67 71 A-2.
FT REPEAT 79 83 A-3.
FT DOMAIN 84 107 2 X 12 AA REPEATS OF MOTIF B.
FT REPEAT 84 95 B-1.
FT REPEAT 96 107 B-2.
FT DOMAIN 87 134 5 X 9 AA REPEATS OF MOTIF C.
FT REPEAT 87 95 C-1.
FT REPEAT 99 107 C-2.
FT REPEAT 108 116 C-3.
FT REPEAT 117 125 C-4.
FT REPEAT 126 134 C-5.
FT DOMAIN 52 138 GLN/PRO-RICH.
FT VARSPLIC 13 49 Missing (in isoform 2).
FT VARIANT 99 107 MISSING (IN VARIANT V12M2).
FT VARIANT 312 316 LILLV -> EVAAG (IN VARIANT V12M2).
FT VARIANT 318 322 VCKAF -> GVOGA (IN VARIANT V12M2).
SQ SEQUENCE 333 AA; 35521 MW; 9A274606139E0EC1 CRC64;

Query March 1.3%; Score 7; DB 1; Length 333;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 NTALIAG 460
Db 292 NTALIAG 298

RESULT 32
BTUC YERPE STANDARD; PRT; 335 AA.
AC OeDkx4;
DT 28-FEB-2003 (Rel. 41, Created).
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin B12 transport system permease protein btuc.
GN BTUC OR YPO2425 OR Y1914.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Bivovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titchell R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,

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RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
RA Leathar S., Moule S., Oyeron P.C.F., Oatli M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
RA "Genome sequence of Yersinia pestis, the causative agent of plague."
RA Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Bivovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Jiss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.,
RA "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611(2002).
CC -1- FUNCTION: Part of the binding-protein-dependent transport system
CC for vitamin B12. Involved in the translocation of the substrate
CC across the membrane (by similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1 SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. FECD SUBFAMILY.
CC -----
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CC -----
DR EMBL; AJ414152; CAC91229.1; -
DR EMBL; AE013794; AAM85481.1; ALT_INIT.
DR PIR; A10295; A10295.
DR HAMAP; MF_01004; -; 1.
DR InterPro; IPR000515; BPD transp.
DR InterPro; IPR000522; FECD.
DR Pfam; PF01032; FECD; 1.
DR ProDom; PD001557; FECD; 1.
DR PROSITE; PS00402; BPD TRANSP. INN MEMBER, FALSE NEG.
KM Transpore; Cobalt transport; Transmembrane; Inner membrane;
KM Complete proteome.
FT TRANSMEM 21 43 POTENTIAL.
FT TRANSMEM 65 87 POTENTIAL.
FT TRANSMEM 94 113 POTENTIAL.
FT TRANSMEM 117 139 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 200 220 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 282 302 POTENTIAL.
FT TRANSMEM 309 329 POTENTIAL.
SQ SEQUENCE 335 AA; 36331 MW; 839381BADF5E5A74 CRC64;

Query March 1.3%; Score 7; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 464 GGVLLLA 470
Db 291 GGVLLLA 297

RESULT 33
BTUC YERPE STANDARD; PRT; 352 AA.
AC OeDkx4;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Zinc finger protein 185 (ZIM-domain protein ZFP185) (P1-A).

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CN ZNF185 OR ZFP185.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96425694; PubMed=8828036;
RA Levin M.L., Chatterjee A., Pragliola A., Worley K.C., Wehnert M.,
RA Zhuchenko O., Smith R.F., Lee C.C., Herman G.E.;
RT "A comparative transcription map of the murine bare patches (Bpa) and
RT striated (Str) critical regions and human Xq28.";
RL Genome Res. 6:465-477(1996).
CC -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF CELLULAR
CC PROLIFERATION AND/OR DIFFERENTIATION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKIN, KIDNEY, OVARY, TESTIS. ALSO
CC EXPRESSED IN BRAIN, CARTILAGE, HEART, LUNG, SPLEEN AND THYMUS.
CC -1- DEVELOPMENTAL STAGE: AT E14.5, ONLY EXPRESSED IN MESENCHYMAL
CC CELLS. AT E16.5 EXPRESSED ALSO IN CELLS LINING THE VERTEBRAE AND
CC TENDONS OF THE PROXIMAL TAIL. IN LATE EMBRYOGENESIS, EXPRESSED IN
CC MESENCHYMAL CELLS ADJACENT TO THE DISTAL LIMB BONES (TIBIA AND
CC CALCANEUM), IN TENDONS AND IN THE CONNECTIVE TISSUE SHEATH
CC (EPIMYSIUM) SURROUNDING THE SKELETAL MUSCLE. ALSO EXPRESSED IN THE
CC EPITHELIA OF THE EPIDIDYMIS OF THE TESTIS.
CC -1- SIMILARITY: contains 1 LIM zinc-binding domain.
-----
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DR EMBL: U46687; AAC52628.1; -.
DR MGI: MGI:108095; Zfp185.
DR InterPro: IPR001781; LIM.
DR ProDom: PD000094; LIM; 1.
DR SMART; SM00132; LIM; 1.
DR PROSITE; PS00478; LIM DOMAIN 1; FALSE_NEG.
DR PROSITE; PS00023; LIM DOMAIN 2; 1.
DR KW LIM domain; Metal-binding; Zinc.
FT DOMAIN 23 26 POLY-GLU.
FT DOMAIN 292 347 LIM.
SQ SEQUENCE 352 AA; 38322 MW; 2AB1F83D7AF1A5C CRC64;

Query Match 1.3%; Score 7; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 SGLSST 27
DB 103 SGLSST 109

RESULT 34
YOCB_ERWCA STANDARD; PRT; 376 AA.
ID YOCB_ERWCA
AC 047417;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Exoenzyme regulation regulon ORF1.
OS Erwinia carotovora.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxId=554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCDO 2054;
RA Vaughan E.E., Pridmore R.D., Moller B.;
RA Golby P., Jones S.E., Stephens S., Reeves P.J., Bycroft B.,
RA Stewart G., Williams P., Salmund G.P.C.;

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RT "Global regulation of Erwinia carotovora exoenzyme virulence
RT factors: multicopy suppression of rex mutants and evidence for a
RT global repression/regulation.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE RLJ FAMILY OF PSEUDOURIDINE SYNTHASES.
CC STRONG, TO E.COLI YOCB.
CC -1- SIMILARITY: IN THE N-TERMINAL, STRONG, TO E.COLI YOCB; IN THE C-
CC TERMINAL, STRONG, TO E.COLI YOCB.
-----
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-----
DR EMBL: X79474; CAA55982.1; -.
DR PIR: S45107; S45107.
DR InterPro: IPR006145; Pseudou synth.
DR InterPro: IPR006224; PSI_RLU.
DR Pfam; PF04287; DUF446; 1.
DR Pfam; PF00849; Pseudou synth. 2; 1.
DR ProDom; PD001819; PSI_RLU; 1.
DR PROSITE; PS01129; PSI_RLU; 1.
DR PROSITE; PS01129; PSI_RLU; 1.
SQ SEQUENCE 376 AA; 43605 MW; F35992CAAD22E30 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 GVLLAL 471
DB 173 GVLLAL 179

RESULT 35
GALI_LACLA STANDARD; PRT; 399 AA.
ID GALI_LACLA
AC Q9R7D7; O87521;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galactokinase (EC 2.7.1.6) (Galactose kinase).
GN GALK OR LI1983.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxId=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 7962;
RA Lee J.M., Chung D.K., Park J.H., Lee W.K., Chang H.C., Kim J.H.,
RA Lee H.J.;
RT "The organization of genes involved in metabolism of gal/lac of
RT Lactococcus lactis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolding A., Wincker P., Manger S., Jallion O., Malarne K.,
RA Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
RN [3]
RP SEQUENCE OF 276-399. FROM N.A.
RC STRAIN=NCDO 2054;
RX MEDLINE=98406043; PubMed=9733593;
RA Vaughan E.E., Pridmore R.D., Moller B.;
RT "Transcriptional regulation and evolution of lactose genes in the
RT galactose-lactose operon of Lactococcus lactis NCDO2054.";
RL J. Bacteriol. 180:4893-4902(1998).

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CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
CC phosphate.
CC -1- PATHWAY: Galactose metabolism; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. GALK SUBFAMILY.
CC -----
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CC -----
CC EMBL; U60828; AAD11510.1; -.
CC EMBL; AE006428; AAK06081.1; -.
CC EMBL; AF008208; AAC63017.1; -.
CC PIR; G86872; G86872.
CC HAMAP; MF_00246; -.
CC DR InterPro; IPR000705; Galactokinase.
CC DR InterPro; IPR001174; Galkinase.
CC DR InterPro; IPR006204; GHMP Kinase.
CC DR InterPro; IPR006203; GHMPkinase ATP.
CC DR InterPro; IPR006206; Mew_galkinase.
CC DR Pfam; PF00288; GHMP_kinases; 1.
CC DR PRINTS; PR00473; GALTOKINASE.
CC DR PRINTS; PR00960; LMPPROTEIN.
CC DR PRINTS; PR00959; MEVGALKINASE.
CC DR TIGRFAMs; TIGR00131; gal_kin; 1.
CC DR PROSITE; PS00106; GALACTOKINASE; 1.
CC DR PROSITE; PS00627; GHMP_KINASES_ATP; 1.
CC DR Transferase; Kinase; Galactose metabolism; ATP-binding;
CC Complete proteome.
CC NP_BIND 131 141 ATP (POTENTIAL).
CC FT CONFLICT 290 T->A (IN REF. 3).
CC SQ SEQUENCE 399 AA; 43824 MW; D013EA01C4CE2EAB CRC64;

Query Match 1.3%; Score 7; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 ASGLSSS 26
DB 133 ASGLSSS 139

RESULT 36
GALI_LACTC STANDARD; PRT; 399 AA.
AC Q9S6S2;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Galactokinase (EC 2.7.1.6) (Galactose Kinase).
GN GALK.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MG1363;
RA Grossbard B.P., Luesink E.J., Vaughan E.E., Kuipers O.P., De Vos W.M.;
RT "Characterization, expressions, and mutations of the Lactococcus lactis
RT galATKRE genes involved in galactose utilization via the leloir
RT pathway."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
CC phosphate.
CC -1- PATHWAY: Galactose metabolism; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. GALK SUBFAMILY.
CC -----
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CC -----
CC EMBL; AJ011653; CAB44216.1; -.
CC HAMAP; MF_00246; -.
CC DR InterPro; IPR000705; Galactokinase.
CC DR InterPro; IPR001174; Galkinase.
CC DR InterPro; IPR006204; GHMP Kinase.
CC DR InterPro; IPR006203; GHMPkinase ATP.
CC DR InterPro; IPR006206; Mew_galkinase.
CC DR Pfam; PF00288; GHMP_kinases; 1.
CC DR PRINTS; PR00473; GALTOKINASE.
CC DR PRINTS; PR00960; LMPPROTEIN.
CC DR PRINTS; PR00959; MEVGALKINASE.
CC DR TIGRFAMs; TIGR00131; gal_kin; 1.
CC DR PROSITE; PS00106; GALACTOKINASE; 1.
CC DR PROSITE; PS00627; GHMP_KINASES_ATP; 1.
CC DR Transferase; Kinase; Galactose metabolism; ATP-binding.
CC NP_BIND 131 141 ATP (POTENTIAL).
CC SQ SEQUENCE 399 AA; 43741 MW; 31EB38F63AE2277 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 ASGLSSS 26
DB 133 ASGLSSS 139

RESULT 37
PEK_TREAC STANDARD; PRT; 408 AA.
AC Q9HJ95;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR TAL075.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=DSM 1728;
RA MERLIN=20479972; PubMed=11029001;
RA Ruepp A., Gremel W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermophilic scavenger Thermoplasma
RT acidophilum."
RL Nature 407:508-513(2000).
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -1- PATHWAY: Second phase of glycolysis; second step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the phosphoglycerate kinase family.
CC -----
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CC -----
CC EMBL; AL445066; CAC12203.1; -.
CC HSP; P07378; 16PK.

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DR HAMAP_MF_00145: -. 1.
DR InterPro: IPR001576; PGK.
DR Pfam: PF00162; PGK; 1.
DR PRINTS: PR00477; PHGLYCKINASE.
DR PROSITE: PS00111; POLYMERASE KINASE; FALSE NEG.
DR TRANSFERASE: Kinase; GLYCOLYSIS; Complete proteome.
SO SEQUENCE 408 AA; 45372 MW; 6F3C6C2357F5B849 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 408;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 PSGORIS 144
DB 284 PSGORIS 290

RESULT 38
VG46_BPP1 STANDARD; PRT; 424 AA.
ID_VG46_BPP1
AC_P25131;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE 46.5 kDa protein (ORF 424).
OS Bacteriophage Pfl.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10871;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25102-B1;
RX MEDLINE=91186399; PubMed=2010913;
RA Hill D.F., Short N.D., Pernam R.N., Petersen G.B.;
RT "DNA sequence of the filamentous bacteriophage Pfl.";
RJ J. Mol. Biol. 218:349-364(1991).
CC
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CC -----
CC EMBL: X52107; CAA36334.1; -.
CC PIR: S15146; S15146.
CC SEQUENCE 424 AA; 46539 MW; 108EA88EA407BEC7 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 424;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALL 472
DB 230 VLLALL 236

RESULT 39
YKJ5_STRCO STANDARD; PRT; 430 AA.
ID_YKJ5_STRCO
AC_09KYS0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-FEB-2003 (Rel. 42, Last annotation update)
DE Hypochemical zinc metalloprotease SC05695 (EC 3.4.24.-).
GN SC05695 OR SC5H4.19.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyces; Streptomyces; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;

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RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cardeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Sanders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wierhorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- COFACTOR: zinc (Probable).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50B.
CC -1- SIMILARITY: Contains 1 PDZ/DRH domain.
CC -----
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CC -----
CC EMBL: AL939124; CAB9131.1; -.
CC InterPro: IPR001478; PDZ.
CC InterPro: IPR006025; Zn_MTPeptide.
CC Pfam: PF00595; PDZ; 1.
CC Pfam: PF02163; Peptidase_M50; 1.
CC SMART: SMO0228; PDZ; 1.
CC PROSITE: PS0106; PDZ; FALSE NEG.
CC PROSITE: PS00142; ZINC_PROTEASE; 1.
CC KW Hypothetical protein; Hydrolase; Metalloprotease; Zinc; Transmembrane;
CC Complete proteome.
CC METAL 20
CC ACT SITE 21
CC METAL 24
CC TRANSMEM 122
CC TRANSMEM 341
CC TRANSMEM 402
CC DOMAIN 146
CC SEQUENCE 430 AA; 46239 MW; 3586ABD3FD1F44F CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 430;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LVLVAD 15
DB 416 LVLVAD 422

RESULT 40
NMTH_CIOAB STANDARD; PRT; 431 AA.
ID_NMTH_CIOAB
AC_097TN5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable manganese transport protein nmth.
GN NMTH OR CAP0063.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

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RA Gibson R., Lee H.M., Dubois J., Qiu D., Hltti J., Wolf Y.I.,
RA Tacusov R.L., Sabathe F., Doucet-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.,
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
CC -1- FUNCTION: H(+)-stimulated, highly selective, manganese uptake
CC system (by similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO THE NRAMP FAMILY.
CC -----
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CC -----
CC EMBL; AE001438; AK76809.1; -
CC HAMAP; MF_00221; -; 1.
CC InterPro; IPR001046; Nramp.
CC Pfam; PF01566; Nramp; 1.
CC PRINTS; PR00447; NATRESASCOMP.
CC PRODOM; PD001861; Nramp; 1.
CC TIGRFAMs; TIGR01197; nramp; 1.
KW Transport; Symport; Manganese; Transmembrane; Plasmid;
KW Complete proteome.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 61 81 POTENTIAL.
FT TRANSMEM 110 130 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
FT TRANSMEM 211 231 POTENTIAL.
FT TRANSMEM 258 278 POTENTIAL.
FT TRANSMEM 307 327 POTENTIAL.
FT TRANSMEM 347 367 POTENTIAL.
FT TRANSMEM 368 388 POTENTIAL.
FT TRANSMEM 406 426 POTENTIAL.
SQ SEQUENCE 431 AA; 47025 MW; C4AD77DDP5028E9 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ASGLSSS 26
|||
Db 315 ASGLSSS 321

Search completed: October 2, 2003, 16:03:48
Job time : 45 secs

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OM protein - protein search, using sw model

Run on: October 2, 2003, 15:51:44 ; Search time 67 Seconds

(without alignments)
1277.511 Million cell updates/sec

Title: US-10-039-770a-1

Perfect score: 2822
Sequence: 1 MGLVGVQLLVADCTIFA.....EAEENIDQDETHVWEGDY 541

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PTC_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PTCUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	404	13.8	478	US-10-271-145-2	Sequence 2, Appl
2	404	13.8	478	US-10-105-717-2	Sequence 2, Appl
3	114	3.9	549	US-10-156-761-8993	Sequence 8993, Ap
4	105.5	3.6	782	US-10-124-436-1	Sequence 1, Appl
5	105	3.6	758	US-09-949-039-66	Sequence 66, Appl
6	104	3.6	1253	US-10-146-473-72	Sequence 72, Appl
7	104	3.6	1253	US-09-769-508-2	Sequence 2, Appl
8	104	3.6	1255	US-09-854-356-1	Sequence 1, Appl
9	104	3.6	1255	US-09-930-125-2	Sequence 6, Appl
10	104	3.6	1255	US-09-441-411-6	Sequence 2, Appl
11	104	3.6	1255	US-10-313-644-2	Sequence 2, Appl
12	104	3.6	1255	US-10-207-655-45	Sequence 45, Appl
13	103.5	3.5	365	US-09-925-299-847	Sequence 847, App
14	103.5	3.5	365	US-09-925-299-847	Sequence 847, App
15	103.5	3.5	365	US-10-106-698-6387	Sequence 6387, Ap

16	103	3.5	1255	9	US-09-811-123-9	Sequence 9, Appl
17	103	3.5	1255	9	US-09-811-115-3	Sequence 3, Appl
18	103	3.5	1255	12	US-10-207-498-6	Sequence 6, Appl
19	103	3.5	1255	12	US-10-338-730-2	Sequence 2, Appl
20	103	3.5	1255	12	US-10-322-892-4	Sequence 4, Appl
21	103	3.5	1255	15	US-10-177-293-126	Sequence 126, App
22	102	3.5	470	10	US-09-859-053-36	Sequence 36, Appl
23	101.5	3.5	418	10	US-09-887-879-14	Sequence 14, Appl
24	101.5	3.5	418	10	US-09-992-964-14	Sequence 14, Appl
25	101.5	3.5	418	12	US-10-242-383-14	Sequence 14, Appl
26	101.5	3.5	467	12	US-10-280-047-6	Sequence 6, Appl
27	101.5	3.5	468	12	US-10-322-673-1	Sequence 1, Appl
28	101.5	3.5	468	13	US-10-039-785-1	Sequence 1, Appl
29	101.5	3.5	468	15	US-10-226-296-2	Sequence 2, Appl
30	101.5	3.5	468	15	US-10-226-318-2	Sequence 2, Appl
31	101.5	3.5	468	15	US-10-175-902-2	Sequence 2, Appl
32	100.5	3.4	1702	10	US-09-738-973-434	Sequence 434, App
33	100.5	3.4	1702	10	US-09-854-133-434	Sequence 434, App
34	100.5	3.4	1702	15	US-10-144-649A-434	Sequence 434, App
35	99	3.4	470	10	US-09-859-053-32	Sequence 32, Appl
36	98.5	3.4	327	9	US-09-820-893-60	Sequence 60, Appl
37	98.5	3.4	327	12	US-10-216-163-236	Sequence 236, App
38	98.5	3.4	327	15	US-10-227-884-236	Sequence 236, App
39	98.5	3.4	327	15	US-10-230-163-236	Sequence 236, App
40	98.5	3.4	327	15	US-10-230-338-236	Sequence 236, App
41	98.5	3.4	327	15	US-10-218-631-236	Sequence 236, App
42	98.5	3.4	327	15	US-10-230-414-236	Sequence 236, App
43	98.5	3.4	327	15	US-10-216-159A-236	Sequence 236, App
44	98.5	3.4	327	15	US-10-218-849-236	Sequence 236, App
45	98.5	3.4	327	15	US-10-227-873-236	Sequence 236, App

ALIGNMENTS

RESULT 1
US-10-271-145-2
Sequence 2, Application US/10271145
Publication No. US20030138450A1
GENERAL INFORMATION:
/4
APPLICANT: Lanar, David E.
APPLICANT: Dutta, Sheetfj
APPLICANT: Ware, Lisa A.
APPLICANT: Nair, Lalitha P. V.
TITLE OR INVENTION: falciparum AMA-1 Protein and Uses Thereof
FILE REFERENCE: 003/255/SAP
CURRENT APPLICATION NUMBER: US/10/271,145
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 10/105,717
PRIOR FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 2
LENGTH: 478
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Expressed partial sequence of Plasmodium falciparum AMA-1
US-10-271-145-2
Query Match 13.8%; Score 404; DB 12; Length 478;
Best Local Similarity 27.0%; Pred. No. 6.3e-30;
Matches 123; Conservative 71; Mismatches 163; Indels 98; Gaps 18;
Qy 41 GNPQANVEKTEMERENLTHHOSGIYVDLGDQKVDGLTYREPAGLCPIMWGHIELOO 100
Db 43 GNPV-----TEVAKYDIEHVGSGIRVDLGEDAVAGQYRLPSGKCPFGGIIEN 96
Qy 101 PDRIPYNNLTLEDPYTEKEYKOSGNPLPGGFNNLFTVPSQORISPFME-----LLEKNSN 156
Db 97 SN-----TTLVTPVATNGOYLKD-----GGFAF-----PTEPLMSPTLDEMRHFYKONKY 143

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Qy 157 IKASTDLGRCAEFAFKTAMDKNNKATKYRYPFVYDSKRLCHILYVSMQMEGKYQSV 216
Db 144 VKNIDELTLCRHHGMMI--PDNDKSNYKTPAYDDDKCHILYIAQENNGRYCN- 200
Qy 217 KGEPPDLTWYCFKPKRYSTENHLLYGSAYGEN-PDAFISCKPQALRGYFGWKKGR 275
Db 201 KQESRNSMFCFRPAKDISFQNY-----TLYSKNVVDMWEKVCPRKLNQNAKFGMLVDCN 255
Qy 276 CLDYTELTD-TVIERVESKAQCWVKTFFENDGVASDQPHYTP--LTSQASMNQWMP----- 327
Db 256 CEDIPHVEFPALDIFE-----CNKLVEFELS--ASDQPKQYEQHLLDYEKIKEGFNKNAS 309
Qy 328 -----LHOSDQPHSGGVGRNYGFYVDTTGEKCALSDQVPCDCLVSDSAVSYTA 377
Db 310 MIKAFKPTGAFKADRYSHGKGNWGNVNTETO---KCEIFNVKPTCLINNSSIYATTA 366
Qy 378 AGSLSEETPNFIIPSN-----PSYTPPTPETAL 405
Db 367 LSHPIEVENN--PCSLYKDEIMKEIERESKRILKNDNDGNNKIIAPRIFISDDKSL 424
Qy 406 OCTADKFPDSFGACDVQACRKQKTSVCGGQIQSTS 440
Db 425 KCPDPEWVSNSTCRFFVCK-----CVERRAEVTS 454

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RESULT 2

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US-10-105-717-2
; Sequence 2, Application US/10105717
; Publication No. US20030032787A1
; GENERAL INFORMATION:
; /4
; APPLICANT: Lanar, David E.
; APPLICANT: Dutta, Sheelji
; APPLICANT: Ware, Lisa A.
; APPLICANT: Nair, Lalitha P. V.
; TITLE OF INVENTION: Plasmodium falciparum AMA-1 Protein and Uses Thereof
; FILE REFERENCE: 003/246/SAP
; CURRENT APPLICATION NUMBER: US/10/105,717
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/278,616
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Expressed partial sequence of Plasmodium falciparum AMA-1
US-10-105-717-2

```

Query Match 13.8%; Score 404; DB 15; Length 478;

Best Local Similarity 27.0%; Pred. No. 6,3e-30;

Matches 123; Conservative 71; Mismatches 163; Indels 98; Gaps 18;

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Qy 41 GNPFOANVMKTFMERFNLTHHOSGIYVDLQDKEVDGTLVREBAGLCPIWGKHIQLQFDR 100
Db 43 GNPW-----TEMAKYDIEEVHSGIRVLDGDAVAGTQYRLPSGKCPVFGKGIITEN 96
Qy 101 PRLRYRNNFLDVPTEKEVKOSGNPLPGFNLNFVTPSGORISPPRME-----LLEKSN 156
Db 97 SN-----TFLTPVATGNQYLD-----GGFAF--PTEPLMSPTLDEMHHFYDNKY 143
Qy 157 IKASTDLGRCAEFAFKTAMDKNNKATKYRYPFVYDSKRLCHILYVSMQMEGKYQSV 216
Db 144 VKNIDELTLCRHHGMMI--PDNDKSNYKTPAYDDDKCHILYIAQENNGRYCN- 200
Qy 217 KGEPPDLTWYCFKPKRYSTENHLLYGSAYGEN-PDAFISCKPQALRGYFGWKKGR 275
Db 201 KQESRNSMFCFRPAKDISFQNY-----TLYSKNVVDMWEKVCPRKLNQNAKFGMLVDCN 255
Qy 276 CLDYTELTD-TVIERVESKAQCWVKTFFENDGVASDQPHYTP--LTSQASMNQWMP----- 327

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Db 256 CEDIPHVEFPALDIFE-----CNKLVEFELS--ASDQPKQYEQHLLDYEKIKEGFNKNAS 309
Qy 328 -----LHOSDQPHSGGVGRNYGFYVDTTGEKCALSDQVPCDCLVSDSAVSYTA 377
Db 310 MIKAFKPTGAFKADRYSHGKGNWGNVNTETO---KCEIFNVKPTCLINNSSIYATTA 366
Qy 378 AGSLSEETPNFIIPSN-----PSYTPPTPETAL 405
Db 367 LSHPIEVENN--PCSLYKDEIMKEIERESKRILKNDNDGNNKIIAPRIFISDDKSL 424
Qy 406 OCTADKFPDSFGACDVQACRKQKTSVCGGQIQSTS 440
Db 425 KCPDPEWVSNSTCRFFVCK-----CVERRAEVTS 454

```

RESULT 3

```

US-10-156-761-8993
; Sequence 8993, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8993
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8993

```

Query Match 3.9%; Score 114; DB 15; Length 549;

Best Local Similarity 20.7%; Pred. No. 0.066;

Matches 76; Conservative 57; Mismatches 107; Indels 128; Gaps 20;

```

Qy 44 FOANYEMKTFMERFNLTHHOSGIYVDLQDKEVDGTLVREBAGLCPIWGKHIQLQFDR 103
Db 151 FRAKVE-----KWLGEGLDLSIRQADGNYYVLP-----GLHEKVGSGYS 189
Qy 104 LPRNNFLD-----DVPTL-----KEYKOS-----GNPLPGFNLNFVTPSG 140
Db 190 LSFRLDVLKKGGLDLPYTWDOYVDLKLKALVDPVYFSDRWGQPTFGGALLNYLGA- 248
Qy 141 QRISPPMELLEKSNINIKASTDLGRCAEFAFKTAMDKNNKATKYRYPFVYDSKRLCHI 200
Db 249 -----FGTKAGMSYANTAMD--TARKKVFVGATDEYQOMLEY 284
Qy 201 L--VYSQMEGKYQSVKGEPPDLTWYCFKPKRYSTENHLLYGSAYGENPDAFISCK 258
Db 285 LRKLVAELKMDPESTQDD-----AVRK-----LTSKSPV-----ISAN 321
Qy 259 PNOALRGYRFGVWK--KGRCLDYTEL-----TDVTI--BRVESKAQCWVKTFFENDVASDQ 310
Db 322 PDELQVNRYYNGKQVKATTEMLPVPIGPTGEVIVGSRLEGLNVAAGRAABGDS----- 376
Qy 311 PHTYPLTQASWMDA-WPLHOSDQPHSGGVGRNYGFYVD-----TTGEGKCALSDQV 364
Db 377 -----FVAMMGVVDLW-----YSDG--GQEPKAYGEGVTYTSAGGRYKVAVDGI-S 421
Qy 365 CLVSDSAA 372
Db 422 YMGSDPSA 429

```

RESULT 4
US-10-124-436-1
; Sequence 1, Application US/10124436
; Publication No. US20030082573A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Yue, Henry
; APPLICANT: Thangavelu, Kavitha
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: CELL CYCLE PROTEIN
; FILE REFERENCE: PV-0005 CIP
; CURRENT APPLICATION NUMBER: US/10/124,436
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US01/26682
; PRIOR FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 782
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; OTHER INFORMATION: Incyte ID No. US20030082573A1 604004550CD1
US-10-124-436-1

Query Match 3 6%; Score 105.5; DB 15; Length 782;

Best Local Similarity 19.0%; Pred. No. 0.75;
Matches 92; Conservative 65; Mismatches 168; Indels 159; Gaps 22;

QY 114 VPTKEVYKQGNP-LPGGFN-LNFVTPSGRISPPFMLEKNINIKASTDLGRC-----166
DB 33 VTPOGHALPRLPCPTDFKSPINSTVTEQLGTP-ESFPRNAGSSSTLTKCKRRS 91
QY 167 -----AEFAFTVAMDKNKATKRYRPFVDSKRLCHILVSMQLEGGKYYCSVK 217
DB 92 AVGARGSPETHNLIFIRAOQNIKNAR-KSPLAQDSPQSGSPALYRVNVLIER-----144
QY 218 GEPRLTYCPRKPRSVENHHLIYGSAYVGENPRAPIFSKCPNOALRGYRFGVMKGRCL 277
DB 145 -----ISAFQSAFHSIKENEMKTG-----CL 165
QY 278 DY-----TELDTVIERVESKACQCVKTFENDGVAHQPTVPLTQASNDMMPLHQS 331
DB 166 EFSENGKSEMTDLT-----RKEGLSACQSGFPVAVSSKRRRISYQDS 210
QY 332 DQPHSGVGRNYGYVDVTGEGKALSDQVDPCLVSDSAVSYTAAGLSLSE-----383
DB 211 DENLTDAEGKVIQLDIFNIDTBRACAVETSVL-LSEISSLKSGTQSGFLVEESLPLSEL 268
QY 384 -ETPFIIPSN-----PSVTPTPTETAL-----OCTADK-----PDSFGA-----418
DB 269 TETSNAGNPTNSANLPAFSAPELILFALKVADCVVKGSSDAVSDTFTFAEVSSDAV 328
QY 419 CDVQ-----ACKRQ-----KTSVCGQIQSTSYVD-CTADEQNEC-----GSNTALIGL 461
DB 329 PDVSPAPACRRDLPTKTFVLRSVLKPSYKMCLESLQEHCHNNLYDDGHPSLISNL 388
QY 462 AVGGVLLALLGGGCFYFAKRLDRNKGVAAHHEHFGSDR-GARKKRPSPDLMDAEPSP 519
DB 389 P-----NCKEKE-----AEDEEFELAPALNKKRKRKRVTFGEDELSPV 427
QY 520 WDEA 523
DB 428 FDES 431

RESULT 5
US-09-949-039-66
; Sequence 66, Application US/09949039
; Publication No. US20030166160A1

; GENERAL INFORMATION:
; APPLICANT: HAMLEY, STEPHEN B.
; TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
; TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS
; FILE REFERENCE: 057220/1101
; CURRENT APPLICATION NUMBER: US/09/949,039
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 66
; LENGTH: 758
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-949-039-66

Query Match 3 6%; Score 105; DB 12; Length 758;

Best Local Similarity 18.8%; Pred. No. 0.8; DB 179; Indels 218; Gaps 25;
Matches 105; Conservative 56; Mismatches 179; Indels 218; Gaps 25;

QY 16 CTIFASGLSSSTRRESQTLASTSGNPFQANVEKTEMERPNLTHHQSGLYV-DLQD 74
DB 56 CRIGAKKRCCTLLISEGYI-----SKDYKGRANLTPFENGTFVMDICHL 100
QY 75 KEVDGTYREBAGL-----NFTLEDVPTKEKYEK-QSGNPLPGGFNL-----134
DB 101 TRGDSGLYKCGIGISSRGLSFQVSLVSGQFGQIGDVHYTTADLSTVTINCPF--KSEN 158
QY 98 LQDPRLPYR-----NFTLEDVPTKEKYEK-QSGNPLPGGFNL-----134
DB 159 AOKPQSV-YKLGQIRLVIDSNGYLNNTFNRAHLSTQTNQVFSFVIRIQRLDAGI 217
QY 135 FVTPSGQRISPPFMLEL-----EKNSNIKASTDLGRCAEFAFTVAMDKNKATRY 185
DB 218 YICQAGDESSADQLKPEBELYEDLRGVTTPDCAIGOMANVAKLCLQKNGKT---274
QY 186 RYPFVYDSKRLCHILVSM-----QMEGKYYCSVK-----217
DB 275 -----CNVINTLGKKAQDFEGRILTPKENSHPVHITGLRKEADAGHYLGA 322
QY 218 ---GEP-----PDLTWYCF-----KPRKSVTEHNLHLYGSAYVGENDAPIFSKCPNAL 263
DB 323 HPDGEPRKQGVQAMQLEINEDTMI PRSSVVRG--VVGSSVAV-----TCPYMPK 371
QY 264 RGYRFGVW-----KGRCLDYTELDTVIERVESKACQCVKTFENDGVAHQPTVPLT 317
DB 372 ETNSLKYCKRMENENGRCPQVLESGLVNDQYGR-----LALVEBPANGFTVILNDLT 427
QY 318 SQASNDMMWPLHQSDQPHSGGVGRNYGYVDVTGEGKALSDQVDPCLVSDSAVSYTA 377
DB 428 N-----RDAGFYW-----CLTNEDSRMRSTV 448
QY 378 AGSLSEETPNFIIPSNBSVTPPTPET-ALQCTADKFPDPSACDVQACKRQKTSVCG---433
DB 449 ELKIVEGEPNKLKEN-VTAMVGETLKLSC--HFPCFKFSYOKYKWKMSNTGCRALPS 503
QY 434 ---GOIYSTSYDCTADEQ 448
DB 504 QDEGQDA-FVNCDKXSQ 520

RESULT 6
US-10-146-473-72
; Sequence 72, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Teeng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)

CURRENT APPLICATION NUMBER: US/10/146,473
 CURRENT FILING DATE: 2002-05-15
 PRIOR APPLICATION NUMBER: US 60/291,150
 PRIOR FILING DATE: 2001-05-15
 NUMBER OF SEQ ID NOS: 82
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 72
 LENGTH: 1253
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-10-146-473-72

Query Match 3.6%; Score 104; DB 15; Length 1253;
 Best Local Similarity 22.5%; Pred. No. 2.2; Indels 156; Gaps 27;
 Matches 108; Conservative 43; Mismatches 174

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QY 81 LYRPAGCPIWGKIEIQDRLPYRNFLFEDVTEKEYKOSGNPLPGG---FNLNFT 137
DB 256 LHPHNSGIC-----ELHCPALVTYNTDTFESMN-----PEGRTFGASCVT 297
QY 138 PSGORISPFPMELLEKNKNISAKSTDLGRCAEFA---FKTYAMDKNKATKRYRPFYD 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPILHNOEVTAEDEGTORCEKSKPCA--- 339
QY 194 KKRLLCH-----ILVSMQLMGKKYC-----SVKGEPPDLTWYCFKPRK 232
DB 340 --RVCYGLGMEHLREVRVAVTSANIQEFAGCKKIFGSLAFLEPSFDGDPASNTAPLQPEOL 397
QY 233 SVTENHHLIYSAVYGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
DB 398 QVFETLEETIGLYISAMPDSLPLDSVFQNLQVIRGRIHNGAYSLTIGLGISMIGRS 457
QY 277 LDYTELDTVIERVESKAQCWVKTENDGVASDQ---PHTYPLTSQASNDMPHLQSD 332
DB 458 L-RELGSGLALHNNHTLCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVGRNYGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAG 379
DB 499 RPEDECVGEGLACHQLCARHCGMPGPTQVNCQFLRGQCEVEECRYLQGLPREYVNR 558
QY 380 SLSEETPNFIIPNSVTPPTETALQCTAD-----KF 412
DB 559 HCLPCHPE-COPQNSVTCFGE-ADQCVACAHKDPFCVARGSPGVKPDLSYMPWKF 616
QY 413 PDSFGACDVQACKROKTSVGGQIOGSTVDTADEONEGSGTALAGLVGVLALL 472
DB 617 PDEBAC--QPC---PINCTHSCVDLDDKGCPRABQR--ASPLTSIS--AVGILLVVL 667
QY 473 G 473
DB 668 G 668

```

RESULT 7
 US-09-769-508-2
 Sequence 2, Application US/09769508
 Patent No. US2002015527A1
 GENERAL INFORMATION:
 APPLICANT: STUART, SUSAN G.
 APPLICANT: MONAHAN, JOHN J.
 APPLICANT: LANGTON, BEATRICE CLAUDIA
 APPLICANT: HANCOCK, MIRIAM E.C.
 APPLICANT: CHAO, LORINE A.
 APPLICANT: BLUFORD, PETER
 TITLE OF INVENTION: C-ERB-2 EXTERNAL DOMAIN: GP75
 FILE REFERENCE: BEBIO-111-C1
 CURRENT APPLICATION NUMBER: US/09/769,508
 CURRENT FILING DATE: 2001-01-26
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 1255
 TYPE: PRF

ORGANISM: Homo sapiens
 US-09-769-508-2

Query Match 3.6%; Score 104; DB 10; Length 1255;
 Best Local Similarity 22.2%; Pred. No. 2.2;
 Matches 107; Conservative 45; Mismatches 173; Indels 156; Gaps 27;

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QY 81 LYRPAGCPIWGKIEIQDRLPYRNFLFEDVTEKEYKOSGNPLPGG---FNLNFT 137
DB 256 LHPHNSGIC-----ELHCPALVTYNTDTFESMN-----PEGRTFGASCVT 297
QY 138 PSGORISPFPMELLEKNKNISAKSTDLGRCAEFA---FKTYAMDKNKATKRYRPFYD 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPILHNOEVTAEDEGTORCEKSKPCA--- 339
QY 194 KKRLLCH-----ILVSMQLMGKKYC-----SVKGEPPDLTWYCFKPRK 232
DB 340 --RVCYGLGMEHLREVRVAVTSANIQEFAGCKKIFGSLAFLEPSFDGDPASNTAPLQPEOL 397
QY 233 SVTENHHLIYSAVYGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
DB 398 QVFETLEETIGLYISAMPDSLPLDSVFQNLQVIRGRIHNGAYSLTIGLGISMIGRS 457
QY 277 LDYTELDTVIERVESKAQCWVKTENDGVASDQ---PHTYPLTSQASNDMPHLQSD 332
DB 458 L-RELGSGLALHNNHTLCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVGRNYGFYVDTTGE-----TGSKCALSDQ-----VPDCLVSDSAVSYTAG 379
DB 499 RPEDECVGEGLACHQLCARALLGSPGPTQVNCQFLRGQCEVEECRYLQGLPREYVNR 558
QY 380 SLSEETPNFIIPNSVTPPTETALQCTAD-----KF 412
DB 559 HCLPCHPE-COPQNSVTCFGE-ADQCVACAHKDPFCVARGSPGVKPDLSYMPWKF 616
QY 413 PDSFGACDVQACKROKTSVGGQIOGSTVDTADEONEGSGTALAGLVGVLALL 472
DB 617 PDEBAC--QPC---PINCTHSCVDLDDKGCPRABQR--ASPLTSIS--AVGILLVVL 667
QY 473 G 473
DB 668 G 668

```

RESULT 8
 US-09-854-356-1
 Sequence 1, Application US/09854356
 Patent No. US20020177567A1
 GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A.
 APPLICANT: Cheever, Martin A.
 APPLICANT: Corixa Corporation
 APPLICANT: SmithKline Beecham Biologicals S. A.
 TITLE OF INVENTION: HER-2/neu Fusion Proteins
 FILE REFERENCE: 014058-009810PC
 CURRENT APPLICATION NUMBER: US/09/854,356
 CURRENT FILING DATE: 2001-05-09
 PRIOR APPLICATION NUMBER: US 09/493,480
 PRIOR FILING DATE: 2000-01-28
 PRIOR APPLICATION NUMBER: US 60/117,976
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 1255
 TYPE: PRF
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: human HER-2/neu protein
 NAME/KEY: DOMAIN
 LOCATION: (1)..(653)
 OTHER INFORMATION: extracellular domain (ECD)
 NAME/KEY: DOMAIN

LOCATION: (676)..(1255)
 OTHER INFORMATION: Intracellular domain (ICD)
 NAME/KEY: DOMAIN
 LOCATION: (990)..(1255)
 OTHER INFORMATION: phosphorylation domain (PD)
 NAME/KEY: DOMAIN
 LOCATION: (990)..(1048)
 OTHER INFORMATION: fragment of the phosphorylation domain, preferred
 OTHER INFORMATION: portion (delta PD)
 US-09-854-356-1

Query Match 3.6%; Score 104; DB 10; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 2.2;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

QY 81 LYREPAGCPIMGHIIELOQDRLPYRNPFLEDPTEKEYKQSGNPLPG---FNLNFT 137
 DQ 256 LHPHSGIC-----ELHCPALVTYNTDTESMNP-----PEGKTTGASCVT 297
 QY 138 PSGORISPPMELLEKNKNIKASTDLGRCAEFA---FKTVAMDKNNKATKRYPPVYDS 193
 DB 298 AC-----PYNVL-----STDVGSCTLVCPHNGEVTABDGTQCEKSKPCA--- 339
 QY 194 KKRLCH-----ILVSMQLMGKKYC-----SVKGPPDLTWICFKPRK 232
 DB 340 --RVCYGLGMEHLREVRVAVTSANIQEFAGCKKIFGSLAFLPESFDGDSNTAPLQPEQL 397
 QY 233 SVTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGR 276
 DB 398 QVFETLEITGYLYISAMPDSLPLSVFQNLQVIRGRILHNGAYSLTQIGISWLGSR 457
 QY 277 LDYTELDTVIERVESKAQCWKTFENDGVASDQ---PHTYPLTSQASNDMPHOSD 332
 DB 458 L-RELGSGLALHNNHLCFVHT---VPMQDLFRNPH-----QAL-----LHTRAN 498
 QY 333 QPHSGGVRNGYFYVDITGE-----GKCALSDQ-----VPDCLVSDAANSYTAAG 379
 DB 499 RPEDECVGEGLAQCLARGHCWGPFGQCVNCSQFLRGCEVCECRVLQGLPREYVNA 558
 QY 380 SLSEBTFPIIPSNPSVTPPTPETALQCTAD-----KFL 412
 DB 559 HCLPCHPE-COPQNGSVTCFGE-ADQCVACAHYKDPFCVACRPSGVKPLSTWPIWK 616
 QY 413 PDSFGACDVQACKQKTSQVGGQIQSTSVDTADEONECGSNTALAGLAVGVLLALL 472
 DB 617 PDESGAC--QPC---PINCTHSCVDLDDKCPAQR--ASPLTSTIS--AVVGLLVVVL 667
 QY 473 G 473
 DB 668 G 668

RESULT 9
 US-09-930-125-2
 Sequence 2, Application US/09930125
 Publication No. US20020193329A1
 GENERAL INFORMATION:
 APPLICANT: Hand-Zimmerman, Susan
 APPLICANT: Cheever, Martin A.
 APPLICANT: Foy, Teresa M.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Kalos, Michael D.
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Vedyick, Thomas S.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
 TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
 FILE REFERENCE: 210121.544
 CURRENT APPLICATION NUMBER: US/09/930.125
 CURRENT FILING DATE: 2001-08-14
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 1255

TYPE: PRT
 ORGANISM: Homo sapien
 US-09-930-125-2

Query Match 3.6%; Score 104; DB 10; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 2.2;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

QY 81 LYREPAGCPIMGHIIELOQDRLPYRNPFLEDPTEKEYKQSGNPLPG---FNLNFT 137
 DB 256 LHPHSGIC-----ELHCPALVTYNTDTESMNP-----PEGKTTGASCVT 297
 QY 138 PSGORISPPMELLEKNKNIKASTDLGRCAEFA---FKTVAMDKNNKATKRYPPVYDS 193
 DB 298 AC-----PYNVL-----STDVGSCTLVCPHNGEVTABDGTQCEKSKPCA--- 339
 QY 194 KKRLCH-----ILVSMQLMGKKYC-----SVKGPPDLTWICFKPRK 232
 DB 340 --RVCYGLGMEHLREVRVAVTSANIQEFAGCKKIFGSLAFLPESFDGDSNTAPLQPEQL 397
 QY 233 SVTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGR 276
 DB 398 QVFETLEITGYLYISAMPDSLPLSVFQNLQVIRGRILHNGAYSLTQIGISWLGSR 457
 QY 277 LDYTELDTVIERVESKAQCWKTFENDGVASDQ---PHTYPLTSQASNDMPHOSD 332
 DB 458 L-RELGSGLALHNNHLCFVHT---VPMQDLFRNPH-----QAL-----LHTRAN 498
 QY 333 QPHSGGVRNGYFYVDITGE-----GKCALSDQ-----VPDCLVSDAANSYTAAG 379
 DB 499 RPEDECVGEGLAQCLARGHCWGPFGQCVNCSQFLRGCEVCECRVLQGLPREYVNA 558
 QY 380 SLSEBTFPIIPSNPSVTPPTPETALQCTAD-----KFL 412
 DB 559 HCLPCHPE-COPQNGSVTCFGE-ADQCVACAHYKDPFCVACRPSGVKPLSTWPIWK 616
 QY 413 PDSFGACDVQACKQKTSQVGGQIQSTSVDTADEONECGSNTALAGLAVGVLLALL 472
 DB 617 PDESGAC--QPC---PINCTHSCVDLDDKCPAQR--ASPLTSTIS--AVVGLLVVVL 667
 QY 473 G 473
 DB 668 G 668

RESULT 10
 US-09-441-411-6
 Sequence 6, Application US/09441411
 Publication No. US20030008342A1
 GENERAL INFORMATION:
 APPLICANT: Scholler, Nathalie B.
 APPLICANT: Disis, Mary L.
 APPLICANT: Hellstrom, Ingegerd
 APPLICANT: Hellstrom, Karl Erik
 TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
 FILE REFERENCE: 730033.409
 CURRENT APPLICATION NUMBER: US/09/441.411
 CURRENT FILING DATE: 1999-11-16
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 1255
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-441-411-6

Query Match 3.6%; Score 104; DB 11; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 2.2;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;
 QY 81 LYREPAGCPIMGHIIELOQDRLPYRNPFLEDPTEKEYKQSGNPLPG---FNLNFT 137
 DB 256 LHPHSGIC-----ELHCPALVTYNTDTESMNP-----PEGKTTGASCVT 297

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QY 138 PSGQRISPPFMELEKNSNIKASTDLGRCAEFA-----FKTVAMDGNKATKRYPFVYDS 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPHNOEVTAEDETQCEKSKRCA--- 339
QY 194 KRRLCH-----ILVSMQMEGKKYC-----SYGEPEDLTWYCFKPRK 232
DB 340 --RVCYGLGMEHLREVRAVTSANIOEPAGCKKIFGSLAFLEPSFGDDPASNTAPLQPEOL 397
QY 233 SVTEHHLLIYGSAYVGENPDAF--ISKCPN--QALRG-----YRFGV-WKKGRG 276
DB 398 QVFETLEITGYLYISAMPDSL.PDLISVFQNLQVIRGRILHNGAYSLTLOGLISWLGSR 457
QY 277 LDYETLDTVIERVESKACQWKTFENDGVASDQ---PHTYPLTSQASWMDMPLHOSD 332
DB 458 L--RELGSGLALIHNNHLCFVHT-----VPMDOLEFRNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVGRNYGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
DB 499 RPEDECVGEGLAGLQCARGHCMGPGPTQCVNCSQFLRGQECVEBCRYLQGLPREVYVAR 558
QY 380 SLSEETPNFIIPNSPVTPTPTETALQCTAD-----KF 412
DB 559 HCLPCHPE--CQPNQSVTCFGE--ADQVCAHAYKDPFCVARGPSGVKPDLSYMPWKF 616
QY 413 PDSFGACDVQACKROKTSVCGQIOSTSVDTADEQNECGSNTALIGLAVGVLLALL 472
DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKGCRAEOR--ASPLTSIIS--AVVGILLVVL 667
QY 473 G 473
DB 668 G 668

```

RESULT 11

```

US-10-313-644-2
; Sequence 2, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-313-644-2

```

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Query Match 3.6%; Score 104; DB 12; Length 1255;
Best Local Similarity 22.5%; Pred. No. 2.2; Indels 156; Gaps 27;
Matches 108; Conservative 43; Mismatches 174;
QY 81 LYREPAGLCPWKGKHELOQPDRLPYRNNFLEDVTEKEYKQSGNPLPGG---FNLNFTV 137
DB 256 LHFNSGIC-----ELHCPALVTYNTDTFESMPN-----PEGRTYFGASCVT 297
QY 138 PSGQRISPPFMELEKNSNIKASTDLGRCAEFA-----FKTVAMDGNKATKRYPFVYDS 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPHNOEVTAEDETQCEKSKRCA--- 339
QY 194 KRRLCH-----ILVSMQMEGKKYC-----SYGEPEDLTWYCFKPRK 232
DB 340 --RVCYGLGMEHLREVRAVTSANIOEPAGCKKIFGSLAFLEPSFGDDPASNTAPLQPEOL 397
QY 233 SVTEHHLLIYGSAYVGENPDAF--ISKCPN--QALRG-----YRFGV-WKKGRG 276

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DB 398 QVFETLEITGYLYISAMPDSL.PDLISVFQNLQVIRGRILHNGAYSLTLOGLISWLGSR 457
QY 277 LDYETLDTVIERVESKACQWKTFENDGVASDQ---PHTYPLTSQASWMDMPLHOSD 332
DB 458 L--RELGSGLALIHNNHLCFVHT-----VPMDOLEFRNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVGRNYGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
DB 499 RPEDECVGEGLAGLQCARGHCMGPGPTQCVNCSQFLRGQECVEBCRYLQGLPREVYVAR 558
QY 380 SLSEETPNFIIPNSPVTPTPTETALQCTAD-----KF 412
DB 559 HCLPCHPE--CQPNQSVTCFGE--ADQVCAHAYKDPFCVARGPSGVKPDLSYMPWKF 616
QY 413 PDSFGACDVQACKROKTSVCGQIOSTSVDTADEQNECGSNTALIGLAVGVLLALL 472
DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKGCRAEOR--ASPLTSIIS--AVVGILLVVL 667
QY 473 G 473
DB 668 G 668

```

RESULT 12

```

US-10-207-655-45
; Sequence 45, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-45

```

```

Query Match 3.6%; Score 104; DB 15; Length 1255;
Best Local Similarity 22.5%; Pred. No. 2.2;
Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;
QY 81 LYREPAGLCPWKGKHELOQPDRLPYRNNFLEDVTEKEYKQSGNPLPGG---FNLNFTV 137
DB 256 LHFNSGIC-----ELHCPALVTYNTDTFESMPN-----PEGRTYFGASCVT 297
QY 138 PSGQRISPPFMELEKNSNIKASTDLGRCAEFA-----FKTVAMDGNKATKRYPFVYDS 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPHNOEVTAEDETQCEKSKRCA--- 339
QY 194 KRRLCH-----ILVSMQMEGKKYC-----SYGEPEDLTWYCFKPRK 232
DB 340 --RVCYGLGMEHLREVRAVTSANIOEPAGCKKIFGSLAFLEPSFGDDPASNTAPLQPEOL 397
QY 233 SVTEHHLLIYGSAYVGENPDAF--ISKCPN--QALRG-----YRFGV-WKKGRG 276
DB 398 QVFETLEITGYLYISAMPDSL.PDLISVFQNLQVIRGRILHNGAYSLTLOGLISWLGSR 457
QY 277 LDYETLDTVIERVESKACQWKTFENDGVASDQ---PHTYPLTSQASWMDMPLHOSD 332
DB 458 L--RELGSGLALIHNNHLCFVHT-----VPMDOLEFRNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVGRNYGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
DB 499 RPEDECVGEGLAGLQCARGHCMGPGPTQCVNCSQFLRGQECVEBCRYLQGLPREVYVAR 558
QY 380 SLSEETPNFIIPNSPVTPTPTETALQCTAD-----KF 412
DB 559 HCLPCHPE--CQPNQSVTCFGE--ADQVCAHAYKDPFCVARGPSGVKPDLSYMPWKF 616

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QY 413 PDSTGACDVQACKQKTSVGGQIQTSTVDTCTADEQNECGSNALIAVLAVGVLLALL 472
Db 617 PDEBGAC--QPC---PINTHSCVLDLDDKGPACQR--ASPLTISII--AVGILLYVL 667
QY 473 G 473
Db 668 G 668

RESULT 13

US-09-925-299-847
Sequence 847, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 847
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-847

Query Match 3.5%; Score 103.5; DB 9; Length 365;
Best Local Similarity 19.7%; Pred. No. 0.36;
Matches 93; Conservative 48; Mismatches 121; Indels 211; Gaps 22;

QY 101 PDRLPYNNFLVDVPTKE---YKQGNP-----LPG-----GFNLNFTPSGQRIS-P 145
Db 6 PGCGPWLPSPLPDTQDLDRPPGSRRTGRPDMAAELPGFLCGALLGFLCLSLAVEVK 65
QY 146 FPMLEKSNINIKASTDLGRCAEFAPKTVAMDKNKATKYRYPFVDSKKRLCHILVSM 205
Db 66 VPTPEPL-----STPLGKTAEILT-----C----- 83
QY 206 QLMGKKYCSVKGEPPDLTYCFKPKRSVTENHLLIYSAVGENPDATFISCPNOLRG 265
Db 84 -----TYSTVSGDSFALWSPVOPGKRISHSHILYFT-----NG 118
QY 266 YRFGVWKKGRCCLDYTELTDIVIERVESKAQCWKTFENDGVASDQPHTYPLTQASWMDW 325
Db 119 HLYPTGSKSRVSLQLNPPTV-----GVA-----TLKLTID----- 148
QY 326 WPLHQSOPHSGGVGRNYGYVVDTTGEGKALSDQVPCLVSAVSYTAAGSLSEET 385
Db 149 --VHPSD-----TGTYLQVNNP-PDFTYNGLGILNLTV----- 179
QY 386 PNFIFPSNP-----SVTPPTETALQCTADK-----FPDSFGACDVQACKR 426
Db 180 --LVPPSNPLCSGSGQTSVGSSTALRCSSSGAKRPYVNWRLGTFTPSGSMVQ----- 233
QY 427 QKTSVGGQIQTSTVDTCTAD-----EQNECGS-----NTALLAGLAVG---G 465
Db 234 ---DEVSGQLITLNLSTLSSGTYRCVATNQMGASCELTLSTVTEPSGGRVAGALIGVLG 290
QY 466 VLLALLGGCGYFAKRLDRNKGVQAHHHEFQSDRGARKRP---SDLMQEA 515
Db 291 VLLLSV-----AAFLVRFQERKKRPETYGGSDLREDA 325

RESULT 14
US-09-925-299-847
Sequence 847, Application US/09925299
Publication No. US20030040617A9

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 847
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-847

Query Match 3.5%; Score 103.5; DB 11; Length 365;
Best Local Similarity 19.7%; Pred. No. 0.36;
Matches 93; Conservative 48; Mismatches 121; Indels 211; Gaps 22;

QY 101 PDRLPYNNFLVDVPTKE---YKQGNP-----LPG-----GFNLNFTPSGQRIS-P 145
Db 6 PGCGPWLPSPLPDTQDLDRPPGSRRTGRPDMAAELPGFLCGALLGFLCLSLAVEVK 65
QY 146 FPMLEKSNINIKASTDLGRCAEFAPKTVAMDKNKATKYRYPFVDSKKRLCHILVSM 205
Db 66 VPTPEPL-----STPLGKTAEILT-----C----- 83
QY 206 QLMGKKYCSVKGEPPDLTYCFKPKRSVTENHLLIYSAVGENPDATFISCPNOLRG 265
Db 84 -----TYSTVSGDSFALWSPVOPGKRISHSHILYFT-----NG 118
QY 266 YRFGVWKKGRCCLDYTELTDIVIERVESKAQCWKTFENDGVASDQPHTYPLTQASWMDW 325
Db 119 HLYPTGSKSRVSLQLNPPTV-----GVA-----TLKLTID----- 148
QY 326 WPLHQSOPHSGGVGRNYGYVVDTTGEGKALSDQVPCLVSAVSYTAAGSLSEET 385
Db 149 --VHPSD-----TGTYLQVNNP-PDFTYNGLGILNLTV----- 179
QY 386 PNFIFPSNP-----SVTPPTETALQCTADK-----FPDSFGACDVQACKR 426
Db 180 --LVPPSNPLCSGSGQTSVGSSTALRCSSSGAKRPYVNWRLGTFTPSGSMVQ----- 233
QY 427 QKTSVGGQIQTSTVDTCTAD-----EQNECGS-----NTALLAGLAVG---G 465
Db 234 ---DEVSGQLITLNLSTLSSGTYRCVATNQMGASCELTLSTVTEPSGGRVAGALIGVLG 290
QY 466 VLLALLGGCGYFAKRLDRNKGVQAHHHEFQSDRGARKRP---SDLMQEA 515
Db 291 VLLLSV-----AAFLVRFQERKKRPETYGGSDLREDA 325

RESULT 15
US-10-106-698-6387
Sequence 6387, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0

SEQ ID NO 6387
 LENGTH: 365
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-698-6387

Query Match 3.5%; Score 103.5; DB 15; Length 365;
 Best Local Similarity 19.7%; Pred. No. 0.36; Indels 211; Gaps 22;
 Matches 93; Conservative 48; Mismatches 121

101 PDRLEPRNNFLEDPTEKE---YKQSGNP---LPQ---GNLNFVTPSGQRIS-P 145
 6 PGCGWVLPSPUDPTQDLDPRPGRSRTGRDPAAMALPQFLCGALLGLGSLAVEVK 65
 146 FPMELLEKNKSNIKASTDLGRCAEFAPKTYAMDKNKATKRYRPFYDSSKKRLCHLYISM 205
 66 VPTBPL---STPLGKTAELE---C----- 83
 206 QLMEEKYCSVKGPEPDLTWYCFKPKSVTENHLLIYGSAYVGENPDAFISKCPQALRG 265
 84 ---TSTVSDSPALEMSFVQPKPTSESHPLVFT-----NG 118
 266 YRFGWKGRCLDYELDTVIERVESKAQCWKTFFENDVASDQPHTYPLTQASNDW 325
 119 HLYPTGSKSKRYSLQNPPTV-----GVA---TLKLTID----- 148
 326 WPLHOSDQPHSGGVGRNRYFYVDITGEGKALSDQVDPCLVSDANASYTAAGSLSEET 385
 149 ---VHPSD-----TGTYLCQVNNP-PDFTYNGLGLMLTV----- 179
 366 PNFIIIPSNP---SVTPPTPEALQCTADK-----FPDSFGACDYOACKR 426
 180 --LVPSNPCLGSGSGCTSVGSTALLKSSSEGAPEKVVWVRLGTFPTSPSSMQ----- 233
 427 QKTSQVSGQISTSVYDCTAD-----EQNEGCS-----NTALIAGLVAG--G 465
 234 ---DEVSGQLITLNTLSITSGTYRCVATNQMSASCELTLSTPEQGRVAGALIGVLG 290
 466 VLLALLGGCCYFANKRLDNKKVQAAHHEHFERQSDRGARKRP---SDLMQEA 515
 291 VLLLSV-----AAFCLVRFQKERGKKPKETGGSDLREDA 325

RESULT 16
 US-09-811-123-9
 Sequence 9, Application US/09811123
 Patent No. US2002001587A1
 GENERAL INFORMATION:
 APPLICANT: Sharon Erickson
 APPLICANT: Ralph Schwall
 APPLICANT: Mark Sliwkowski
 TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
 FILE REFERENCE: GENENT. 073A2
 CURRENT APPLICATION NUMBER: US/09/811,123
 CURRENT FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/238,327
 PRIOR FILING DATE: 2000-10-05
 PRIOR APPLICATION NUMBER: 09/602,530
 PRIOR FILING DATE: 2000-06-23
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9
 LENGTH: 1255
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-811-123-9

Query Match 3.5%; Score 103; DB 9; Length 1255;
 Best Local Similarity 22.2%; Pred. No. 2.7;
 Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;
 81 LVREPRAGLCPIWKGHIELOQPDRLPRNNFLEDPTEKEVKQSGNPLPGS---FNINFTV 137

DB 256 LHFHNSGIC-----ELHCPALVTYNTDFESMWN-----PEGRTFGASCVT 297
 QY 138 PSQGRISBPFMELLEKNKSNIKASTDLGRCAEFA---FKTYAMDKNKATKRYRPFYVDS 193
 DB 298 AC-----PYNVY-----STDVSGCTLVCPHLNQEVTAEEDGTORCEKSKPCA--- 339
 QY 194 KKRLLCH-----ILVSMQLMGKKYCC-----SVKGEPPDLTWYCFKPRK 232
 DB 340 --RVCYGLGMHLREVRVAVTSANIQEFAGCKKIGSLAFLPESDGDPASTALQPEQL 397
 QY 233 SVTENHLLIYGSAYVGENPDFAF--ISKCPN-QALRG-----YRFGV-WKKGR 276
 DB 398 QVFETLEETGYLVISAMPDLPDLSTVFQNLVIRGRILHNGAYSLTLQIGIGISMLGRS 457
 QY 277 LDYIELDTVIERVESKAQCWKTFFENDVASDQ---PHTYPLTQASNDWMPHOSD 332
 DB 458 L--RELGSGLALIHNNTHLCFVHT---VWMDLFRNPH---QAL-----LHTAN 498
 QY 333 QPHSGVGRNRYFYVDITGE-----GKCALSDQ-----VPCLVSDANASYTAAG 379
 DB 499 RPEDECVEGELACHQLCARHGMGPPTQCVNCSQFLRGQECVECRVLOGLPREYNNAR 558
 QY 380 SLSEETPNFIIPSNPSVTPPTPEALQCTAD-----KF 412
 DB 559 HCLPCHPE-CQPOKGSVTCFQPE-ADQVACAHYKDPFCVARGPSGVKPDLSYMPWK 616
 QY 413 PDSRACVQACKQKTSQVSGQISTSVYDCTABQNEGCSNTALIAGLVAGVLLALL 472
 DB 617 PDEBQAC--QPC---PINCHSCVDLDKGGCPAOR--ASPLTIVS--AVVGLLVVL 667
 QY 473 G 473
 DB 668 G 668

RESULT 17
 US-09-811-115-3
 Sequence 3, Application US/09811115
 Patent No. US2002005736A1
 GENERAL INFORMATION:
 APPLICANT: Erickson, Sharon
 APPLICANT: Schwall, Ralph
 APPLICANT: King, Kathleen
 TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
 FILE REFERENCE: GENENT. 034A
 CURRENT APPLICATION NUMBER: US/09/811,115
 CURRENT FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/189,844
 PRIOR FILING DATE: 2000-03-16
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 1255
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-811-115-3

Query Match 3.5%; Score 103; DB 9; Length 1255;
 Best Local Similarity 22.2%; Pred. No. 2.7;
 Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;
 81 LVREPRAGLCPIWKGHIELOQPDRLPRNNFLEDPTEKEVKQSGNPLPGS---FNINFTV 137
 DB 256 LHFHNSGIC-----ELHCPALVTYNTDFESMWN-----PEGRTFGASCVT 297
 QY 138 PSQGRISBPFMELLEKNKSNIKASTDLGRCAEFA---FKTYAMDKNKATKRYRPFYVDS 193
 DB 298 AC-----PYNVY-----STDVSGCTLVCPHLNQEVTAEEDGTORCEKSKPCA--- 339
 QY 194 KKRLLCH-----ILVSMQLMGKKYCC-----SVKGEPPDLTWYCFKPRK 232
 DB 340 --RVCYGLGMHLREVRVAVTSANIQEFAGCKKIFGSLAFLPESDGDPASTALQPEQL 397

QY 223 SYTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
DB 398 QVFETLEBITGYLISAMPDSL.PDLVSFQNLQVIRGLHNGAYSLTQGLGISMGLRS 457
QY 277 LDYELTDTVIERVESAQAQCKVKTENDGVASDQ---PHYTYPLTSQASNDMPHLOSD 332
DB 458 L--RELGGGLALIHNNHLCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVGRNYGFYYVDITGE-----GKCALSDQ-----VPDCLVSDSAAVSYTAAG 379
DB 499 RPEDCEVGEGLACHQLCARGHCWGPPTQCVNCSQFLRGQCEVBCRYLQGLPREYVNAK 558
QY 380 SLSEETPNFIIPSNPSVTPPTETALQCTAD-----KF 412
DB 559 HCLPCHPE-COPONGSVTCFGE-ADQVCAHYKDPFCVARGSPGVKPDLSYMPIMKF 616
QY 413 PDSFGACDVQACKROKTSVCGGOIOSTSVDTADEQNECGSNTALLAGLAVGVLLALL 472
DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKGCPEQR--ASPLTSIVS--AVVGILLVVL 667
QY 473 G 473
DB 668 G 668

RESULT 18

US-10-207-498-6
; Sequence 6, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizebeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HERGULIN AND HER3
; FILE REFERENCE: 30448.103-US-01
; CURRENT APPLICATION NUMBER: US/10/207,498
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-498-6

Query Match 3.5%; Score 103; DB 12; Length 1255;
Best Local Similarity 22.2%; Pred. No. 2.7; Indels 156; Gaps 27;
Matches 107; Conservative 44; Mismatches 174;

QY 81 LYREPAGLCPIWKGHIELQOPDRLPYNNFLEDPTEKEYKQSGNPLPGG---FNLFNVT 137
DB 256 LHFHNSGIC-----ELHCPALVTYNTDTFESMNP-----DEGRYTFGASCVT 297
QY 138 PSGQRISFPFMELEKSNINIKASTDLGRCAEFA---FKTVAMDKNKATKYRYPVYDS 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPHLHNOEVTAEADGTQCEKSKPCA--- 339
QY 194 KKRLLCH-----ILVSMQLMGKKYC-----SYKGEPPDLTWYCFKPRK 232
DB 340 --RVCYGIGMEHLREVRATVSANIOPAGCKKIFGSLAFLEPSFDGDPASNTAPLQPEQL 397
QY 233 SVTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
DB 398 QVFETLEBITGYLISAMPDSL.PDLVSFQNLQVIRGLHNGAYSLTQGLGISMGLRS 457
QY 277 LDYELTDTVIERVESAQAQCKVKTENDGVASDQ---PHYTYPLTSQASNDMPHLOSD 332
DB 458 L--RELGGGLALIHNNHLCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498

QY 333 QPHSGGVGRNYGFYYVDITGE-----GKCALSDQ-----VPDCLVSDSAAVSYTAAG 379
DB 499 RPEDCEVGEGLACHQLCARGHCWGPPTQCVNCSQFLRGQCEVBCRYLQGLPREYVNAK 558
QY 380 SLSEETPNFIIPSNPSVTPPTETALQCTAD-----KF 412
DB 559 HCLPCHPE-COPONGSVTCFGE-ADQVCAHYKDPFCVARGSPGVKPDLSYMPIMKF 616
QY 413 PDSFGACDVQACKROKTSVCGGOIOSTSVDTADEQNECGSNTALLAGLAVGVLLALL 472
DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKGCPEQR--ASPLTSIVS--AVVGILLVVL 667
QY 473 G 473
DB 668 G 668

RESULT 19

US-10-338-730-2
; Sequence 2, Application US/10338730
; Publication No. US20030147905A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS
; FILE REFERENCE: 5017C
; CURRENT APPLICATION NUMBER: US/10/338,730
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: US 09/527,487
; PRIOR FILING DATE: 2002-03-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-730-2

Query Match 3.5%; Score 103; DB 12; Length 1255;
Best Local Similarity 22.2%; Pred. No. 2.7; Indels 156; Gaps 27;
Matches 107; Conservative 44; Mismatches 174;

QY 81 LYREPAGLCPIWKGHIELQOPDRLPYNNFLEDPTEKEYKQSGNPLPGG---FNLFNVT 137
DB 256 LHFHNSGIC-----ELHCPALVTYNTDTFESMNP-----DEGRYTFGASCVT 297
QY 138 PSGQRISFPFMELEKSNINIKASTDLGRCAEFA---FKTVAMDKNKATKYRYPVYDS 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPHLHNOEVTAEADGTQCEKSKPCA--- 339
QY 194 KKRLLCH-----ILVSMQLMGKKYC-----SYKGEPPDLTWYCFKPRK 232
DB 340 --RVCYGIGMEHLREVRATVSANIOPAGCKKIFGSLAFLEPSFDGDPASNTAPLQPEQL 397
QY 233 SVTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
DB 398 QVFETLEBITGYLISAMPDSL.PDLVSFQNLQVIRGLHNGAYSLTQGLGISMGLRS 457
QY 277 LDYELTDTVIERVESAQAQCKVKTENDGVASDQ---PHYTYPLTSQASNDMPHLOSD 332
DB 458 L--RELGGGLALIHNNHLCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVGRNYGFYYVDITGE-----GKCALSDQ-----VPDCLVSDSAAVSYTAAG 379
DB 499 RPEDCEVGEGLACHQLCARGHCWGPPTQCVNCSQFLRGQCEVBCRYLQGLPREYVNAK 558
QY 380 SLSEETPNFIIPSNPSVTPPTETALQCTAD-----KF 412
DB 559 HCLPCHPE-COPONGSVTCFGE-ADQVCAHYKDPFCVARGSPGVKPDLSYMPIMKF 616
QY 413 PDSFGACDVQACKROKTSVCGGOIOSTSVDTADEQNECGSNTALLAGLAVGVLLALL 472

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Db      617 PDEBAC--QPC---PINCHSCVDLDDKCPAEOR--ASPLTSIVS--AVVIGILLVVVL 667
QY      473 G 473
Db      668 G 668

RESULT 20
US-10-322-892-4
; Sequence 4, Application US/10322892
; Publication No. US20030171257A1
; GENERAL INFORMATION:
; APPLICANT: STIRBL, ROBERT C.
; APPLICANT: SNEAD, MALCOLM L.
; APPLICANT: XU, JIMMY
; APPLICANT: VILETTA, ELLEN S.
; APPLICANT: WILK, PETER J.
; TITLE OF INVENTION: METHOD AND RELATED COMPOSITION EMPLOYING NANOSTRUCTURES
; FILE REFERENCE: M07-505
; CURRENT APPLICATION NUMBER: US/10/322,892
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/342,894
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-892-4

Query Match      3.5%; Score 103; DB 12; Length 1255;
Best Local Similarity 22.2%; Pred. No. 2.7; 174; Indels 156; Gaps 27;
Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;

QY      81 LYREPAGLCPIWKGKHELOQPDRLPYRNNFLEDVPTKEKYKSGNPLPGG---FNLNFT 137
      256 LHFNNHSGIC-----ELHCPALVTYNTDTFESMNP-----PEGRTFGASCVT 297
      138 PEGQRISPPMELLEKNISIKASTDLCRCABFA---FTVAMDKNKATKRYPFVYDS 193
      298 AC-----PYYVL-----STDVGSCTLVCPHNGEVLTAEDGTQRCCKSKCA--- 339
      194 KKRLLCH-----ILVYSQMLEGKKYC-----SVKGEPPDLTWYCFKPRK 232
      340 --RVCGGLGMEHLREVRAVTSANIQEPAGCKIFGSLAFLPESFDGDPASNTAPLOPEOL 397
      233 SVTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGR 276
      398 QVFETLEETITGYLIYAWPDSLPDLSVPQNLQVIRGRILHNGAYSLTGLGISWGLRS 457
      277 LDYTELDTVIERVESKACQWVKTFFENDGVASDQ---PHTYPLTSQASWMDMPLHOSD 332
      458 L--RELGSGLALIHNTLHCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
      333 QHSGGVGNNGYVYDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
      499 RPEDECVGGLACHQICARHGCGPGPTQCVNCSQFLRGQECVEEGRVLAGLREYVNAH 558
      380 SLSEETPNFIIPSNPVTPTPETALQCTAD-----XK 412
      559 HCLPCHPE-CQPNQSVTCGPRE-ADQVACAHYKDPFCVACSPSGVAPDLSYMIWKF 616
      413 PDSFGACDVQACKRQRTSCVGGQIOSTSVDTCTADEONEGCSNTALAGLAVGVLALL 472
      617 PDEBAC--QPC---PINCHSCVDLDDKCPAEOR--ASPLTSIVS--AVVIGILLVVVL 667

QY      473 G 473
Db      668 G 668

RESULT 21

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US-10-177-293-126
; Sequence 126, Application US/10177293
; Publication No. US20030124126A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatc, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Metrens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Baet Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzatzi, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sabin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-126

Query Match      3.5%; Score 103; DB 15; Length 1255;
Best Local Similarity 22.2%; Pred. No. 2.7;
Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;

QY      81 LYREPAGLCPIWKGKHELOQPDRLPYRNNFLEDVPTKEKYKSGNPLPGG---FNLNFT 137
      256 LHFNNHSGIC-----ELHCPALVTYNTDTFESMNP-----PEGRTFGASCVT 297
      138 PEGQRISPPMELLEKNISIKASTDLCRCABFA---FTVAMDKNKATKRYPFVYDS 193
      298 AC-----PYYVL-----STDVGSCTLVCPHNGEVLTAEDGTQRCCKSKCA--- 339
      194 KKRLLCH-----ILVYSQMLEGKKYC-----SVKGEPPDLTWYCFKPRK 232
      340 --RVCGGLGMEHLREVRAVTSANIQEPAGCKIFGSLAFLPESFDGDPASNTAPLOPEOL 397
      233 SVTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGR 276
      398 QVFETLEETITGYLIYAWPDSLPDLSVPQNLQVIRGRILHNGAYSLTGLGISWGLRS 457
      277 LDYTELDTVIERVESKACQWVKTFFENDGVASDQ---PHTYPLTSQASWMDMPLHOSD 332
      458 L--RELGSGLALIHNTLHCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
      333 QHSGGVGNNGYVYDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379

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Db 499 RPEDECBEGLAGHOLCARHGCHGPGFPQCVNCSQFLRGQCEBCECVLQGLPREYVAR 558
Qy 380 SLSEETPNFIIPNSPVTPTPTALQCTAD-----KF 412
Db 559 HCLPCHPE-CQPNCSVTCFGE-ADQVACHMYKDPFCVACRCSGVKPDLSYPIKPF 616
Qy 413 PDSFACVQACROKTCSCVGGQISTVDCTADEQNECGSNTALIALAGVGLLALL 472
Db 617 PDEBAC--QPC---PINCTHSCVDLDDKGCFAQR--ASPLTISV--AVVGILLVVVL 667
Qy 473 G 473
Db 668 G 668

RESULT 22

US-09-859-053-36
Sequence 36, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tezuka, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859, 053
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-36

Query Match 3.5%; Score 102; DB 10; Length 470;
Best Local Similarity 22.2%; Pred. No. 0.74;
Matches 70; Conservative 34; Mismatches 140; Indels 72; Gaps 14;

Qy 111 LEDVTEKXYKQSGNPL--PGGFNLFTYTPSGQRISPPMBLEKNSIKXSTDLGRCAE 168
Db 14 LEGVQCEVQVLVESGGGLVQPGGSLRLSCAASGFTFSYDMH-----VROATGKLEWV 67
Qy 169 FAFKTVAMDKNKATKYRYPFYVDSKRLCHILVSMQMEGKKYCSVKGSPDLTWYCF 228
Db 68 SALGTAGGTYYPGSVKGRFT---SRENAKSLYQNMSLA-----GD--TRVYICV 115
Qy 229 KPRSVSTENHLIYGSAYVENPDAFISKPNQALRGYRFGVKKGRCLDYTELDTVIE 288
Db 116 RDKRTVTEHHYYGMDVWGCTVTVVSASTGP-----SVFLAPCSRST----- 163
Qy 289 RVESKAO--CWKTF-----ENDGVAADPHYPLTSSQSNKMDMPLHQ----- 330
Db 164 --ESTALGCLVKDFPEPVTVSNMGSALTSGLVHFFPVLQSS--GLYSLSVYVPSN 219
Qy 331 -SDPHSGVGRNRYFYVDTTGEKCALSDOVPDCLVSDSAVSTAAGSLSEETPNFI 389
Db 220 FGTQVTCNVDHKRENTKVDKVERKCV--ECPPCAPPAVAGPSV-----FL 265
Qy 390 IPSNPSVT--PTPE 402
Db 266 FPPKPKDTLMISRTPE 281

RESULT 23
US-09-887-879-14
Sequence 14, Application US/09887879

Patent No. US20020102706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Chutcharapai, Anan
APPLICANT: Gurney, Austin
APPLICANT: Kim, Kyung Jin
APPLICANT: Wood, William I.
TITLE OF INVENTION: Apo-2DCR
FILE REFERENCE: P1110P1
CURRENT APPLICATION NUMBER: US/09/887, 879
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 09/096, 500
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/049, 911
PRIOR FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 14
LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapiens
US-09-887-879-14

Query Match 3.5%; Score 101.5; DB 10; Length 418;
Best Local Similarity 24.2%; Pred. No. 0.69;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

Qy 313 TYPLTQASNDW---PL-----HSDQPHSGVGRNRYFYVDTTGEKCALSDQ 361
Db 60 TIKHDSIGTQOQHESPLGELCPGSHRSER--GACNR-----CTEVGYTNASN 110
Qy 362 VPDCVDSAAVSTAAAGSLSEETPNFIIPNSPVTPTPTALQCTADKPPDSFGACDV 421
Db 111 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACQCRPGTFRNNSA--- 151
Qy 422 QACRQKTCSCVGGQISTVDCTADEQNEC-----GSN-----TALIALAGVGL 467
Db 152 EMCRKSGTCGPRGMVKV--DCTPMSDIECVHKGSGNHNIWLVTVLVPLLVAVLI 209
Qy 468 LIALGGG-----CYFAKRLDRNGVQ-AAHHE-----HEFQSDGARKKR 507
Db 210 VCCIGSGCGGDPKCMRVCFWRIGLLRGPAEDNANEILSNADSLSTFVSEQMESQE 269
Qy 508 PSDL 511
Db 270 PADL 273

RESULT 24

US-09-992-964-14
Sequence 14, Application US/09992964
Patent No. US20020161202A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin
APPLICANT: Gurney, Austin
APPLICANT: Wood, William
TITLE OF INVENTION: Apo-2DCR
FILE REFERENCE: P1110
CURRENT APPLICATION NUMBER: US/09/992, 964
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 08/876, 168
PRIOR FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 14
LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapiens
US-09-992-964-14

Query Match 3.5%; Score 101.5; DB 10; Length 418;
Best Local Similarity 24.2%; Pred. No. 0.69;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;


```
QY 313 TYPLTSQASWMDW---PL-----HOSDOPHSGVGRNGFYVDTTSGKCALSDQ 361
DB 60 TKLHDQSIGTQOWHSPFLGELCPGSHRSER--GACNR-----CTEGVGYMASNN 110
QY 362 VPDCLVSDAASVYTAAGSLSEETPNFIIPSNPVTPTPTALQCTADKFPDSPGACDV 421
DB 111 LFACL-----PCTACKSDEEB-----RSPCTT--TRNTACQCKGTFRNDNSA--- 151
QY 422 QACKRQKTSVGGQIOSTSVDTCTADEQNEC-----GSN-----TALINGLAVGVL 467
DB 152 EMCRCKSTGCPRGWVKV--DCTPMSDIECVHESGNGHNIWLVTLVPLLVAVLI 209
QY 468 LIALIGGG-----CYFAKRLDRKNGVQ-AAHHE-----HEFOSDRGARKKR 507
DB 210 VCCICGGGGGPKCMDRVCFWRLGLRGPABDNNAHNIISNADSLSTFVSEQMESOE 269
QY 508 PSDL 511
DB 270 PADL 273

RESULT 25
US-10-242-383-14
; Sequence 14, Application US/10242383
; Publication No. US20030138915A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntcharapai, Anan
; APPLICANT: Gurney, Auestin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P110P1
; CURRENT APPLICATION NUMBER: US/10/242,383
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/887,879
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 14
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-383-14

Query Match 3.5%; Score 101.5; DB 12; Length 418;
Best Local Similarity 24.2%; Pred. No. 0.69; Indels 75; Gaps 14;
Matches 59; Conservative 27; Mismatches 83;

QY 313 TYPLTSQASWMDW---PL-----HOSDOPHSGVGRNGFYVDTTSGKCALSDQ 361
DB 60 TKLHDQSIGTQOWHSPFLGELCPGSHRSER--GACNR-----CTEGVGYMASNN 110
QY 362 VPDCLVSDAASVYTAAGSLSEETPNFIIPSNPVTPTPTALQCTADKFPDSPGACDV 421
DB 111 LFACL-----PCTACKSDEEB-----RSPCTT--TRNTACQCKGTFRNDNSA--- 151
QY 422 QACKRQKTSVGGQIOSTSVDTCTADEQNEC-----GSN-----TALINGLAVGVL 467
DB 152 EMCRCKSTGCPRGWVKV--DCTPMSDIECVHESGNGHNIWLVTLVPLLVAVLI 209
QY 468 LIALIGGG-----CYFAKRLDRKNGVQ-AAHHE-----HEFOSDRGARKKR 507
DB 210 VCCICGGGGGPKCMDRVCFWRLGLRGPABDNNAHNIISNADSLSTFVSEQMESOE 269
QY 508 PSDL 511
DB 270 PADL 273
```

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RESULT 26
US-10-280-047-6
; Sequence 6, Application US/10280047
; Publication No. US20030180883A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10
; FILE REFERENCE: P379P1D1
; CURRENT APPLICATION NUMBER: US/10/280,047
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 09/580,212
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/086,483
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/069,112
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/050,936
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/144,023
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/142,563
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/136,766
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 467
; TYPE: PRT
; ORGANISM: human
US-10-280-047-6

Query Match 3.5%; Score 101.5; DB 12; Length 467;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPLTSQASWMDW---PL-----HOSDOPHSGVGRNGFYVDTTSGKCALSDQ 361
DB 110 TKLHDQSIGTQOWHSPFLGELCPGSHRSER--GACNR-----CTEGVGYMASNN 160
QY 362 VPDCLVSDAASVYTAAGSLSEETPNFIIPSNPVTPTPTALQCTADKFPDSPGACDV 421
DB 161 LFACL-----PCTACKSDEEB-----RSPCTT--TRNTACQCKGTFRNDNSA--- 201
QY 422 QACKRQKTSVGGQIOSTSVDTCTADEQNEC-----GSN-----TALINGLAVGVL 467
DB 202 EMCRCKSTGCPRGWVKV--DCTPMSDIECVHESGNGHNIWLVTLVPLLVAVLI 259
QY 468 LIALIGGG-----CYFAKRLDRKNGVQ-AAHHE-----HEFOSDRGARKKR 507
DB 260 VCCICGGGGGPKCMDRVCFWRLGLRGPABDNNAHNIISNADSLSTFVSEQMESOE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 27
US-10-322-673-1
; Sequence 1, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL
; FILE REFERENCE: PE585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
```



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; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 1
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-1

```

```

Query Match      3.5%; Score 101.5; DB 12; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

```

```

Qy 313 TYPLTSQASNDW---PL-----HSDQPHSGVGRNYGYVDTTGEKCALSDQ 361
Db 110 TIKLHDQSIGTQWEHSPLEGCPGSHRSERP--GACNR-----CTEGVGYTNASN 160
Qy 362 VPDCLVSDSAVSYTAAGSLSEETPNFLIPSNPVTPTPTALQCTADKFPDSFGACDV 421
Db 161 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACCKRGTRNDNSA--- 201
Qy 422 QACKROKTSQVGGQIGSTVSDCTADEQNEC-----GSN-----TALAGLAVGVL 467
Db 202 EMCRKSTGCPRGWVKV--DCTPMSDIECVHKSNGHNIMVILVTVLVLVAVLI 259
Qy 468 LIALGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFQSDRGARKR 507
Db 260 VCCIGSGCGGDPKCMDRVCFWRGLRGPAEDNAHNEILSNADSLSTFVSEQMESOE 319
Qy 508 PSDL 511
Db 320 PADL 323

```

```

RESULT 28
US-10-039-785-1
; Sequence 1, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1

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```

; SEQ ID NO 1
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-1

```

```

Query Match      3.5%; Score 101.5; DB 13; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

```

```

Qy 313 TYPLTSQASNDW---PL-----HSDQPHSGVGRNYGYVDTTGEKCALSDQ 361
Db 110 TIKLHDQSIGTQWEHSPLEGCPGSHRSERP--GACNR-----CTEGVGYTNASN 160
Qy 362 VPDCLVSDSAVSYTAAGSLSEETPNFLIPSNPVTPTPTALQCTADKFPDSFGACDV 421
Db 161 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACCKRGTRNDNSA--- 201
Qy 422 QACKROKTSQVGGQIGSTVSDCTADEQNEC-----GSN-----TALAGLAVGVL 467
Db 202 EMCRKSTGCPRGWVKV--DCTPMSDIECVHKSNGHNIMVILVTVLVLVAVLI 259
Qy 468 LIALGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFQSDRGARKR 507
Db 260 VCCIGSGCGGDPKCMDRVCFWRGLRGPAEDNAHNEILSNADSLSTFVSEQMESOE 319
Qy 508 PSDL 511
Db 320 PADL 323

```

```

RESULT 29
US-10-226-296-2
; Sequence 2, Application US/10226296
; Publication No. US20030036168A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Rosen, Craig A.
; Pan, James G.
; Gentz, Reiner L.
; Dixie, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; Receptor 4), Member of the TNF-Receptor
; Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/226,296
; FILING DATE: 23-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: STEEFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540

```

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-226-296-2

Query Match 3.5%; Score 101.5; DB 15; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPPLTSQASNDWM---PL-----HOSDQPHSGGVGRNYGYVDTTGEKCALSDQ 361
DB 110 TIKLHDQSIGTQOWEHSPLGELCPGSHRSERP--GACNR-----CTEGVGYTNASN 160
QY 362 VPDCLVSDSAVSYTAAGSLSEETPNFIIPNSVTPPTPETALQCTADKPPDSFGACDV 421
DB 161 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACQCKRGTRNDNSA---- 201
QY 422 QACKRKQKTSVCGGQIOGSTVDTCTADEQNEC-----GSN-----TALAGLAVGV 467
DB 202 EMCRCRQKSTGCPRGWVK--DCTPMSDIECVHKSNGHNIMVILVTLVPLLVAVLI 259
QY 468 LIALIGG-----CYFAKRLDRNKKVQ-AAHHE-----HEFQSDRGARKKR 507
DB 260 VCCICGSGCGGDPKCMDRVCFWRLGLRGPAEDNAHNEILSNADSLSTFVSEQMESOE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 30

US-10-226-318-2
Sequence 2, Application US/10226318
Publication No. US20030073187A1
GENERAL INFORMATION:

APPLICANT: NI, Jian

Rosen, Craig A.
Pan, James G.
Gentz, Reiner L.

Dixit, Vishva M.

TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death
Receptor 4), Member of the TNF-Receptor
Superfamily and Binding to Trail (Ap02-L)

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE

STATE: MD
COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/226,318
FILING DATE: 23-Aug-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/448,868
FILING DATE: <Unknown>

APPLICATION NUMBER: 09/013,895
FILING DATE: 27-Jan-1998

ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488,1300004

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-226-318-2

Query Match 3.5%; Score 101.5; DB 15; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPPLTSQASNDWM---PL-----HOSDQPHSGGVGRNYGYVDTTGEKCALSDQ 361
DB 110 TIKLHDQSIGTQOWEHSPLGELCPGSHRSERP--GACNR-----CTEGVGYTNASN 160
QY 362 VPDCLVSDSAVSYTAAGSLSEETPNFIIPNSVTPPTPETALQCTADKPPDSFGACDV 421
DB 161 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACQCKRGTRNDNSA---- 201
QY 422 QACKRKQKTSVCGGQIOGSTVDTCTADEQNEC-----GSN-----TALAGLAVGV 467
DB 202 EMCRCRQKSTGCPRGWVK--DCTPMSDIECVHKSNGHNIMVILVTLVPLLVAVLI 259
QY 468 LIALIGG-----CYFAKRLDRNKKVQ-AAHHE-----HEFQSDRGARKKR 507
DB 260 VCCICGSGCGGDPKCMDRVCFWRLGLRGPAEDNAHNEILSNADSLSTFVSEQMESOE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 31

US-10-175-902-2
Sequence 2, Application US/10175902
Publication No. US20030108516A1
GENERAL INFORMATION:

APPLICANT: NI, Jian

Rosen, Craig A.
Pan, James G.
Gentz, Reiner L.

Dixit, Vishva M.

TITLE OF INVENTION: Death Domain Containing Receptor 4

FILE REFERENCE: 1488,1300005
CURRENT APPLICATION NUMBER: US/10/175,902

PRIOR FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 09/565,918

PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,922

PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: US 09/013,895

PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: US 60/037,829

PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: US 60/035,722

PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 2

LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 3.5%; Score 101.5; DB 15; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPILTSQASWMDW---PL-----HOSDOPHSGGVRNGYFYVDTTGSGKCALSDQ 361
DB 110 TIKHDOISGTOQWHSPLGELCPGSHRSERP--GACNR-----CTEGVGTNASSN 160
QY 352 VPDCLVSSAASVYRAGSLSEETNFIIPSNPSVTPPTPETALQCTADKFPDSCGADV 421
DB 161 LFACL-----PCTACKSDEEB-----RSPCTT--TRNTACCKPCTGFNDNSA-- 201
QY 422 QACKROKTSVCGOISTSVDTCTADEQNEC-----GSN-----TALINGLAVGV 467
DB 202 EMCRCRSGTCCPRGMVVK--DCTPMSDIECHKESGNGHNIWVILVTLVPLLVAVLI 259
QY 468 LIALIGG-----CYAKSLDRNKVQ-AAHNE-----HEFOSDRGARKR 507
DB 260 VCCGSGGGGDPKCMDRVCFWRLGLRPGAEADNAHNEILSNADSLSTFVSEQMESQE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 32

US-09-738-973-434
; Sequence 434, Application US/09738973
; Patient No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Eliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 1702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-738-973-434

Query Match 3.4%; Score 100.5; DB 10; Length 1702;

Best Local Similarity 20.1%; Pred. No. 7.5; Mismatches 183; Indels 245; Gaps 30;

QY 20 ASGLSSSTRRESOT-----LSASTG-----NPFQANVE 49
DB 312 AEGTLRAKSEBSLISLAHVODSKLFRPRRPRSSDLSASFNGEMLGRNCNSYD-- 367
QY 50 MKTFRERFNLTHHOSGIYVDLGQDKEVDGTLVREPAGLCPITWGHIELQOPD----- 102
DB 368 -----NLPHDNS-----EEGGLHLPALMSPHSAEDVDLSPPDIGVASLD 409
QY 103 -----RLPYRNNFLVDVPTKEKYKQGN-----PLPGFNLNF 135
DB 410 FDPMSFOCSPPRASECELESASFL-DSFGYSKDPSPANKKDAETGSSQCOTPGS----- 463
QY 136 VTPSGORISPPMELERKSNIKASTDLGRCAEFAFTVAM-----DKNNKATKYRPFVY 191
DB 464 -TASEPVS-----LQKLS-----PFTLDSLPTEDKSKSPSTTEKVVY 504
QY 192 DSKRLCHILVYSQMLMEGKKYCSVKGPPDLTWYCFPRKSVTENHHLIYGSAYVGENP 251

DB 505 AFSPKIGRLKSKSPSM-----SI-SEPISTV--LPPRVS----- 535
QY 252 DAFISKCPNQLRGRCFGVWKGRCLDYTELDVIERVESKACQWTFENDGVASD-- 309
DB 536 -EVIGTYSNTTAQNAASSWTDK--CVERDXTN-----RSPQT--VMMKTNETVQAEAY 585
QY 310 QPHTYPLTSQASWMDWMLHOSDOPHSGGVRNGYFYVDTTGSGKCALSDQVDPCLVSD 369
DB 586 ESEVQPLDQVAA-----BEVELP-----GK---EQGSVSSGSQK 616
QY 370 SAASVYRAGSLSEETNFIIP-SNPSV--TPPTPETALQCTADKFPDSCGADVQACKR 426
DB 617 AVASGQRTGTGAVTHDPPQDSVPSVSLIPPPPKVYARMIALALAESAOASTQSILKR 676
QY 427 QKTGCVG-----GOIQTSVDTCTADEQNECSNTALLINGLAVGVLLALLGGGCVFAARL 482
DB 677 PGTISOAGTYNYGDI--AVATTEBNLS-----SSYSAYAL 708
QY 483 DRNKGVOAAHNEHEFOSDRGARKRPSDLMQAEAP-----SFWDEAEENIEODG 531
DB 709 DK-----AYFQTDRAPEQFH-----LONNAPGNDHPLPPTTATGDTHTSNTTESG 754

RESULT 33

US-09-854-133-434
; Sequence 434, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 1702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-133-434

Query Match 3.4%; Score 100.5; DB 10; Length 1702;

Best Local Similarity 20.1%; Pred. No. 7.5; Mismatches 183; Indels 245; Gaps 30;

QY 20 ASGLSSSTRRESOT-----LSASTG-----NPFQANVE 49
DB 312 AEGTLRAKSEBSLISLAHVODSKLFRPRRPRSSDLSASFNGEMLGRNCNSYD-- 367
QY 50 MKTFRERFNLTHHOSGIYVDLGQDKEVDGTLVREPAGLCPITWGHIELQOPD----- 102
DB 368 -----NLPHDNS-----EEGGLHLPALMSPHSAEDVDLSPPDIGVASLD 409
QY 103 -----RLPYRNNFLVDVPTKEKYKQGN-----PLPGFNLNF 135
DB 410 FDPMSFOCSPPRASECELESASFL-DSFGYSKDPSPANKKDAETGSSQCOTPGS----- 463
QY 136 VTPSGORISPPMELERKSNIKASTDLGRCAEFAFTVAM-----DKNNKATKYRPFVY 191
DB 464 -TASEPVS-----LQKLS-----PFTLDSLPTEDKSKSPSTTEKVVY 504
QY 192 DSKRLCHILVYSQMLMEGKKYCSVKGPPDLTWYCFPRKSVTENHHLIYGSAYVGENP 251
DB 505 AFSPKIGRLKSKSPSM-----SI-SEPISTV--LPPRVS----- 535

```

QY 252 DAFISCPNOLRGVRFVWKKGRCLDYTELDTVIERVESKAQCWKTFFENDGVASD-- 309
DB 536 -EVIGTSTNTTAQNASSSTWDX--CVERDATN-----RSPQTQ-VKMKTNETVAQAEY 585
QY 310 QPHTYPLTSQASWMDMWPMLHOSDOPHSGVGRNRYFYVDTTGGKCALSDQVPCLVSD 369
DB 586 ESEVQPLQOVAA-----EEVELP-----GK---EDQSVSSSQSK 616
QY 370 SAAVSYTAAGSLSEETPNFIIP-SNPSV--TPPTETALQCTADKFPDSFGACDVQACKR 426
DB 617 AVASGOTGTGAVTHDPQDSVPVSSVSLIPPPPKVVARMLALALAESAOQASTQSLKR 676
QY 427 OKTSCVG---GOIOSTSVDCETADEONEGCSNTALIALAGVGVLLALLGGGCVFAPRL 482
DB 677 PGTSGAGTYNGDI---AVATTEDNLS-----SSYSAAVL 708
QY 483 DRNKGVQAHHHEHFEOSDRGARKRPSDLMQEAEP-----SFWDAEENIEODG 531
DB 709 DK-----AVFQTRPAEQFH-----LQNNAPGNCDBLPETATGDPTHSNTTSSG 754
QY 532 ETHWVE 538
DB 755 EQHQVD 761

```

RESULT 34

```

US-10-144-649A-434
; Sequence 434, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongrong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 1702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-649A-434

```

Query Match 3.4%; Score 100.5; DB 15; Length 1702;

Best Local Similarity 20.1%; Pred. No. 7.5; Indels 245; Gaps 30;

Matches 122; Conservative 57; Mismatches 183; Indels 245; Gaps 30;

```

QY 20 ASGLSSSTRSRESOT-----LASTSG-----NPFQANVE 49
DB 312 AGCTLRASASBSSTLSHAVDGSKLFRPRRSSDALASAFNGMLNRCNSVD----- 367
QY 50 MKTFERENLTHHOSGIYVDLQDKEVDGTLYREPAGLCPTWGKHIELQDP----- 102
DB 368 -----NLPHDNES-----EEEGGLHIFALMSPHSABEDVDSLSPDIGVASLD 409
QY 103 -----RLPYRNNFLEDVPTKEVKYOSGN-----PLPGGNLNF 135
DB 410 FDPWFSQSPPAESECLESASFL-DSFGYSKDKPSAKKKAQAEFGSSQCTPFGS----- 463
QY 136 VTPSGQRISPFPMELKKNKNIKASTDLGRCAEFAKTYAM-----DKNNKATKYRYFPY 191
DB 464 -TASESEVP-----LQEKLS-----PFTIDLSPTEDKSSKSPSTFEKXY 504
QY 192 DSKRRLCHILYVSMQMEGKTCYVKGEPPDLTWYCFKPKSVTENHLLIYSAYVGENP 251
DB 505 AFSPIKGRKLSKSPSM-----SI-SEPISVT-----LPPRVS----- 535

```

```

QY 252 DAFISCPNOLRGVRFVWKKGRCLDYTELDTVIERVESKAQCWKTFFENDGVASD-- 309
DB 536 -EVIGTSTNTTAQNASSSTWDX--CVERDATN-----RSPQTQ-VKMKTNETVAQAEY 585
QY 310 QPHTYPLTSQASWMDMWPMLHOSDOPHSGVGRNRYFYVDTTGGKCALSDQVPCLVSD 369
DB 586 ESEVQPLQOVAA-----EEVELP-----GK---EDQSVSSSQSK 616
QY 370 SAAVSYTAAGSLSEETPNFIIP-SNPSV--TPPTETALQCTADKFPDSFGACDVQACKR 426
DB 617 AVASGOTGTGAVTHDPQDSVPVSSVSLIPPPPKVVARMLALALAESAOQASTQSLKR 676
QY 427 OKTSCVG---GOIOSTSVDCETADEONEGCSNTALIALAGVGVLLALLGGGCVFAPRL 482
DB 677 PGTSGAGTYNGDI---AVATTEDNLS-----SSYSAAVL 708
QY 483 DRNKGVQAHHHEHFEOSDRGARKRPSDLMQEAEP-----SFWDAEENIEODG 531
DB 709 DK-----AVFQTRPAEQFH-----LQNNAPGNCDBLPETATGDPTHSNTTSSG 754
QY 532 ETHWVE 538
DB 755 EQHQVD 761

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RESULT 35

```

US-09-859-053-32
; Sequence 32, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-32

```

Query Match 3.4%; Score 99; DB 10; Length 470;

Best Local Similarity 22.2%; Pred. No. 1.4; Indels 72; Gaps 14;

Matches 70; Conservative 32; Mismatches 142; Indels 72; Gaps 14;

```

QY 111 LEDVTEKVKYOSGNPL--PGGFNLNFTVTPSGQRISPFPMELKKNKNIKASTDLGRCAE 168
DB 14 LEVQCEVQVLVESGGGLVQPGSLRLSCAAGFTTSSIDMTM-----VRQATGGLMEV 67
QY 169 FAFKTVANDKNNKATKYRYPPVYDSKRLCHILYVSMQMEGKTCYVKGEPPDLTWYCF 228
DB 68 SAIGTAGDTYYPGVSKGFTI---SRENAKSLYLQNNSLRA-----GD--TAVYVCV 115
QY 229 KPRKSVTENHLLIYSAYVGENPDAFISCPNOLRGVRFVWKKGRCLDYTELDTVIE 288
DB 116 RDNRYVTEHHYYGMDVWGQGTIVTVSSASTGP-----SVFLAPCSRSTS----- 163
QY 289 RVESKAQ--CWYKTF-----ENDGVAQDPHTYPLTSQASWMDMWPMLH----- 330
DB 164 --ESTALGCLVKDYFPPPVVSNMNGALTVGHTFPAVLOS--GLYSLSSVTVPPSSN 219
QY 331 -SDQPHSGVGRNRYFYVDTTGGKCALSDQVPCLVDSAAVSYTAAGSLSEETPNFI 389

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Db 220 FCTOTYTCNVHDKBSNTKVDKTEKCCV--ECPPCAPPVAGPSV-----FL 265
Qy 390 IPSNPSVT--PPTPE 402
Db 266 PPPKPKDTLMISRTPE 281

RESULT 36
US-09-820-893-60
Sequence 60, Application US/09820893
Patent No. US20020076705A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: P2033p1
CURRENT APPLICATION NUMBER: US/09/820,893
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/531,119
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/102,895
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 60
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-820-893-60

Query Match 3.4%; Score 98.5; DB 9; Length 327;
Best Local Similarity 19.2%; Pred. No. 0.92;
Matches 84; Conservative 43; Mismatches 109; Indels 201; Gaps 19;

Qy 127 LPG---GFNINFTVPSGORIS-PPMELLEKNINIKASTDLCRCACFAFTVAMDKNK 181
Db 4 LRGPLCALGLFLCLSLGLAVEVVKPTPEPL-----STPLGKTAELT----- 44
Qy 182 ATKRYRPFVYDSKRLCHILYVSMQMEGKKYCSVKGEPPDLTWYCFKPKRSVTENHILI 241
Db 45 -----C-----TYSTVSDSFALWMSFVQPGKPKISHSPIIL 75
Qy 242 YGSAVGENPDPAFISCKPNQALRGYRFGVWKGRCLDTYELTDVIERVESKACQWVTF 301
Db 76 YFT-----NGHLYPTGSKSRVSLQNPPTV----- 101
Qy 302 ENDGASDQPHTYPLTQASNMNDWMLHSDQPHSGGVGRNYGFYVDTTGEKCALSDQ 361
Db 102 ---GVA---TLKLTID-----VHPSD-----TGTYLCOVNNP 126
Qy 362 VPDLVSDSAVSYTAAGSLSEETPNFIIPSNP-----SVTPPTETALQCTADK----- 411
Db 127 -PDFYTNGLGLINLTV-----LVPSNPLCSGSGGTSVGSSTALRCSSSEGAKP 175
Qy 412 -----FPDSFGACDVQACKROKTSVGGQIQSTSVDTCTABEONEGCSNTAL----- 457
Db 176 VYNNVRLGTFPTPSGSMVQ-----DEVSGQLITLNLITLSGTYRCVATNMGASASC 228
Qy 458 -----TAGLAVG---GVLLALLGGCGYFAKRLDRNKGCVQAHHNHEFOSDR 501
Db 229 ELTSLVTEPPQGRVAGALIGVLLGLVLLSV-----AACLVRFPQKER 270
Qy 502 GAKKKRP---SDLMQEA 515
Db 271 GKPKRETYGSDLREDA 287

RESULT 37
US-10-216-163-236
Sequence 236, Application US/10216163
Publication No. US20030149239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc

APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACTIS ENCODING THE SAME
FILE REFERENCE: P3530PIC3
CURRENT APPLICATION NUMBER: US/10/216,163
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 236
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-10-216-163-236

Query Match 3.4%; Score 98.5; DB 12; Length 327;
Best Local Similarity 19.7%; Pred. No. 0.92;
Matches 86; Conservative 43; Mismatches 107; Indels 201; Gaps 20;

Qy 127 LPG---GFNINFTVPSGORIS-PPMELLEKNINIKASTDLCRCACFAFTVAMDKNK 181
Db 4 LRGPLCALGLFLCLSLGLAVEVVKPTPEPL-----STPLGKTAELT----- 44
Qy 182 ATKRYRPFVYDSKRLCHILYVSMQMEGKKYCSVKGEPPDLTWYCFKPKRSVTENHILI 241
Db 45 -----C-----TYSTVSDSFALWMSFVQPGKPKISHSPIIL 75
Qy 242 YGSAVGENPDPAFISCKPNQALRGYRFGVWKGRCLDTYELTDVIERVESKACQWVTF 301
Db 76 YFT-----NGHLYPTGSKSRVSLQNPPTV----- 101
Qy 302 ENDGASDQPHTYPLTQASNMNDWMLHSDQPHSGGVGRNYGFYVDTTGEKCALSDQ 361
Db 102 ---GVA---TLKLTID-----VHPSD-----TGTYLCOVNNP 126
Qy 362 VPDLVSDSAVSYTAAGSLSEETPNFIIPSNP-----SVTPPTETALQCTADK----- 411
Db 127 -PDFYTNGLGLINLTV-----LVPSNPLCSGSGGTSVGSSTALRCSSSEGAKP 175
Qy 412 -----FPDSFGACDVQACKROKTSVGGQIQSTSVDTCTAD-----EONEGCS--- 453
Db 176 VYNNVRLGTFPTPSGSMVQ-----DEVSGQLITLNLITLSGTYRCVATNMGASASC 228
Qy 454 -----NTALTAGLAVG---GVLLALLGGCGYFAKRLDRNKGCVQAHHNHEFOSDR 501
Db 229 ELTSLVTEPPQGRVAGALIGVLLGLVLLSV-----AACLVRFPQKER 270

OY 502 GAKKRP---SDLMQEA 515
Db 271 GKPKETVYGSDLRDA 287

RESULT 38
US-10-227-884-236
; Sequence 236, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deanoys, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; PRIOR APPLICATION NUMBER: 2002-08-26
; PRIOR FILING DATE: 10/119,480
; PRIOR APPLICATION NUMBER: 2002-04-09
; PRIOR FILING DATE: 60/059113
; PRIOR APPLICATION NUMBER: 1997-09-17
; PRIOR FILING DATE: 60/062287
; PRIOR APPLICATION NUMBER: 1997-10-17
; PRIOR FILING DATE: 60/063549
; PRIOR APPLICATION NUMBER: 1997-10-28
; PRIOR FILING DATE: 60/064103
; PRIOR APPLICATION NUMBER: 1997-10-31
; PRIOR FILING DATE: 60/069873
; PRIOR APPLICATION NUMBER: 1997-12-17
; PRIOR FILING DATE: 60/078910
; PRIOR APPLICATION NUMBER: 1998-03-20
; PRIOR FILING DATE: 60/079294
; PRIOR APPLICATION NUMBER: 1998-03-25
; PRIOR FILING DATE: 60/079556
; PRIOR APPLICATION NUMBER: 1998-03-26
; PRIOR FILING DATE: 60/079728
; PRIOR APPLICATION NUMBER: 1998-03-27
; PRIOR FILING DATE: 60/081819
; PRIOR APPLICATION NUMBER: 1998-04-15
; PRIOR FILING DATE: 60/081955
; PRIOR APPLICATION NUMBER: 1998-04-15
; PRIOR FILING DATE: 60/082804
; PRIOR APPLICATION NUMBER: 1998-04-22
; PRIOR FILING DATE: 60/084441
; PRIOR APPLICATION NUMBER: 1998-05-06
; PRIOR FILING DATE: 60/085323
; PRIOR APPLICATION NUMBER: 1998-05-13
; PRIOR FILING DATE: 60/085579
; PRIOR APPLICATION NUMBER: 1998-05-15
; PRIOR FILING DATE: 60/086392
; PRIOR APPLICATION NUMBER: 1998-05-22
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; PRIOR APPLICATION NUMBER: 1998-06-17
; PRIOR FILING DATE: 60/089538
; PRIOR APPLICATION NUMBER: 1998-06-17
; PRIOR FILING DATE: 60/089905
; PRIOR APPLICATION NUMBER: 1998-06-18
; PRIOR FILING DATE: 60/090472
; PRIOR APPLICATION NUMBER: 1998-06-24
; PRIOR FILING DATE: 60/090557
; PRIOR APPLICATION NUMBER: 1998-06-24
; PRIOR FILING DATE: 60/090691
; PRIOR APPLICATION NUMBER: 1998-06-25

; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR APPLICATION NUMBER: 60/100038
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; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605

PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
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PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
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PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-04-28
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
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PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 3.4%; Score 98.5; DB 15; Length 327;

Beet local similarity 19.7%; Pred. No. 0.92;

Matches 86; Conservative 43; Mismatches 107; Indels 201; Gaps 20;

QY 127 LFG-----GFNFVTPSGORIS-PPMELLENKSNIKASTDLGRCAEFAPKTVMADKKNK 181
DB 4 LFGPLCALGLFGLSLGLAVEVKYPTPL-----STPLGKTAELT----- 44
QY 182 ATKRYRPFVYDSKKRLCHILYVSMQJMGKKYCSVKGEPDDLTYWCYFKPRKSVTEHHLI 241

DB 45 -----C-----TYSTVSGDSFALEWSFYVQPKISEHPI 75
QY 242 YGSAVGENPDFAISKCPNOLRGYRFGWKGRCLDYTELTDYIEVESKACQWXTF 301
DB 76 YFT-----NGHLPTGSKSRVSLLOMPPIV----- 101
QY 302 ENDGVASDQPHPTPLTSQASWMDWPLHQSDQPHSGVGRVYGYVDTTSEGCALSDQ 361
DB 102 ---GVA-----TLKLTID-----VHPSD-----TCTYLCQVNNP 126
QY 362 VPDCLVSDASAVSTTAAGSLSEETPNFIIPNP-----SVTPPIPETALQCTADK----- 411
DB 127 -PDFYVWGLGLINTV-----LVPSPNPLCSQSGQTSVGSTALRCSSSGAKRP 175
QY 412 -----FPDSGACDQVQCKRQKTSVCGQIQSTSVDCAD-----EQNEGCS--- 453
DB 176 VYNNVRLCTFTPTSPGSAVQ-----DEVGQLITNLISLSTGTCVATNQGSASC 228
QY 454 -----NTALJAGLVG-----GVLLALIGGCGCYFAKRLDRKKGVQAAHHEHFGSDR 501
DB 229 ELTLSTVTEPSQGRVAGALIGVLGLLSTV-----AFCVLVRFOKER 270
QY 502 GAKKRP---SDIWOEA 515
DB 271 GKRPETVYGSDLREDA 287
RESULT 39
US-10-230-163-236
Sequence 236, Application US/10230163
Publication No. US20030036635M1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geertsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephanie, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC96
CURRENT APPLICATION NUMBER: US/10/230,163
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
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PRIOR APPLICATION NUMBER: 60/082804

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PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
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PRIOR FILING DATE: 1999-01-12
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PRIOR FILING DATE: 1999-01-12
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PRIOR FILING DATE: 1999-02-10
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PRIOR FILING DATE: 1999-03-10
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PRIOR FILING DATE: 1999-05-14
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PRIOR FILING DATE: 1999-06-22
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PRIOR FILING DATE: 1999-06-23
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PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
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PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733

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 PRIOR APPLICATION NUMBER: 60/164418
 PRIOR FILING DATE: 1999-11-09
 PRIOR APPLICATION NUMBER: 60/166361
 PRIOR FILING DATE: 1999-11-16
 PRIOR APPLICATION NUMBER: 60/169445
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: 60/169495
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: 60/169835

Query Match 3.4%; Score 98.5; DB 15; Length 327;
 Best Local Similarity 19.7%; Pred. No. 0.92;
 Matches 86; Conservative 43; Mismatches 107; Indels 201; Gaps 20;

127 LRG-----GFNINFTVPSGGRIS-PPMELLEKNSNIKASTDGRCAEFAFTVAMDKNK 181
 4 LRGPFGLGALGFLGLSLAVEVKVTEPL-----STPLGKTAELT----- 44
 182 ATKRYRPFVYDSKKRLCHILVYSQMMEGKYYCSVKGEPPDLTWYCFKPKSVTEHHLI 241
 45 -----C-----TSTSVGDSFALWESFVQPKPKISHSHPL 75
 242 YGSAVGENPDAPFISKCPNQLRGYRFGVWKGRCLDYTELTDVIEVESKACQWXTF 301
 76 YFT-----NGHLVPTGSKSKRVSLQNPPTV----- 101
 302 ENDGVASDQPHTYPLTSQASWMDWPLHQSOPHSGGVGRNYGFYVDTTGEKCALSDQ 361
 102 --GVA-----TLKLTLD-----VHPSD-----TGYLCOVNNP 126
 362 VPDLVSDSAVSYTAAGSLSEETPNFIIPSNP-----SVTPPTPETALQCTADK----- 411
 127 -PDFTYNGLGILNLTV-----LVPPSNPLCSQSGQTSVGSSTALRCSSSEGAKP 175
 412 -----PPDSFGACDVQACKRQKTSVCGQIQSTSVDTAD-----EQNEGGS----- 453
 176 VYNNVRLGTFTPTSPGSMVQ-----DEVSGQILTNLSITSSGTYRCVATNMGMSASC 228
 454 -----NTALJAGLAVG---GVLLALLGGCGYFAKRLDRNKGVQAAHHEHFFQSDR 501
 229 ELTSLVTEPSQGRVAGALIGVLLGVLLSV-----AACLVRFOKER 270
 502 GAKKRP---SDLMQEA 515
 271 GKPKETYGSDLREDA 287

RESULT 40
 US-10-230-338-236
 Sequence 236, Application US/10230338
 Publication No. US20030044934A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Deenoyers, Luc
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Goddard, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Macanabe, Colin L.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3530P1C92
 CURRENT FILING DATE: 2002-08-28
 PRIOR FILING DATE: 2002-04-09
 PRIOR APPLICATION NUMBER: 10/119,480
 PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/063549
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/064103
 PRIOR FILING DATE: 1997-10-31
 PRIOR APPLICATION NUMBER: 60/069873
 PRIOR FILING DATE: 1997-12-17
 PRIOR APPLICATION NUMBER: 60/078910
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 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 Remaining Prior Application data removed - See file wrapper or PALM.
 NUMBER OF SEQ ID NOS: 246
 SEQ ID NO 236
 LENGTH: 327
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-230-338-236

Query Match 3.4%; Score 98.5; DB 15; Length 327;
 Best Local Similarity 19.7%; Pred. No. 0.92;
 Matches 86; Conservative 43; Mismatches 107; Indels 201; Gaps 20;

127 LRG-----GFNINFTVPSGGRIS-PPMELLEKNSNIKASTDGRCAEFAFTVAMDKNK 181
 4 LRGPFGLGALGFLGLSLAVEVKVTEPL-----STPLGKTAELT----- 44
 182 ATKRYRPFVYDSKKRLCHILVYSQMMEGKYYCSVKGEPPDLTWYCFKPKSVTEHHLI 241
 45 -----C-----TSTSVGDSFALWESFVQPKPKISHSHPL 75
 242 YGSAVGENPDAPFISKCPNQLRGYRFGVWKGRCLDYTELTDVIEVESKACQWXTF 301
 76 YFT-----NGHLVPTGSKSKRVSLQNPPTV----- 101
 302 ENDGVASDQPHTYPLTSQASWMDWPLHQSOPHSGGVGRNYGFYVDTTGEKCALSDQ 361
 102 --GVA-----TLKLTLD-----VHPSD-----TGYLCOVNNP 126
 362 VPDLVSDSAVSYTAAGSLSEETPNFIIPSNP-----SVTPPTPETALQCTADK----- 411
 127 -PDFTYNGLGILNLTV-----LVPPSNPLCSQSGQTSVGSSTALRCSSSEGAKP 175
 412 -----PPDSFGACDVQACKRQKTSVCGQIQSTSVDTAD-----EQNEGGS----- 453
 176 VYNNVRLGTFTPTSPGSMVQ-----DEVSGQILTNLSITSSGTYRCVATNMGMSASC 228
 454 -----NTALJAGLAVG---GVLLALLGGCGYFAKRLDRNKGVQAAHHEHFFQSDR 501
 229 ELTSLVTEPSQGRVAGALIGVLLGVLLSV-----AACLVRFOKER 270
 502 GAKKRP---SDLMQEA 515
 271 GKPKETYGSDLREDA 287

Search completed: October 2, 2003, 16:01:31
 Job time : 73 secs

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OM protein - protein search, using sw model

Run on: October 2, 2003, 15:46:34 ; Search time 43 Seconds
(without alignments)
1209.936 Million cell updates/sec

Title: US-10-039-770A-1
Perfect score: 2922
Sequence: 1 MGLVGVQVLTVLVADCTIFA.....EAEENIBODETHVWESGDY 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	447	15.3	562	2 A49944	apical membrane an
2	431	14.8	622	2 A44986	apical membrane an
3	431	14.8	622	2 A32499	apical membrane an
4	421.5	14.4	563	2 A39238	66k merzofite surf
5	415	14.2	622	2 A44986	apical membrane an
6	412	14.1	622	2 A44986	apical membrane an
7	410	14.0	622	2 C44986	apical membrane an
8	398.5	13.6	558	2 A44964	apical membrane an
9	127	4.3	2364	2 A56577	microtubule-associ
10	125	4.3	863	2 S06017	neuraxin - rat
11	120	4.1	1701	1 T09127	probable erythrocy
12	120	4.1	2464	1 QRMSP1	microtubule-associ
13	112	3.8	993	2 T09129	probable erythrocy
14	111	3.8	600	2 T34757	probable oligopept
15	109	3.7	724	2 A48569	antigen Em100 - Bi
16	108	3.7	768	2 T00073	hypothetical prote
17	107.5	3.7	1104	2 T38869	transcription fact
18	107	3.7	1009	2 T48727	retinoblastoma bin
19	106	3.6	415	2 A35560	lysosomal membrane
20	104.5	3.6	6658	2 T13931	proectin - fruit
21	104	3.6	1255	1 A24571	protein-tyrosine k
22	104	3.6	1611	2 T38236	hypothetical prote
23	103	3.5	360	2 S69063	probable membrane
24	103	3.5	1332	2 T23024	hypothetical prote
25	102	3.5	3002	2 A47221	fibrillin 1 precur
26	101.5	3.5	287	2 A60643	antigen 5401 - Rim
27	101.5	3.5	320	2 S07296	plastocyanin-plast
28	100.5	3.4	715	2 T14812	hypothetical prote
29	99.5	3.4	732	1 J00132	acylaminoacyl-pept

30	99.5	3.4	1606	2 T49219	translacion initia
31	99	3.4	2331	2 S44054	genome polyprotein
32	98	3.4	444	2 E65203	probable dehydroge
33	98	3.4	521	2 A1525	interanal like pr
34	97.5	3.3	1280	2 B95031	alaine amylopolur
35	97.5	3.3	2871	2 A55624	fibrillin-1 precu
36	97	3.3	468	2 B40228	neuraxin I-beta pr
37	97	3.3	694	2 F97279	TPR-repeat-contain
38	97	3.3	1507	2 A40228	neuraxin I-alpha p
39	96	3.3	1020	2 B86414	hypothetical prote
40	96	3.3	1256	2 G97902	alpha-amyase (EC
41	95.5	3.3	320	1 C8R2	plastocyanin-plast
42	95.5	3.3	376	2 C81272	probable aminotran
43	95.5	3.3	482	2 JC5092	E-selectin - pig
44	95	3.3	357	1 TVHUR2	transforming prote
45	95	3.3	571	2 D90157	hypothetical prote

ALIGNMENTS

RESULT 1

A49944
C:Species: Plasmodium fragile
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C:Accession: A49944
R:Peterson, M.G.; Nguyen-Dinh, P.; Marshall, V.M.; Elliott, J.F.; Collins, W.E.; Anders, M.O. Biochem. Parasitol. 39, 279-284, 1999
A:Title: Apical membrane antigen 1 precursor - Plasmodium fragile.
A:Reference number: A49944; MUID:90205978; PMID:2181309
A:Accession: A49944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-562 <Per>
A:Cross-references: GB:M29898

Query Match 15.3%; Score 447; DB 2; Length 562;
Best Local Similarity 25.9%; Pred. No. 5.9e-27;
Matches 159; Conservative 91; Mismatches 231; Indels 132; Gaps 26;

QY	6	VQVLLVAVDCTIF-----ASGLSSSTRS---RESQTLASTSGNPPQANVENKT	52
DB	4	IYCLFLSAQCLVHMGKCEPQKPSRLRSKNTLLEQEPWVERSTRMSNPW-----KA	57
QY	53	FMERFNLTHHSGIYVDIGDQKVDGTLVEEPAGLCPIWKGKHELOQPDLLPYRNPLE	112
DB	58	FMEKYDIEKTRSSGIRVDLGSDAEVSYSRIPAKCPVFGKGIYQNSE-----VSFLT	112
QY	113	DVPT-EKEVYKSGNPLPGCFNLNFTPSGQRISPPPM-----ELLEKSNIRASTDLGRCA	167
DB	113	PVALGNQKLKDGCFAPF-----QANDHISISITIKNLRERKENNDLKKNDLALCK	163
QY	168	EPAFKTV-AMDKNKATRYRPFYVDSKRIKILVYSWQMLEGKYCSVKGPEPDLTWY	226
DB	164	THAASFVWEMDKN---SSYRHPAVYDEDKICVWLYLSAQNMSPRYCSKDAENKD-AMF	219
QY	227	CFKRRKSTENHHLIYSAAYGEN-PDAFISKCNQMLRGRRPQVWKKGRCLDYTELDT	285
DB	220	CFKDKMETFDH-----LAYLSKVVNDWQNKCRKNGSKFGIWDNGCEELPYVDV	274
QY	286	VIEFVESKAOQVMTFENDGVASDQPHYPLTISOASNDWMPHLQSDQPHSGV-----	339
DB	275	---QAKDLRECNRIYFE--ASASQPPQY---BEELTDYKIQIGFQNGQMIKSAFL	325
QY	340	-----GRNYGFYVDTTGECK-CALSDQVDCIVSDSAVSYPAAG---SLS	382
DB	326	PVGAFNDSNDFKSGRGVWMAFDT--ENKVCYLFNAKPTCLINDKNFIATLASHPOEVD	383
QY	383	EETNFIIPSN-----PSTPPTPETAQCTADKPPDSGA	418
DB	384	NEPFSIYKDEMEREMKRESNMSLVNDKARIYLPRLFISNDKSLKCPCAPEHTWTST	443

```

Qy 419 CDVQAKCKKQKTSV--GGQIOSTSVDTCTADE-----QNEGSGNTLLIAGLAVGVLL 468
Db 444 CNFYVC-----NCVKKRAEIKENNEVAIKKEFKQDYQAQGSCKOMLIIITIGTGVCV 498
Qy 469 LALLGGCGYFAKRLDRNKGVQAHHHEFQSDRGARKKRPDLMOEAPSFMDAEENIE 528
Db 499 VA-LASMFYFRKKANDK-----YDKMEQADQYGVPTTRKDBMLDEPASFGEER--R 548
Qy 529 ODGEHVMVEGDY 541
Db 549 ASHTTPVLMKEPY 561

```

RESULT 2

```

B44986
A:apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain Thai Tn)
C:Species: Plasmodium falciparum
C>Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C:Accession: B44986
R:Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Biochem. Parasitol. 42, 285-286, 1990
A:Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate anti
A:Reference number: A44986; MUID:91101665; PMID:2270110
A:Accession: B44986
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-622 <THO>
A:Cross-References: GB:M34553
C:Keywords: membrane protein; surface antigen

```

Query Match 14.8%; Score 431; DB 2; Length 622;

Best Local Similarity 26.7%; Pred. No. 1.2e-25;

Matches 153; Conservative 81; Mismatches 209; Indels 130; Gaps 25;

```

Qy 41 GNPQANVEMKTFMERFNLTHHSGIYVDLGQDKVDGTLREBAGLCPIWGKHIELQ 100
Db 107 GNPW-----TEYMAKYDIEVHSGIRVDLGEDAVAGTQYRLPSGKCPVFGKIIEN 160
Qy 101 PDRLEPRNNFLDVPTE--KEYKOSGNPLDGGFNLFVTSGORISFPME---LLEKNS 155
Db 161 S-----KTFLETPVATENODLKDGGFAFP-----PTEPLISMPTLDQMKHLKXDE 206
Qy 156 NIKASTDLGRCAEFKATVAMDKNNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYSV 215
Db 207 YKANDELTLCSHAGNM--PNNDKSNYKIPAVYDDDKCHILYIAQENNGRYCN- 264
Qy 216 VKGEPPDLTWYCFKPKRK-SVTENHHLIYGSAYGEN-PDAFISKCPNOLRGYRGVWK 273
Db 265 -KDESKRSMFCRPAKDIKFENY-----TYLSKVVNDWMEKVCPRKNLQNAKFGGLAVD 317
Qy 274 GRCLDYTELTVIERVESKAQCVKTFENDGVASQPHYTP--LTSQASNDWMP----- 327
Db 318 GNCEIDIPHYNEF--SANDLFECNKLVFELS--ASDQPKQYEQHLDYERIKIEGFQNKQA 372
Qy 328 -----LHOSQPHSGGVGRNYGFYVDTTEGKCALSDQVPCIVSASAVSYT 376
Db 373 SMKSAFLPTGAFKARVYKSHGKGYMGNVNTETO--KCEIFNVKPTCLINNSSVIATTA 429
Qy 377 AAGSLSEETPNFIIIPSN-----PSVTPPPTETA 404
Db 430 ALSHPREVENNF--PCSLYKDEIKKEIERESKRRIKLNDDDEGNKKIIPRIPIISDKOS 487
Qy 405 LOCTADKFPDSFGACVQACKKQKTSQVGGIOSTG-----VDCTAD--EQNEGG 452
Db 488 LKCPDCEPIVSNSTCNFVCK-----CVERRAVTSNNEVVVEKYKDEYADIPKHKPTY 542
Qy 453 SNTALI-----AGLAVGVLLALLGGCYFAKRLDRNKGVQAHHHEFQSDRGARKKRP 508
Db 543 DNKKIIIASAAVAVALTILM-----VLYKR-----KNAEKYDGMDEPQYKGSNSR- 591
Qy 509 SDLMQAEPSFMDAEENIEODGEHVMVEGDY 541
Db 592 NDEMIDPEASFGEER--RASHTTPVLMKEPY 621

```

RESULT 3

```

A32499
A:apical membrane antigen 1 - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jun-2000
C:Accession: A32499
R:Peterson, M.G.; Marshall, V.M.; Smythe, J.A.; Crewther, P.E.; Lew, A.; Silva, A.; Ande
Mol. Cell. Biol. 9, 3151-3154, 1989
A:Title: Integral membrane protein located in the apical complex of Plasmodium falciparu
A:Reference number: A32499; MUID:89384584; PMID:2701947
A:Accession: A32499
A:Status: preliminary
A:Molecule type: DNA, mRNA
A:Residues: 1-622 <PEI>
A:Cross-References: GB:M27133; NID:9160072; PID:9160073
C:Keywords: membrane protein; surface antigen

```

Query Match 14.8%; Score 431; DB 2; Length 622;

Best Local Similarity 26.2%; Pred. No. 1.2e-25;

Matches 149; Conservative 86; Mismatches 212; Indels 122; Gaps 24;

```

Qy 41 GNPQANVEMKTFMERFNLTHHSGIYVDLGQDKVDGTLREBAGLCPIWGKHIELQ 100
Db 107 GNPW-----TEYMAKYDIEVHSGIRVDLGEDAVAGTQYRLPSGKCPVFGKIIEN 160
Qy 101 PDRLEPRNNFLDVPTE--KEYKOSGNPLDGGFNLFVTSGORISFPME---LLEKNS 156
Db 161 SN-----TTFLETPVATGNQYLKD-----GGFAFP-----PTEPLISMPTLDQMKHLYKXNY 207
Qy 157 IKASTDLGRCAEFKATVAMDKNNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYSV 216
Db 208 VANLDELTLCSHAGNM--PNNDKSNYKIPAVYDDDKCHILYIAQENNGRYCN- 264
Qy 217 KGEPPDLTWYCFKPKRSYTENHHLIYGSAYGEN-PDAFISKCPNOLRGYRGVWKGR 275
Db 265 KDESKRSMFCRPAKDIKFQNY-----TYLSKVVNDWMEKVCPRKNLQNAKFGGLAVDGN 319
Qy 276 CLDYTELTD--TYIERVESKAQCVKTFENDGVASQPHYTP--LTSQASNDWMP----- 327
Db 320 CEDIPHYNEFSAIDFE---CNKLVFELS--ASDQPKQYEQHLDYERIKIEGFQNKQAS 373
Qy 328 -----LHOSQPHSGGVGRNYGFYVDTTEGKCALSDQVPCIVSASAVSYTA 377
Db 374 MKSAFLPTGAFKARVYKSHGKGYMGNVNTETO--KCEIFNVKPTCLINNSSVIATTA 430
Qy 378 AAGSLSEETPNFIIIPSN-----PSVTPPPTETA 405
Db 431 LSHPREVENNF--PCSLYKDEIKKEIERESKRRIKLNDDDEGNKKIIPRIPIISDKOSL 488
Qy 406 OCTADKFPDSFGACVQACKKQKTSQVGGIOSTVDCTA-----DEQNEGGS----- 454
Db 489 KCPDCEPIVSNSTCNFVCK-----CVERRAVTSNNEVVVEKYKDEYADIPKHKPTYD 543
Qy 455 --TALIAGLAVGVLLALLGGCYFAKRLDRNKGVQAHHHEFQSDRGARKKRPDL 512
Db 544 KMKIIIASAAVAVALTILM-----VLYKR-----KNAEKYDGMDEPQYKGSNSR- 595
Qy 513 QEAPSPFMDAEENIEODGEHVMVEGDY 541
Db 596 LDPEASFGEER--RASHTTPVLMKEPY 621

```

RESULT 4

```

A39238
A:66k merozoite surface antigen precursor - Plasmodium knowlesi
C:Species: Plasmodium knowlesi
C>Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 07-Feb-1997
C:Accession: A39238
R:Waters, A.P.; Thomas, A.W.; Deans, J.A.; Mitchell, G.H.; Hudson, D.E.; Miller, L.H.; M
J. Biol. Chem. 265, 17974-17979, 1990
A:Title: A merozoite receptor protein from Plasmodium knowlesi is highly conserved and d

```

A:Reference number: A39238; MUID:91009268; PMID:2211675
 A:Accession: A39238
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-563 <WMT>
 A:Cross-references: GB:J05631
 C:Keywords: surface antigen

Query Match 14.4%; Score 421.5; DB 2; Length 563;
 Best Local Similarity 24.6%; Pred. No. 5.9e-25;
 Matches 148; Conservative 96; Mismatches 250; Indels 107; Gaps 24;

```

QY 6 VOULLVADCTTASGL---SSSTRRESQTLASSTSGNPQANVEN---KTFMEREN 58
DB 4 IYVLFISAQCLVMKGCERNQKTRTLRSANNASLEKGPPIERSIRMSPMKAFMEKYD 63
QY LTHHOSGIYVDLGDQKVEDGTLREPAICPIWGHIELQOQPRPLPRNNFLDVPF-E 117
DB 64 LERHNSGIRIDLEBDAVNSKTRIPAGKCPVFGKIVENS---VSFLTPVATGA 118
QY 118 KEYKOSGNPLPGGFNLNFTPSGORISFPFM---ELLEKSNIKASTDLGRCAEFAPKT 173
DB 119 QRLKEGFAFPN-----ADHISITITANKERKENADLMKLANDLCTHAASF 169
QY 174 VAMDKNKATKYRYPYVDSKRLCHILYVSMQMEGKRYCSVKGEPDLTWYCFKPKRS 233
DB 170 VIAEDQN--TSYRPAVYDEKTKCYMLYLSAQENMGPRYCSPPSQND--AMFCFKEDKN 226
QY 234 VTEHHHLYGSAVYGENPDAFISKCPNALRGYRFGWKKRCLDYTELDTVIEREYSK 293
DB 227 -EKFDNLVYLSKNVSN--WENKCPKRLGNAFGLWVDCBEI-----PYNEVEAR 277
QY 294 A--QCWKTENDVADSDQPHTY--PLTQASNDMWPRLHOSDQPHSG----- 337
DB 278 SLRCKNIVFE--ASADQPRQYEEBELTAYEKIOEGFRQNRDITKAFPLVGAPNSDNF 335
QY 338 -GGRNATGYVDTTGSCKCALSDQVDCVSDSAVSYTAAG--SLSEETPNFIIPSN 393
DB 336 KSKRGYWMANFDSV--NNKCYIFNTKPTCLINDKRFATLASHQEVDFPESYVDE 394
QY 394 -----PSVTPPETALQCTADKFPDSGACVQACROKT 429
DB 395 IEREIKQSRNNLVSVDKERIVLPRIFISTDKESIKCPCEPHISNCTCFYVC----- 449
QY 430 SCV--GGQIOSTS-----VDCTADEONECGSN--TALIAGLAVGVLLTALLGGCYFAK 480
DB 450 NCVKRAEIKENNVIIKEFKEDYENPDGKHKKMLIITIGTAVCVAVASLFFPRK 509
QY 481 RLDRNKGVQAHHHEFQSDRGARKRPSDLMQEAEPSPFMDAEBENIEODETHVWEGD 540
DB 510 KAQDDK-----YDKMDQAEAVGKTANTRKDEMLDPEASFWGCDK---RASHTTIVLMKRP 561
QY 541 Y 541
DB 562 Y 562

```

RESULT 5
 A:Reference number: A39238; MUID:91009268; PMID:2211675
 A:Accession: A39238
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-563 <WMT>
 A:Cross-references: GB:J05631
 C:Keywords: surface antigen

Query Match 14.2%; Score 415; DB 2; Length 622;
 Best Local Similarity 25.8%; Pred. No. 2.2e-24;
 Matches 147; Conservative 82; Mismatches 218; Indels 122; Gaps 23;

```

QY 41 GNPFQANVEKTFERNRLTHHOSGIYVDLGDQKVEDGTLREPAICPIWGHIELQO 100
DB 107 GNPF-----TEYMAKDIEKVGSGIRVDLGEDAVAGTQYRLPSGKCPVFGKIIEN 160
QY 101 PDRLPYNNFLDVPF-E-EKEYKOSGNPLPGGFNLNFTPSGORISFPFM---ELLEKNS 155
DB 161 SN-----TTLKPVATGNQDLKOGFAFP-----PTNPLISPMTLDHMRPYKNE 206
QY 156 NIKASTDLGRCAEFAPFTVAMDKNKATKYRYPYVDSKRLCHILYVSMQMEGKRYCS 215
DB 207 YVKNLDELTLCSRAAG--NMPDQDNKSNKYPAVYDYNKCKHILYIAQENNGPRCN 264
QY 216 VKGEPDLTWYCFKPKRSVTENHHLIYSAVYGEN--DPAFISKCPNALRGYRFGWKKG 274
DB 265 -KDSKNSMFCFRPAKDKSFQNY-----TYSKNVVDNMEKVPKRLLENAKFGLWVDG 318
QY 275 RCLDYTELDTVIERVSKAQCWKTENDVADSDQPHTY--LTQASNDMWP----- 327
DB 319 NCEDI PHVNEF---SANDLEFCNKLVFELS--ASDQKQYEOHLTDYEKIKEGKKNAS 373
QY 328 -----LHOSDQPHSGGVGRNRYGYVDTTGSCKCALSDQVDCVSDSAVSYTA 377
DB 374 MISAFLPTGAFAKDRKYSKSGKYNMGYNRKTO---KCEIFNVKPTCLINSSYIATTA 430
QY 378 AGSLSEETPNFIIPSN-----PSVTPPETAL 405
DB 431 LSHNEVEHNF--PCSLYKDEIKKEIERESKRIKLANDNDEGNKIIAPRIFISDDKSL 488
QY 406 QCTADKRPDQFAGCDVQACROKTSYCVGQIOSTSVDTA-----DEONECGSN----- 454
DB 489 KCPCDPRIVNSNCTNFPVCK-----CVKRAEVTSSNEVVVKEEYKQEVADIPEHKPTD 543
QY 455 -TALIAGLAVGVLLTALLGGCYFAKRLDRNKGVQAHHHEFQSDRGARKRPSDLM 512
DB 544 KMKIITISSAAVAVLATILM---VYLYKR-----KGNAEKDKDMEPODYGSNSR--NDEM 595
QY 513 QEAEPSPFMDAEBENIEODETHVWEGDY 541
DB 596 LDPEASFWGCEK---RASHTTIVLMKRPY 621

```

RESULT 6
 A:Reference number: A39238; MUID:91009268; PMID:2211675
 A:Accession: A39238
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-622 <THO>
 A:Cross-references: GB:M34552
 C:Keywords: membrane protein; surface antigen

Query Match 14.1%; Score 412; DB 2; Length 622;
 Best Local Similarity 26.2%; Pred. No. 3.8e-24;
 Matches 150; Conservative 80; Mismatches 214; Indels 128; Gaps 25;

```

QY 41 GNPFQANVEKTFERNRLTHHOSGIYVDLGDQKVEDGTLREPAICPIWGHIELQO 100
DB 107 GNPF-----TEYMAKDIEKVGSGIRVDLGEDAVAGTQYRLPSGKCPVFGKIIEN 160
QY 101 PDRLPYNNFLDVPF-E-EKEYKOSGNPLPGGFNLNFTPSGORISFPFM---ELLEKNS 155

```

Db 161 SN-----TFLKPVATGNQDLKDGFAFP-----PTEPLISPMTLNMGDPFYKNE 206
Qy 156 NIKASTDLGRCAFAFKTVAMDKNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYYCS 215
Db 207 YVKNLDELTLCSRNA-GNMNPDKQON--SNKYKPAVYDDKDKCHILYIAQENNGPRYCN 264
Qy 216 VKGEPPDLTWYCFKPKRSVTENHLLYGSAYVGEN-PAFISKCPNOALRGYRFGVWK 274
Db 265 -KDESKRSMWCFRPAKDKLFENY-----TYLSKNVVDNWEKVCPRKLENAKRGLWVDG 318
Qy 275 RCLVTELTDTVIERVESKAQCVMTFENDGVAADQPHYTP--LTSQASNDWMP----- 327
Db 319 NCEDIPIHNER--SANDLFECKLVFELS--ASQPRQYEQHLLDYEKIKEGFNKNAS 373
Qy 328 -----LHSDQPHSGVGRNRYGYVDTTGEKCALSDQVPCLVSDSAVSYTA 377
Db 374 MIKSAFLPTGAFKADRYKSHGKGYMGNVNRKT--HKCEIFNVKPTCLINNSYIATTA 430
Qy 378 AGSLSEETPNFIIPSN-----PSVTPPTPETA 405
Db 431 LSHPIEVNNF--PCSLYKNEIMKEIERESKRKIKLNDNDGKNKIAPRIFISDKDSL 488
Qy 406 OCTADKFPDSFGACDVQACRQKTSVCGQIQSTS-----VDCTAD--EQNEGCS 453
Db 489 KCPCDPEMVSNSCRFPVCK-----CVERRAEVTSNNEVVKKEKYDEYADIDPEHKPTY 543
Qy 454 NTALI-----AGLAVGVLLALLGGCGYFPAKRLDRNKGYOAAHNEHFGSDRGARKRPS 509
Db 544 NMKIIASSAAVAVLATILMV-----YLYKR-----KGAKEYDKMDQPODYGKSTSR-N 592
Qy 510 DLMQEAEPFWDFAEENIEQDGETHWVWEGDY 541
Db 593 DEMLDPEASFWGEEK--RASHTTPVLMKPY 621

RESULT 7

A:apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain FCR 3)
C:Species: Plasmodium falciparum
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C:Accession: C44986
R:Thomas, A.W.; Water, A.P.; Carr, D.
Mol. Biochem. Parasitol. 42, 285-288, 1990
A:Title: Analysis of variation in Pf83, an erythrocytic merozoite vaccine candidate anti-
A:Reference number: A44986; MUID:91101665; PMID:2270110
A:Accession: C44986
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-622 <THO>
A:Cross-references: GB:M34554
C:Keywords: membrane protein; surface antigen

Query Match 14.0%; Score 410; DB 2; Length 622;
Best Local Similarity 26.0%; Pred. No. 5, 4e-24;
Matches 149; Conservative 80; Mismatches 214; Indels 130; Gaps 25;
Qy 41 GNPQANVEMKTFMERFNLTHHQSIGIYVDLGDKVEDGTLREPAGLCPIMKHIETLOQ 100
Db 107 GNPW-----TEYAKYDIEEYVHSGIRYDLGEDAVAGYQYRLPSGKCPVFGKGIILIN 160
Qy 101 PRLPLRNNFLEVPF-EKEYKQSGNPLPGGFNLNVTSPGQRISEPFM-----ELLEKNS 155
Db 161 SN-----TFLKPVATGNQDLKDGFAFP-----PTNPLISPMTLNMGDPFYKNE 206
Qy 156 NIKASTDLGRCAFAFKTVAMDKNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYYCS 215
Db 207 YVKNLDELTLCSRNA--MNPNDKSNKYKPAVYDDKDKCHILYIAQENNGPRYCN 264
Qy 216 VKGEPPDLTWYCFKPKR-SVTENHLLYGSAYVGEN-PAFISKCPNOALRGYRFGVWK 273
Db 265 -KQSKRSMWCFRPAKDKLFENY-----TYLSKNVVDNWEKVCPRKLENAKRGLWVD 317
Qy 274 GRCLDTLTDTVIERVESKAQCVMTFENDGVAADQPHYTP--LTSQASNDWMP----- 327

Db 318 GNCEDIPIHNER--SANDLFECKLVFELS--ASDQPRQYEQHLLDYEKIKEGFNKNNA 372
Qy 328 -----LHSDQPHSGVGRNRYGYVDTTGEKCALSDQVPCLVSDSAVSYT 376
Db 373 SMKSAFLPTGAFKADRYKSHGKGYMGNVNRKT--HKCEIFNVKPTCLINNSYIATTA 429
Qy 377 AGSLSEETPNFIIPSN-----PSVTPPTPETA 404
Db 430 LSHPIEVNNF--PCSLYKNEIMKEIERESKRKIKLNDNDGKNKIAPRIFISDKDSL 487
Qy 405 OCTADKFPDSFGACDVQACRQKTSVCGQIQSTS-----VDCTAD--EQNEGCS 452
Db 488 KCPCDPEMVSNSCRFPVCK-----CVERRAEVTSNNEVVKKEKYDEYADIDPEHKPTY 542
Qy 453 NTALI-----AGLAVGVLLALLGGCGYFPAKRLDRNKGYOAAHNEHFGSDRGARKRPS 508
Db 543 NMKIIASSAAVAVLATILMV-----YLYKR-----KGAKEYDKMDQPODYGKSTSR 591
Qy 509 DLMQEAEPFWDFAEENIEQDGETHWVWEGDY 541
Db 592 DEMLDPEASFWGEEK--RASHTTPVLMKPY 621

RESULT 8

A:apical membrane antigen 1 - Plasmodium chabaudi adami
C:Species: Plasmodium chabaudi adami
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Sep-1997
C:Accession: A44964
R:Marshall, V.M.; Peterson, M.G.; Lew, A.M.; Kemp, D.J.
Mol. Biochem. Parasitol. 37, 281-283, 1989
A:Title: Structure of the apical membrane antigen 1 (AMA-1) of Plasmodium chabaudi.
A:Reference number: A44964; MUID:90114335; PMID:2608101
A:Accession: A44964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-558 <MAR>
A:Cross-references: GB:M25248; NID:G160076; PID:G160077
C:Keywords: membrane protein; surface antigen

Query Match 13.6%; Score 398.5; DB 2; Length 558;
Best Local Similarity 25.8%; Pred. No. 3, 7e-23;
Matches 147; Conservative 86; Mismatches 202; Indels 135; Gaps 24;
Qy 42 NPPQANVEMKTFMERFNLTHHQSIGIYVDLGDKVEDGTLREPAGLCPIMKHIETLOP 101
Db 53 NPWE-----KMEKYDIEEYVHSGIRYDLGEDAVENQDYRIIPSGKCPVWGKGIITONS 106
Qy 102 DRLPLRNNFLEVPF-EKEYKQSGNPLPGGFNLNVTSPGQRISEPFM-----LLEKNSN 156
Db 107 -----KVSFLRVATGNQKVRBGLAF-----QTDVNIISPTIIDNLKMWKDHKE 152
Qy 157 IKASTDLRCAFAFKTVAMDKNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYYCSV 216
Db 153 ILALNDMSLCAGHA--SFVPGTNNVTAVRHRAVYDDKKNKCYILLYVAQENWGGRYCS- 209
Qy 217 KEPPDLTWYCFKPKRSVTENHLLYGSAYVGENDAFISKCPNOALRGYRFGVWKGRG 276
Db 210 NEEDENOPFCFTPEKK-DEYKNLSYLTGNLEED--WETSCPNKSIQNAKGVWVDGVC 265
Qy 277 LDY--TELDTVIERVESKAQCVMTFENDGVAADQPHY----- 314
Db 266 SEYQKKEVHND-----KTLLEGNOIVFNS--ASQPRQYEQHLLDYEKIKRGIYDRNGK 318
Qy 315 -----PLTSQASNDWMP-LHSDQPHSGVGRNRYGYVDTTGEKCALSDQVPCLV 367
Db 319 LTGELALPIGS-----YRADQVSKSGKGYMANVADKKTG--KCYIFNKKPTCLT 365
Qy 368 SLSAAVSYTAASLSSEETPNFIIPSN-----PSVTPPT 400
Db 366 NDKDFVATYALASL-EEGQESFPDIDYKKKIAEELKVNANRNNNGNDTIKPRIFISD 424

Qy 401 PETLOCTADKFPSPFCACVQAC---KROKTCVSGQIOSTSYDVTADPQNEGCS--- 453
Db 425 DKESINCEPCEPTLOLQSTCKEFCVNCVCKEKFQFIS-----ENNEVEIDEKFEKSEYSPIN 478
Qy 454 --NNTALAGLAVGVLLALLGGCGYFAKRDYKNGVQAHHNEHFGQDRACKKRPBDL 511
Db 479 ORMLIILITLITGAILMSLLI---FYFK---SNK--RGDDYDKMGQADYVKAQSRKDE 530
Qy 512 MQBAEPEFMDAEENIEQDGETHWVVEGDY 541
Db 531 MLDEPVSFWGDK---RASHTTPVLMKEPY 557

RESULT 9

microtubule-associated protein MAP 1B - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Feb-1997
C:Accession: A56577
R:Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G.
Eur. J. Cell Biol. 57, 66-74, 1992
A:Title: Identification of two distinct microtubule binding domains on recombinant rat M
A:Reference number: A56577; MUID:92347374; PMID:1639092
A:Accession: A56577
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2364 <ZAU>
A:Cross-references: GB:X60550
A:Experimental source: brain
A>Note: nucleotide sequence not given; conceptual translation not complete
C:Superfamily: microtubule-associated protein MAP1B

Query Match 4.3%; Score 127; DB 2; Length 2364;
Best Local Similarity 19.4%; Pred. No. 0.54; Mismatches 181; Indels 168; Gaps 21;
Matches .97; Conservative 55;

Qy 15 DCTIFASGLSSSTRSRESQTLASTSGNPFQANVEMKTFMERF--NLTHHQSGIYYDLG 72
Db 1654 DMSLYASLASBKVQSLGEEKLSPKSDISPLTPRESSPTSPGFSDSTGAKESYAAVQTS 1713
Qy 73 QDKVDDGLVREPAG---LCPIWKGHIELOQDRLPYRNPFLEDPTEKEYQSGNPL 127
Db 1714 SSPPIDAAA-AEPPGFSSMLFTMOHLLLSR-----DLTSSVEKONGGKT 1760
Qy 128 PGCFNLNFTVPSGORISP-----FPM 149
Db 1761 PGDNVAYQKPESTESDEEDYDSEHKTQAHVGVGYEKTERTKSPCSGYSYE 1820
Qy 150 LLEKNSNIKASTDLGRCAEFAKTV-----AMDKNKATK-----YRPFVYDSKK 195
Db 1821 TIEKTY--KTPEDGVCETETKTRPEEGGYSEISEKTRTRPEVSGTYEKTERRSR 1878
Qy 196 RL-----CHLYVSMQLM---EGKY---CSVKGEPPLTWYCF 228
Db 1879 LDDISNGYDDEGHTLGDGYSYETETKITSFPSESYSYETTKTRSPPTSAVCY 1938
Qy 229 KPRKSVTENHLLIYSAVGENPDPAFISKCPNQLRGYRGVWKGRCLDYTELDTVIE 288
Db 1939 ETMEKITKTPQ--ASTYSYETSD-----RC--YTPERKSPSE 1971
Qy 289 RVESKAOQWKTENDVASDQPHYPLTQASWN--DMW---PLHQSDQF--HSGVG 340
Db 1972 ARQGVDDCLVSSCE---FKHPKTELSPFINPNLEWFAGEPTESSEKPLTQSGAP 2026
Qy 341 RNYGFYVDDTTEGKCALSDQVPCLVSDA-----AVSYTAGLSSETP 386
Db 2027 PPSG-----GKQOGRQCDPTPTSVSESAPQOTSDVPEETECPSTADANLDEDE 2079
Qy 387 NFIIPSNPSTV-----PPTP 401
Db 2080 SETIPTDKTYTYKMDPPAP 2100

RESULT 10

506017
neuxxin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Sep-1990 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: S06017
R:Rientz, A.; Grennahl, G.; Hermans-Borgmeyer, I.; Kirsch, J.; Litaauer, U.Z.; Prior
EMBO J. 8, 2879-2888, 1989
A:Title: Neuxxin, a novel putative structural protein of the rat central nervous system
A:Reference number: S06017; MUID:9005871; PMID:2555150
A:Accession: S06017
A:Molecule type: mRNA
A:Residues: 1-863 <RIE>
A:Cross-references: EMBL:X16623; NID:957826; PIDN:CA434620.1; PID:957827
A>Note: the authors translated the codon GCA for residue 723 as His
C:Keywords: brain; spinal cord; tandem repeat; tubulin binding
F:258-461/Region: 17-residue repeats
F:628-741/Region: arginine/lysine-rich

Query Match 4.3%; Score 125; DB 2; Length 863;
Best Local Similarity 19.2%; Pred. No. 0.18; Mismatches 181; Indels 168; Gaps 21;
Matches .96; Conservative 56;

Qy 15 DCTIFASGLSSSTRSRESQTLASTSGNPFQANVEMKTFMERF--NLTHHQSGIYYDLG 72
Db 153 DMSLYASLASBKVQSLGEEKLSPKSDISPLTPRESSPTSPGFSDSTGAKESYAAVQTS 212
Qy 73 QDKVDDGLVREPAG---LCPIWKGHIELOQDRLPYRNPFLEDPTEKEYQSGNPL 127
Db 213 SSPPIDAAA-AEPPGFSSMLFTMOHLLLSR-----DLTSSVEKONGGKT 259
Qy 128 PGCFNLNFTVPSGORISP-----FPM 149
Db 260 PGDNVAYQKPESTESDEEDYDSEHKTQAHVGVGYEKTERTKSPCSGYSYE 319
Qy 150 LLEKNSNIKASTDLGRCAEFAKTV-----AMDKNKATK-----YRPFVYDSKK 195
Db 320 TIEKTY--KTPEDGVCETETKTRPEEGGYSEISEKTRTRPEVSGTYEKTERRSR 377
Qy 196 RL-----CHLYVSMQLM---EGKY---CSVKGEPPLTWYCF 228
Db 378 LDDISNGYDDEGHTLGDGYSYETETKITSFPSESYSYETTKTRSPPTSAVCY 437
Qy 229 KPRKSVTENHLLIYSAVGENPDPAFISKCPNQLRGYRGVWKGRCLDYTELDTVIE 288
Db 438 ETMEKITKTPQ--ASTYSYETSD-----RC--YTPERKSPSE 470
Qy 289 RVESKAOQWKTENDVASDQPHYPLTQASWN--DMW---PLHQSDQF--HSGVG 340
Db 471 ARQGVDDCLVSSCE---FKHPKTELSPFINPNLEWFAGEPTESSEKPLTQSGAP 525
Qy 341 RNYGFYVDDTTEGKCALSDQVPCLVSDA-----AVSYTAGLSSETP 386
Db 526 PPSG-----GKQOGRQCDPTPTSVSESAPQOTSDVPEETECPSTADANLDEDE 578
Qy 387 NFIIPSNPSTV-----PPTP 401
Db 579 SETIPTDKTYTYKMDPPAP 599

RESULT 11

709127
probable erythrocyte-binding protein MABR - Plasmodium yoelii
C:Species: Plasmodium yoelii
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T09127
R:Kapre, S.H.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998
A:Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
A:Reference number: Z16577; MUID:98115903; PMID:9448314
A:Accession: T09127
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

A:Residues: 1-1701 <KAP>
 A:Cross-references: EMBL:AF031886; NID:G2947227; PID:G2947228
 A:Experimental source: subspecies yeoelli; strain YM
 C:Genetics:
 A:Gene: maebl
 A:introns: 62/1; 1648/1; 1674/2; 1697/1
 C:Keywords: alternative splicing; cell binding; erythrocyte invasion

Query Match 4.1%; Score 120; DB 2; Length 1701;
 Best Local Similarity 18.8%; Pred. No. 1.2;
 Matches 87; Conservative 52; Mismatches 151; Indels 172; Gaps 21;

```

QY 34 TLSTASGNPFOANEMKTFMERFNLTHHH-----QSGIYVDLGQDKEVD--- 78
DB 18 TFSIAIDNP-----QEDFMDRFDLNNHVNIAIKTNGSLAQGNLKFPIYEDNINSLK 71
QY 79 -----GTYREPAAGLCPIMGKH-----I 96
DB 72 NSLENARLCPNNEKNIVR---GSCPDYGTFTSMDLKDDEYSEDFLNEISLGLNKLII 128
QY 97 ELIQQDRL-----PYRNNFLEDVPTKEK-----KQSGNPLRGGFNL 133
DB 129 DVEIPIVNNISGLMAYOGLFANCPYDKNHVNIDIKNEKEDMCFDKFYSNKQD----- 178
QY 134 NVTPTSGORISPPMELLEKNINIKR---STDLGRCAEPFAFTVAMDKNNKATKRY--- 187
DB 179 -----ISTRIKKYP--LISKTYTPGSHGLGRLGNTPEPLHIVPIEYTRTKKRYPTL 231
QY 188 -----PFVYDSKKRLCHILYVSMQLMGKKYCSVK 217
DB 222 VETLEDCSIYSHCIQCPDRDFDNKCFRDLPAFPHNKTKECIIIGTH-----EKKTTNCG 287
QY 218 GEPDPLTWYCFPRKSVTNNHLLIYGSAYVGENPDAFISKC-PNQNLRGRRGV--WKKG 274
DB 288 SONSRRNNGRCFSSIKK-EKQKDMWTYASSEL--RPD-YETKCPRPYPLNNSFGYFNYNTG 343
QY 275 RCLADYTELDTYIERVSKAQCWVKTFENDGVASDOPHTYPLTQASXNDMMPLHOSDOP 334
DB 344 NCESPTKLD---NSYISNECEIEKLF-NFNYNANEPE--EKKNNTLKGWVVLGNKQNTL 397
QY 335 HSGGVGRNYGFYVDTTGEKCALSDQVPCLVSDSAVSYT 376
DB 398 NS-----MNDLGVCALLKEKPTCVLKQNYYSFT 426

```

RESULT 12

ORMSP1

microtubule-associated protein MAP1B - mouse
 N:Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protei

C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000
 C:Accession: S07549; S44387; A33645
 R:Noble, M.; Lewis, S.A.; Cowan, N.J.
 J. Cell Biol. 109, 3367-3376, 1989
 A:Title: The microtubule binding domain of microtubule-associated protein MAP1B contains
 A:Reference number: A33645; MUID:90094559; PMID:2480963
 A:Accession: S07549
 A:Accession: S07549
 A:Molecule type: mRNA
 A:Residues: 1-2464 <NOB>
 A:Cross-references: EMBL:X51396; NID:G52999; PIDN:CAA35761.1; PID:G53000
 R:Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.
 Arch. Biochem. Biophys. 310, 428-432, 1994
 A:Title: Binding of heat-shock protein 70 (hsp70) to tubulin.
 A:Reference number: S44387; MUID:94234720; PMID:8179328
 A:Accession: S44387
 A:Accession: S44387
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 653-663; 'IC' <SAN>
 C:Superfamily: microtubule-associated protein MAP1B
 C:Keywords: microtubule binding; phosphoprotein; tandem repeat
 F:589-786/Domain: microtubule binding #status experimental <MTB>
 F:589-592, 639-642, 649-652, 655-658, 660-663, 668-671, 674-677, 679-682, 683-686, 687-690, 691-69
 R-K-E/D-X)

F:1861-2064/Region: 17-residue repeats
 F:91, 116, 351, 888, 1124, 1153, 1168, 1208, 1662, 1877, 1918, 2003, 2030, 2054, 2083/Binding site: ph
 F:147, 969, 1336, 1563, 1563, 1702, 1708, 1990, 2057, 2063, 2419/Binding site: phosphate (Thr) (co
 F:1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.1%; Score 120; DB 1; Length 2464;
 Best Local Similarity 19.3%; Pred. No. 2;
 Matches 98; Conservative 53; Mismatches 174; Indels 184; Gaps 22;

```

QY 15 DCTIFASGLSSSTRRESQTSASTSGNPFOANEMKTFMERFN-----LTHHQ 64
DB 1754 EMLVYASLASRKYVSLSEKLSPKSDISPLTPRESSPLYSQGFSDSAKETAHAHQAS 1813
QY 65 SGIVYDLDQDKEVDQTLVREPAG-----LCPIWGCHIELQOPDLRYNNFLEDVPTKE 119
DB 1814 SSPPIDAT-----AEPIYGRSSMLPDTMCHHLNLR-----DLTSSV 1852
QY 120 YKQGNPLPGGFNLVFTPSGORISP----- 145
DB 1853 EKDSGKTPGDFENVAYQKPEANAGSPDEEDYDYESQEKTRTHDVVRYYEKTERTKISP 1912
QY 146 -----FPMELLEKNINIKASTDLGRCAEPFAFTV-----AMDKNKATK-----YRY 187
DB 1913 CDSGYSTETIEKTY--KTPEDGGYTCETETKTRTPREGYSYELSEKTRTPREVSTY 1970
QY 188 PFVYDSKKRL-----CHILYVSMQLM-----EGKY-----CSVK--GEP 220
DB 1971 EXTENSRRLDDISNGYDTEDEGHTLADCSYVTEKTRISFPSEBSYVETSKTRIS 2030
QY 221 PDLTWYCFPRKSVTNNHLLIYGSAYVGENPDAFISKC-PNQNLRGRRGV--WKKG 280
DB 2031 PDSAYCYETMEKTKTPQ---ASTYSYETSD-----RC--YT 2063
QY 281 ELTDVIERVSKAQCWVKTFENDGVASDOPHTYPLTQASXNDMMPLHOSDOP 334
DB 2064 TEKSPSARQDQVPCLVSSCE-----FKHPETELSPFINPFLWFAGEPTESKXP 2118
QY 335 -HSGGVGRNYGFYVDTTGEKCALSDQVPCLVSDSAVSYTAA 378
DB 2119 LTQSGAAPPSG-----GKQGRQCBETPTPTSSEAPSGTDSVPEPTEECSTIND 2171
QY 379 GSLSEETPNFIIPNSPSVT-----PTTP 401
DB 2172 ANIDSEDESERIPTDKVTYKMDPPAP 2200

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RESULT 13

T09129

probable erythrocyte-binding protein MAEBL - Plasmodium berghei (fragment)
 C:Species: Plasmodium berghei

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: T09129
 R:Kappe, S.H.; I. Noe, A.R.; Frazer, T.S.; Blair, P.L.; Adams, J.H.
 Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998
 A:Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
 A:Reference number: Z16577; MUID:98115903; PMID:9448314
 A:Accession: T09129

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-993 <KAP>
 A:Cross-references: EMBL:AF031887; NID:G2947229; PIDN:AA005367.1; PID:G2947230
 A:Experimental source: strain ANKA
 C:Genetics:
 A:Gene: maebl
 A:introns: 62/1

C:Keywords: alternative splicing; cell binding; erythrocyte invasion; malaria

Query Match 3.8%; Score 112; DB 2; Length 993;
 Best Local Similarity 20.4%; Pred. No. 2.3; Indels 170; Gaps 24;
 Matches 91; Conservative 49; Mismatches 135;
 QY 53 FMERNLTHHH-----QSG-----IY-----VDLGQDKEVDGTLV 82

Db 31 FMDRFDLNNHVNKWTNLSGLKGDFFKFDIYDEDNINSKENTLESQALCSNHNEDG-1Y 89
QY 83 REPAGLCPIWGRH-----TELQOPDL-----104
Db 90 R---GSCPDYGTPEMNLDKOEYNEDFLNEISLGLNKKLLIDLEIPVMSGLAYQGLF 146
QY 105 ---PYRNNFLBVDVPEKEY-----KOS-----GNPLFGFNL 133
Db 147 ANCPDKHNDIKKEKEYDMCFKRYNNKQINSTRICKOLLISKYTFYSGSLGRLGSLG 206
QY 134 NFVTPSGGRISPPFMELEKNSNIKA-----STDGRCHEFAFKIVA 175
Db 207 N-----TEYFPHITNPTEINTYTKQMRPKVLETLEDSCISYSHCIGPCFD-----250
QY 176 MDKNKATKRYRYPFYVDSKKRLCHILYVSMQLEKSKYCVGKEPPDLTWYCFKPKRSVT 235
Db 251 RDPDKRCR-DLPVAFNFKTECIIIGH---EKKTKNCSNDSRRNNGCFSSIKR-E 304
QY 236 ENHHLIYSANVGENPDFAFISKC-PNQLRGYRGV-WKGRCLDYELTD-TVIERVE 291
Db 305 KGKMTYVSSFL-RPD-YETKCPRPYPLNNSEFGYFNNYTKCESPTKYDNTVI-----357
QY 292 SKAOCWVTFENPDGVAHQPHYPLTSGASNDMMPLHQSDQPHSGGVGRNYGVYVDTT 351
Db 358 SPNOIEKLF-SFNYANENPD-QKRSNYLWGVWLENKQNKLS-----MN 401
QY 352 GEGKALSDQVDDCLVSDAAVSYT 376
Db 402 DLGVCVLKERPTCVLKKQNYYSFT 426

RESULT 14

probable oligopeptide-binding lipoprotein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
C:Accession: J34757
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z21556
A:Accession: J34757
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-600 <MNU>
A:Cross-references: EMBL:AL031184; PIDN:CAA20180.1; GSPDB:GN00070; SCOEDB:SC2A11.11
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC2A11.11
C:Superfamily: dipeptide transport protein

Query Match 3.8%; Score 111; DB 2; Length 600;
Best local similarity 21.4%; Pred. No. 1.4; Matches 59; Mismatches 99; Indels 80; Gaps 14;
Db 15 DCTIFASGLSSSTRSRESQTLASTSGNPFQANVEMKT---MERFNLTHHSGIYVDL 71
Db 305 DIDLQGTGLSPQGRITLAKHKANLD-NPVSGYIRYAFQNVKPFQDNIHCKKAVLY---360
QY 72 GQDEVDGTLYRPAAGLCPIWGRHTELQOPDLRYRNNFLBVDVPEKEYKOSGNPLFG-130
Db 361 GAD-----HVSLO-----TARGGVAGGD 379
QY 131 FNLNFTPS-----GORISPPFMELEKNSNI-KASTDLGRCAE-FAKTVAMDKNKAT 183
Db 380 IGTMLPFAVPSGQKIDPIEMSGANKKVEAKELKACNDPNGKTTIYAVRNKPV 439
QY 184 KY-RYPVYDSKKRLCHILYVSMQLEKSKYCVGKEPPDLTWYCFKPKRSVTENHLY 242
Db 440 EVATAESLQASLKKVG-IDVEIDQYDSQYASVIGSSNV-----QKKG-----Y 483
QY 243 GSAVGENPDFAFISCKPQALRGYRFVWKKGRCLD 278
Db 484 GIITMGWGPDE-----PSVOGYGLPLMHSYILD 512

RESULT 15

A48569
antigen Eml100 - Elmeria maxima
C:Species: Elmeria maxima
C>Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C:Accession: A48569
R:Parmentier, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Biochem. Parasitol. 57, 171-174, 1993
A>Title: Sequence of a major Elmeria maxima antigen homologous to the Elmeria tenella m...
A:Reference number: A48569; MUID:93149203; PMID:842611
A:Accession: A48569
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-724 <PAS>
A:Cross-references: GB:M9058; NID:g158890; PID:g158891
A>Note: sequence extracted from NCBI backbone (NCBI:123776, NCBI:123777)
C:Superfamily: thrombospondin type 1 repeat homology; von Willebrand factor type A repeat
F:45-218/Domain: von Willebrand factor type A repeat homology <VWA2>
F:238-286/Domain: thrombospondin type 1 repeat homology <THR1>
F:309-371/Domain: thrombospondin type 1 repeat homology <THR2>
F:372-432/Domain: thrombospondin type 1 repeat homology <THR3>
F:433-493/Domain: thrombospondin type 1 repeat homology <THR4>
F:494-556/Domain: thrombospondin type 1 repeat homology <THR5>
F:560-610/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 3.7%; Score 109; DB 2; Length 724;
Best local similarity 21.0%; Pred. No. 2.6; Matches 73; Conservative 36; Mismatches 123; Indels 116; Gaps 17;

QY 211 KKYCVKGEF-----PDLTWYC-----FKPKRSVTENHLYGSAY-----V 247
Db 367 KSPPEVQOQPGPWSMDSCATCGGTRRYRREYRPGELFGQTLQAGLDVRENDTC 426
QY 248 GENPDATISKCPNQLRGYRGVWKKGRCLDYELTDVIERV-----ESKAOCWTF 301
Db 427 NENP-----CPVDA-----TCGWTEFSD--CSRYCGCGTKERRRRPWLDNA 466
QY 302 ENDGVAHQPHYPLTJGQ-----ASNDMMPLHQSDQPHSGGVGRNYGVYVDTT 347
Db 467 QFGGRSCSQHQPEGPTSSVECNHPCPVDEYVGEWEMGPC--SEQ-----CGRGROFRY 519
QY 348 ----VDTTGEKCALSOQVPDCLVSDAAVSYTAAAGSLSEETPNFIIPNSVTPPET 403
Db 520 RGPLQOAMRGKTIHQ-----NAGVEEQKILKVEBPCNDVPCGCTLPFTWT 571
QY 404 ALQ-CTADKPEPSGACDV--QACK--ROKTSQ-----431
Db 572 ACESCSGTRFDSVAVFYDDRCQNPTHEESCDAVCEESASGGVGGAGAGGGGG 631
QY 432 -VGQIOTSTVDCIADQNEGSGNTALIAGLAVGVLLALLGGGCTF 478
Db 632 SAGEGSGNAGPGEDEESKGFPTAAVAGVAGVLAIA-AGAGAFY 678

RESULT 16

hypochemical protein KIAA0527 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C:Accession: T00073
R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1998
A>Title: Prediction of the coding sequences of unidentified human genes. IX. The complet...
A:Reference number: Z14086; MUID:98290545; PMID:9628581
A:Accession: T00073
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-768 <NAG>
A:Cross-references: EMBL:AB011099; NID:g3043577; PIDN:BAA25453.1; PID:g3043578
A:Experimental source: brain; clone HG2246
C:Genetics:

A>Note: KIA0527

Query Match 3.7%; Score 108; DB 2; Length 768;
 Best Local Similarity 22.0%; Pred. No. 3.3;
 Matches 105; Conservative 38; Mismatches 160; Indels 174; Gaps 23;

QY 97 ELQGDRLPY-----RNNFLD-----VPTKEKYKQSGNPLPGGFNLNFVPSGGRISP----- 145
 DB 382 EAPKQDRIVSISVSGENIARDKVFPVT-----TSSP-GAGSSVPADSPGSHLLQKHLFW 434
 QY 146 FPMELLEKNINIKASTDLGRCAEFAKTVAMDKNKATKYRPFYVDSKSKRLCHILYYSM 205
 DB 435 FPAEAFHKRGLEKEVD-----DITK----- 455
 QY 206 QLMESKRYCSYK--GEPPDLTWYCFKPKRSVTENHHLIYSA-----YGENP----D 252
 DB 456 QFSAGDNHSGVTLVNGEP-----ETKVLYGNTDPSGPFVSKDNKSKAD 499
 QY 253 AFISCKPQALRGYF--GVWKGRCLDYTELTDVIVIEVESKACQWTFENDGVASDQ 310
 DB 500 PIVSSSDSSWLDGYFVTDGAMRK-----TEABEEDGDRGDSVGLDENLVLPDQ 550
 QY 311 P-----HTYPLTSQASWMDWMPPLHQSQDPHSGGVGRNYGYVYDT 350
 DB 551 PIVLVKKPKKSTLTPSEGMTSSVLPQMLDVEALALRPVNASFEGIGDGDILTKYST 610
 QY 351 -----TSGKCALSDQVPCDCLVSDSAVSYTAAGSLF-----ETPNFIISNPSV 396
 DB 611 LPMREITE-----SPMATLSYEILSTLEILTNTVTKQPHNIPSTIMAT 656
 QY 397 TPPTPETALQCTADKFP-----DSFGACQVQACKQKTSQVCG--QIGSTVDTCADEON 449
 DB 657 TOPVEYTVPEIQDSEFVYLSDFG-----QEGCGPASEELHATLESCTGCD--- 704
 QY 450 ECG--SNTALLAGLVGVLLALLGGCYFAKRLDRNK-----GVQAHHHE 496
 DB 705 GCGPGRGVATITVTLCLLLLAGVGVWGRKQKHSSVYKLVNGQRQARHYNQ 761

RESULT 17

138869 transcritpion.factor NFX1 [imported] - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 02-Sep-2000
 C:Accession: I38869
 R:Song, Z.; Krishna, S.; Thanos, D.; Strominger, J.L.; Ono, S.J.
 J. Exp. Med. 180, 1763-1774, 1994
 A:Title: A novel cysteine-rich sequence-specific DNA-binding protein interacts with the
 n and functions as a transcriptional repressor.
 A:Reference number: I38869; MID:95053707; PMID:7964459
 A:Accession: I38869
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1104 <RES>
 A:Superfamily: RING finger homology
 C:Superfamily: RING finger homology
 F:338-398/Domain: RING finger homology <RRN>

Query Match 3.7%; Score 107.5; DB 2; Length 1104;
 Best Local Similarity 19.7%; Pred. No. 6.1;
 Matches 103; Conservative 61; Mismatches 159; Indels 199; Gaps 29;

QY 85 PGLGCPWKGKHELQOPDLRPLPRNNFLDYPTKEKYKQSGNPLPGGFNLNFVPSGGRIS 144
 DB 579 PGGQFPL-SQLLELSSS-----RKTCDMPVPCG--KVGCKPLPG-SLDFHTCEKICH 630
 QY 145 PPMELLEKNINIKASTDLGRCAEFAKTVAMD-----KNNKATKYRPFVYD---SKRL 197
 DB 631 EBGDCGVSRTSVISC-----RC--SFRTELPCTSLKSDAT-----PMCKRCKKKL 677
 QY 198 CHILYVSMQLMGKRYCSYKGEPPDLTWYCFKPKRSVTENHHLIYSAVYGENPDAFISK 257
 DB 678 C-----GRHKCN-----IC-----CVDKEH-----K 694

QY 258 CPNALNGREGVWK-----KGRCLDYTELTDVIVIEVESKACQWTFENDGVASDQ 311
 DB 695 CPLNGGRRLRGHLRCEBPCRHNC-----QTCWQASFDE----- 729

QY 312 HTYPLTSQASWMDWMP-----LHSDQD--HSGG----- 338
 DB 730 ----LTCGASVYIPRPGCTRPPECTQTGARHNECHPYVYHSHSEKPCPTFLTK 785
 QY 339 --VGR-----NYGYVYDT-----GEGKALSDQVPCDCLVSDSAVSYTAAGS 380
 DB 786 WCMGKHEFRSNI PCHLVDISGLPCSATLPCGMKCRCLCHKGBCLVDE----- 834
 QY 381 LSEETPNFIISNPSVPTPETALQCTADKFPDSFGACDVQACK-RQKTSQVSGQIOST 439
 DB 835 -----PCQPCCTPRADCGHPCAPCHTSS--PCPYTACKAKVELQCEGR-RKE 881
 QY 440 SVDCTADEQNECGSNTALLAGLVGVLLALLGGCYFAKRLDRNKGVQAHHHEFQS 499
 DB 882 MVIC-----SEASVYQRIAIMASAKITDQLGGSVEISKLITK-KEVQARLECBEC 935
 QY 500 DRGARKKRPD--LMQEAEP-----SFWEAENEIED 530
 DB 936 SALERKRLAEAFHISEDSPFNIRSSGSKFSDLKEDARD 977

RESULT 18

748727 retinoblastoma binding protein 2 related protein [imported] - Neurospora crassa (fragment)
 N:Alternate names: protein 8D4.10
 C:Species: Neurospora crassa
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 03-Nov-2000
 C:Accession: T48727
 R:Schultz, U.; Aigen, V.; Hohnes, J.; Brandt, P.; Farman, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24541
 A:Accession: T48727
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1009 <SCH>
 A:Cross-references: EMBL:AL353819; GSPDB:GN00112; NCSP:8D4.10
 A:Experimental source: cosmid contig 8D4; strain 74
 C:Genetics:
 A:Gene: NCSP:8D4.10
 A:Map position: 2
 A:Insertions: 153/2; 480/1
 C:Superfamily: human retinoblastoma binding protein 2

Query Match 3.7%; Score 107; DB 2; Length 1009;
 Best Local Similarity 19.4%; Pred. No. 5.9;
 Matches 111; Conservative 97; Mismatches 191; Indels 172; Gaps 29;

QY 18 IFASGLSSSTNS-RESQTLASSTSGNPQAVENKTEFRNLTHHOSGIYDLGQDK 76
 DB 13 VAAAGTSNNASARASPVVTHSS-----NGSKTAAVNSNGVHPPTSQLPLSPKSEBP 66
 QY 77 VD-GLYEPAGLCIWKIKHELQOPDLRPLPRNNFLDYPTKEKYKQSGNPLPGGF 131
 DB 67 IDLNSVER-----QOPTACKEPSSKKRPHGLEBAPSYCPTEEWK----- 109
 QY 132 NLNFYTPSGORISPPMELLEKNINIKASTDLGRCAEFAKTVAMDKNKATKYR 187
 DB 110 -----PFYIRKIT--PASKRGICKIIPRESWMDPAIDTEVRSIARQ 152
 QY 188 PFVDSKRLCHILYVSMQLMGKRYCSYKGEPPDLTWYCFKPKRSVTENHHLIYSAV 247
 DB 153 PNFHFRTRQ-----ELNSIEGSSGRANIN-----YDALQFHRQHGNNLTRLPV 197
 QY 248 GENP-DATISCPNALGY-----RFGVKK-GRCLDYT-ELTDVIVIEVESKACQWTF 300
 DB 198 DKRPDLRLKKAIVARSGFDVCLKKMAELGRDLGSGKMSLSLSLKSQYKMLCP 257
 QY 301 FEN-----DGVASDQPTY--PLTSQASWMDWMPLEHSD--QPHSGGVGRNYGYVYDT 351

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Db      258 YEDYIRVAKPGVHQOLEYGGPLTPSPAPS---PMKSKSNMAGTPPDLGSESPSRPTPA 314
Oy      352 GEGKCALSDQVDPCLVSDSAAY-----SYTAAGSLSEETPNFIIPNSV 396
Db      315 VNGHAKDSDR--DYMTDAPSPAPVPSGPTAINTGFTAINSGFTSINRLAPASAI 372
Oy      397 TP-----PTPETALQCTADKFPDSFGACDVQACKRQKTSVCGGQISTSVDTAD----- 446
Db      373 TPLSSAKNTPEVR-----PSAAGS---SELKQ-----LSPSTDSAKKE 410
Oy      447 -----EQNECGSNLTALINGLAVGVLLALGCGCYPAKRLDRKNGVQAHHHEFGSDR 501
Db      411 SSVDDKDEAGSR-----SKRLKKGR-----SYHFPHLQAYQ 443
Oy      502 GARKK-----RPSDLMOEAEP-----FWDEAE 525
Db      444 GSRAEACGAARSLYCEARTSPHLFWNLCSB 474

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RESULT 19
A:Accession: A35560
Lysosomal membrane glycoprotein 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Aug-1999
C:Accession: A35560
R:Cha, Y.; Holland, S.M.; August, J.T.
J. Biol. Chem. 265, 5008-5013, 1990
A:Title: The cDNA sequence of mouse LAMP-2. Evidence for two classes of lysosomal membra
A:Reference number: A35560; MUID:90202978; PMID:231880
A:Accession: A35560
A:Status: not compared with conceptual translation
A:Residues: 1-415 <CHA>
A:Residues: 1-415 <CHA>
A:Cross-references: GB:J05287; NID:g198708; PIDN:AAA39412.1; PID:g293693
C:Superfamily: lysosome-associated membrane protein
C:Keywords: glycoprotein; membrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-415/Product: lysosomal membrane glycoprotein 2 #status predicted <MAT>

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Query Match      3.6%; Score 106; DB 2; Length 415;
Best Local Similarity 21.1%; Pred. No. 2;
Matches 71; Conservative 24; Mismatches 91; Indels 150; Gaps 15;
Oy      277 LDYTELTIVIERVESKAQCWKTENDGVASD-----QPHYPLTSGASWMDWPLHQ 330
Db      112 LSYNTSDTVFPGAAKGVHTVKNPKVPLDVIFKNSVLTNLTPLVV--QKTMGHL 169
Oy      331 SDQPHSGGVGRNYGFYVDTTGEKCALSDQVDPCLVSDSAVSYTAAGSLSEETPNEFI 390
Db      170 QAFVQNGTVSKN-----EQVCE-EDQPTTV-----APIHTTAPS-----TTTLT 210
Oy      391 P-SNPSVTP-PTPEPA-----LOCTADKFPDSF-----GAC 419
Db      211 PTPPTPTPTPTPTVGNYSIRNGNTTCLLATWGLQLTITEKVPPIFINPATNTFTSC 270
Oy      420 DVQA----- 423
Db      271 QPQSAQLRLANSQIKYLDLIRAVKNEKRFYKEVNVVTYLANGSAFNISKNLSFWAPL 330
Oy      424 -----CKRQKTSVCGGQIQ-----STVDTCTADEQNECGSNLTALING 460
Db      331 GSSVYCNKEQVLSVBARQINTFNLKVPFMTVKGQSTADCSADBNPL--VPLAVG 387
Oy      461 LAVGULLLALLGGCGYPAKLDKRYQAAHHEHE 496
Db      388 AALGGVLLVL--AYPI-----GLKRRHTYE 413

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RESULT 20
T13931
Projectin - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster

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C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13931
R:Daley, J.; Southgate, R.; Ayne-Southgate, A.
J. Mol. Biol. 279, 201-210, 1998
A:Title: Structure of the Drosophila projectin protein: isoforms and implication for pro
A:Reference number: Z17815; MUID:96300333; PMID:9636710
A:Accession: T13931
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6658 <DAL>
A:Cross-references: EMBL:AF047475; NID:g3337430; PID:g3337431; PIDN:AA27550.1
C:Genetics:
A:Gene: projectin
A:Cross-references: FlyBase:FBgn0005666
A:Map position: 4
A:Note: intron positions not resolved (incomplete sequence)
C:Keywords: muscle

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Query Match      3.6%; Score 104.5; DB 2; Length 6658;
Best Local Similarity 19.0%; Pred. No. 1.4e+02;
Matches 76; Conservative 49; Mismatches 123; Indels 151; Gaps 20;
Oy      124 GNPLPGENLNFVTPSGQRISSPPEMLLEKNSNIKASTDLGRCA--EPAFTVAMDKNK 181
Db      2340 GSPIQG-----YIVEVDKYSPLWEKALETWSPTPTAVQGLIGNEYQFVALNKGNTL 2394
Oy      182 ATKRYRPFVYDSKRLHLIYV-----SMQWLEG---KKYCVKGP-PDLTWYC 227
Db      2395 SEBDSKIFAKKR-----YIAPKIDRLRNLTSSGTLKUDANITGQPAKRVW-- 2447
Oy      228 FKPRKVTENHLLIYGSAYVGENPDAF---ISKCPNALRG----- 265
Db      2448 -----KLSNHLQSGKNVITETPDYTKLVIRPQGTDSSEVLVTAINTSGKSVLVNV 2501
Oy      266 -----YRFGV---WKK-----GRCLDYELTDVIERVESQAQCWK 299
Db      2502 VITDKPSPNGPLQISDVHKEGCHLKKWRPSHDGTPIEYFQ-----IDKLEPTGCMIP 2556
Oy      300 TFEHDVGAADQPHRYPLTQSAWMDWPLHQSDQPHSGGVGRNYGFYVDTTGEKCAL 359
Db      2557 SCRSTAQVDVTGSP-----GNEYKFRVSAVNAEGE----- 2588
Oy      360 DQVDPCLVSDSAVSYTAAGSLSEETPNFIIPSNP-----SVTPPTPE-- 402
Db      2589 ---SQPLVGESIVA-----RNP-FDEPKRENLKATDMDKHVDLAWTPFVIDCG 2635
Oy      403 TALQCTADKFPDSFG---ACDVQA--CKRQKTSVCGGQ 435
Db      2636 SPISCIYIERKQDKYKWERALDVADQCKATIPDLVEGQ 2674

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RESULT 21
A24571
protein-tyrosine kinase (EC 2.7.1.112). erbB2 precursor - human
N:Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB
C:Species: Homo sapiens (man)
C:Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C:Accession: A24571; A25491; A41488; B44188; I55509; I57622
R:Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
Nature 319, 230-234, 1986
A:Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f
A:Reference number: A24571; MUID:86118663; PMID:3003577
A:Accession: A24571
A:Molecule type: mRNA
A:Residues: 1-1255 <YAM>
A:Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
R:Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A:Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm
A:Reference number: A25491; MUID:86016729; PMID:2995967
A:Accession: A25491
A:Molecule type: DNA
A:Residues: 737-1031 <SEM>

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Db 266 ASATVLETRTPAASSTWATSSSHQSPSADSOAEELSKQVAKDDPEFVVSNTANSDP 325
 Qy 462 AVGGTLTLLALGGCGYFAKRLD-----RNKGVAHHEHEFQSDRGARKRP----- 508
 Db 326 ASSSKPAKPLTDLNRAFAQNLDPQKPKSQGSEISEQEBDYDAESDEHSPSYSTHEP 385
 Qy 509 -SDLMQEAEPSPFWEAEENIEQDGE 532
 Db 386 ESEPEDDQDEPESEKDEKNDKVEEED 410

RESULT 23

569063

probable membrane protein YPR075c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein P9513.9

C:Species: Saccharomyces cerevisiae

C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 06-Feb-1998

C:Accession: S69063

R:Couch, J.

A:Submitted to the EMBL Data Library, March 1996

A:Description: The sequence of S. cerevisiae cosmid 9513.

A:Reference number: S69057

A:Accession: S69063

A:Molecule type: DNA

A:Residues: 1-360 <COO>

A:Cross-references: EMBL:U51033; NID:g1230676; PID:g1230683; MIPS:YPR075c

C:Genetics:

A:Gene: SGD:OPY2

A:Cross-references: SGD:S0006279; MIPS:YPR075c

A:Map position: 16R

A:Keywords: transmembrane protein

F:96-112/Domain: transmembrane #status predicted <TM>

Query Match 3.5%; Score 103; DB 2; Length 360;

Best Local Similarity 23.4%; Pred. No. 2.8;

Matches 48; Conservative 23; Mismatches 58; Indels 76; Gaps 10;

Qy 350 TTGGKCALSDQVDPCLVSDSAVSYTAAGSLSEETPFIIIPSNPVTPTPTALQCTA 409
 Db 24 TRGSDGCVVCSTASCPV--CASGEYCVMTSL-----TC 55
 Qy 410 DKFPDSFQACDVOAKCRQKTSQVGGQLOSTSVDTADQNECGSNTALIAGLA--YGV 466
 Db 56 DKCSTY-----CAKQSDS---QLSSLSSSSSSSSSSNSNETSLIVFTVIGVGA 104
 Qy 467 LLLALLGGCGCYFA-KRLDRNGVQAHHHEHEFQSDRGARKRP-PSDLMQEAEPSPFWEAE- 524
 Db 105 MLIALV--ALYFINKRWKPK-----RQKNKALKLEBASQSYGNEBEY 145
 Qy 525 -----ENIEODG-----ETHW 536
 Db 146 FDEDDDDDEDDGGMKDESHTL 170

RESULT 24

T23024

hypothetical protein H02112.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T23024

R:McLay, K.

A:Submitted to the EMBL Data Library, March 1997

A:Reference number: Z19656

A:Accession: T23024

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1332 <MTL>

A:Cross-references: EMBL:292789; PIDN:CAB07215.1; GSPDB:GN00022; CESP:H02112.1

C:Genetics:

A:Gene: CESP:H02112.1

A:Map position: 4

A:Introns: 12/3; 29/1; 60/3; 246/1; 449/1; 756/1; 849/1; 961/1; 1103/3; 1214/3
 Query Match 3.5%; Score 103; DB 2; Length 1332;
 Best Local Similarity 18.0%; Pred. No. 18;
 Matches 123; Conservative 74; Mismatches 237; Indels 248; Gaps 30;

Qy 37 ASTGNPFOANVENKTFMERFNLTH-----HSGIYVD--L 71
 Db 386 SDTIVSPDENVRALKPRDRRKXHHGKPSGYPVNGSYLENPFIPRHGGSHRDHRY 445
 Qy 72 GQDKXVD---GTLREPAAGLCPIWGKHELO---QPD--RLPYRNFLDEVPTKEKYQ 122
 Db 446 GYCPAIDSPFSTAFRGAAALSDQFKDYRRAMGKIQGFARXVDNKGFLIDDEFE--- 500
 Qy 123 SGNPLPGFNLPFTPSGQRTSPPEMLEKNSIKASTDGRCAEPFAKTVANDKXNKA 182
 Db 501 -----GPNKPFESNIEQVFP-----GNRSK--KQKG----- 526
 Qy 183 TKRYPPFYVDSKK-----RLCHILYVMQMEGKKYGSVKGEPPDLTWYCFKP 230
 Db 527 -PHDDPGYDEKTFDAKDLFGATRRKRSAYTGEQSYGQSQNQSARQNVKKD--- 582
 Qy 231 KKSVTENHLLIYGSAVYGENDAFI-----SKCP-----NQLRGYRFGVWKGR 275
 Db 583 -QQYTFPTFLTFGDCF-----DQFIKSGNGINMAACPIGETPDKTLRS----- 626
 Qy 276 CLDYTELDPTVY-----ERVSKAQCVKTFENGVA-----SDQPHT----- 313
 Db 627 CSETCGVSTTIVAVTIGTQTSDDLSAPSEYIENGQVTTOSTWNDQPTTQAPNSYESYTT 686
 Qy 314 -----YPLTSQASMNWMLPHQSDQPHSGGVGHVY-----GFYYVDPTTG 352
 Db 687 QYSNDVPSISAAIIGRCSLDASGL--FSLGCSQKTIQCSGAIYVRGCSLYFNEVQ 745
 Qy 353 EKGKALSDQVDPCLVSDSAVSYTAAGSLSEETPFIIIPSNPVTPTPTETA----- 404
 Db 746 E--CTYRDEVCEGSCQSTSPVITTPGQDSSNYGIGPSDD--VPSTTQPPVGDRCAYV 801
 Qy 405 -----LQCTADKRPDSFGACDVQAK-----RQKNSC----- 431
 Db 802 ASGLFDLGSQKTIQCSDSASVRECEGSLYFDERSGSCRPDEVPKQTDVSSSSTVP 861
 Qy 432 -----VGGQIQTSTVD-----CTADQNECGSNTALIAGLAVG 465
 Db 862 YLDFTTTPASPSDEPTTYESVAPYIPSVYVNVDTCTSLSDTHGCGSSFVYCHG 921
 Qy 466 VLLIALLGGCGCYFAKRLDRN-KGVQA-----AHHEHEFQSDRGARKRP-PSDLMQEAEP 517
 Db 922 RLISS---GNCQLGEGVDPSVQGCRTFSIIPARACDEQEVTTDAGLVQLMYKTLLEVL 978
 Qy 518 SFMDEAEENIEQDETHWVWG 539
 Db 979 T--TEAATVANDGPTDTYITG 998

RESULT 25

A47221

fibrillin 1 precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002

C:Accession: A47221; I54355; S17064; I59574; S17065; S62111; A34198

R:Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

Genomic 17, 476-484, 1993

A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure

A:Reference number: A47221; MUID:94010947; PMID:7691719

A:Accession: A47221

A:Molecule type: mRNA

A:Residues: 1-337; 'T', 339-1029 <COR>

A:Cross-references: GB:X63556

R:Peirata, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangillan, T.; Bonad

Hum. Mol. Genet. 2, 961-968, 1993

A:Title: Genomic organization of the sequence coding for fibrillin, the defective gene p

A:Reference number: I54355; MUID:93372860; PMID:8364578

A:Accession: 154355
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 132-3002 <PER>
 A:Cross-references: GB:LI3923; NID:9306745; PIDN:AAB02036.1; PID:9306746
 R:Maalen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.
 Nature 352, 334-337, 1991
 A:Title: Partial sequence of a candidate gene for the Marfan syndrome.
 A:Reference number: S17064; MUID:91304568; PMID:1852207
 A:Accession: S17064
 A:Molecule type: mRNA
 A:Residues: 1030-3002 <MAS>
 A:Cross-references: EMBL:X63556
 R:Dietz, H.C.; Valle, D.; Franccomano, C.A.; Kendzior, R.J.
 Science 259, 680-683, 1993
 A:Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
 A:Reference number: 159574; MUID:93157831; PMID:8430317
 A:Accession: 159574
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 2217-2288, 'I', 2290-2325 <RES>
 A:Cross-references: GB:S54426; NID:9264860; PIDN:AAB5244.1; PID:9264861
 R:Lee, B.; Godfrey, M.; Vitale, E.; Horl, H.; Mattei, M.G.; Sarfarazi, M.; Tsiipouras, P.
 Nature 352, 330-334, 1991
 A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different
 A:Reference number: S17062; MUID:91304567; PMID:1852206
 A:Accession: S17062
 A:Molecule type: mRNA
 A:Residues: 'VLTVVFIFLSYKML', 944-1444 <LEE1>
 A:Cross-references: EMBL:X62008; NID:931398; PIDN:CA556534.1; PID:95924015
 A:Accession: S62111
 A:Molecule type: protein
 A:Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEE2>
 R:Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
 J. Biol. Chem. 264, 21381-21385, 1989
 A:Title: Connective tissue microfibrils. Isolation and characterization of three large F
 A:Reference number: A34198; MUID:90078246; PMID:2512293
 A:Accession: A34198
 A:Molecule type: protein
 A:Residues: 565-575, 1890-1892, 'I', 1894-1900 <MAD>
 C:Comment: Fibrillin is a major component of elastin-associated microfibrils.
 C:Genetic: C
 A:Gene: GDB:FBN1
 A:Cross-references: GDB:127115; OMIM:134797; OMIM:154700
 A:Map position: 15q21.1-15q21.1
 A:Introns: 2236/1; 2258/1; 2297/1
 C:Superfamily: fibrillin 1; EGF homology
 C:Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; M
 F:1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predicted <MATC>
 F:1332-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC>
 F:1332-1367/Domain: EGF homology <EGF>
 F:1457-1492/Domain: EGF homology <EGF>
 F:2262-2295/Domain: EGF homology <EGF>

Query Match 3.5%; Score 102; DB 2; Length 3002;
 Best Local Similarity 21.9%; Pred. No. 69;
 Matches 114; Conservative 61; Mismatches 212; Indels 134; Gaps 32;

19 PASGLSSSTRSR--ESQTLASTSGNPFQANVEMKTFM--ERFNLTHHQSGLYVDLGD 74
 2196 FEGGCKSSPKSRHNSQEOCCALKBGKWDPCGLCTPEPEARQACPGSSGIIVG-PDD 2254
 75 KEYDGLYNEPACLCPIWGKHELOPD-----RLPYRNFLBDVPEPEYKQSGNPLRG 129
 2255 SAVIDMECKEP-DVC-----KHGQCINTDGSYRCECFGYTLAINECVDTDECSVGNPCGN 2309
 130 GFPLN-----FVTSQGRISPFPEWELLEKSNINASTDLGCAFAPATVAMDGNATKY 185
 2310 GTCKNIVGECTCEGFEFGPMTC-----DINECAQ-----NPLICAF 2350
 186 RYFVYDSKRLCHILYVSMQLEWKKYCSVKGEPPDLTYCFKPR---KSVTENHLLY 242
 2351 RCNNTGSGYCKCPGVV---LAEEDRMCMDEDECEGKKIDCEKQMECNILGTWCIC 2407

243 GSAYGVNPDFAISKCPNALRGYRFGWKKRGCD-----YT-ELTDTVI-----ERVE 291
 2408 GPGY-QRRPDG--BQVDNENCCQRPGLCENGRLNTRGSTTCBCNDGFTASPNODELD 2464
 292 SK-AQCWKTREN--DQVADOPHYPLTSQASWMDWPLHQSDQPHSGV----- 339
 2465 NREGYCFTEVLQNMCOIGSSNRNPVTSECCCDGGRGWG-FHCBICPFGQTVARFKLCPH 2523
 340 GRNNGF-----YVDTTEGKCALSDQVPD-----CLVSDSAVSYTAAGSL 381
 2524 GR-GFMTNGADIDECKVIHVCNNGEC-----VNDKSHYCTKTYTPDITGTSCVDL 2576
 382 SE-ETP---NFIPSNPSVTPPTPTALQCTADK---FPDSFGACDVQACKRQKTS-C 431
 2577 NECDAPRPPCFICKNT-----ESGYQSCSKGYILQDGRSCKDLDBCATKQNHQ 2628
 432 ---VGG-----QISTSV-D--CTADEQNEGGS 453
 2629 FLQVNTIGFTCKCPGPGFTGHTSCIDINNECTSD-INLCGS 2668

RESULT 26
 A60643
 antigen 5401 - Elmeria tenella (fragment)
 C:Species: Elmeria tenella
 C:Date: 14-May-1993 #sequence_revision 14-May-1993.#text_change 18-Jun-1993
 C:Accession: A60643
 R:Danthorh, H.D.; Augustine, P.C.; Ruff, M.D.; McCandlish, R.; Strauberg, R.L.; Likel,
 Poult. Sci. 68, 1643-1652, 1989
 A:Title: Genetically engineered antigen confers partial protection against avian coccidi
 A:Reference number: A60643; MUID:90160107; PMID:2622819
 A:Accession: A60643
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-287 <DNA>
 F:11-120/Region: 22-residue repeats (A-G-X-X-G-G-S-G-G-X-A-E-L-P-G-E-E-G-G-A-G)

Query Match 3.5%; Score 101.5; DB 2; Length 287;
 Best Local Similarity 24.6%; Pred. No. 27;
 Matches 49; Conservative 20; Mismatches 69; Indels 61; Gaps 9;

336 SGVGRNRYFYVVD---TGECKALSDQVDPCLVSDAASVYTAAGSLSEBTPFIIPS 392
 135 AGGAEAGGEGEGEVQVPEGASGEGQVP-----ETPEPEPE 174
 393 NPSVTPPTPTALQCTADKFPDSFGACDVQACKRQKTSVGGQISTSVDTADQNECG 452
 175 TPEARPEPEPTPTPEAB-PTGGA-----EEBEKEBG 207
 453 SN--TALTAGLVGVLLALLGCGCYPAKRLDRNKGVQAAHH-EHEFOSDRGARKKPS 509
 208 SGPPTAAVAG-GVGGVLLAAVGGVAAYSGGGGGGGAEEQVFEBSGGAALFPE 266

510 -----DLMOEAEPFWDNA 523
 267 ADTVIDITDED--YWADS 283

RESULT 27
 S07296
 plastocyanin-plastocyanin reductase (EC 1.10.99.1) cytochrome f precursor - wheat chloro
 N:Alternate names: cytochrome b-f complex cytochrome f
 C:Species: chloroplast Triticum aestivum (common wheat)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993.#text_change 03-Jun-2002
 C:Accession: S07296; S27220
 R:Wiley, D.L.; Howe, C.J.; Aufricht, A.D.; Bowman, C.M.; Dyer, T.A.; Gray, J.C.
 Mol. Gen. Genet. 194, 416-422, 1984
 A:Title: Location and nucleotide sequence of the gene for cytochrome f in wheat chloropl
 A:Reference number: S07296
 A:Accession: S07296
 A:Molecule type: DNA
 A:Residues: 1-320 <WIL>

QY 440 SVDCTADEQ-----NEGSGNTALAGLAVGVLLAL 471
 DB 377 VFDSPQRSDRLFAVDQMGSVTSLTAGSGGSKMLTT 415

RESULT 30

translation initiation factor eIF-4 gamma homolog F27H5.30 [similarity] - Arabidopsis th
 N:Alternate names: protein F27H5.30
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 20-Jun-2000
 C:Accession: T49219
 R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: 225018
 A:Accession: T49219
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1606 <RIB>
 A:Cross-references: EMBL:AL163852; GSPDB:GNO0061; ATSP:F27H5.30
 A:Experimental source: cultivar Columbia; BAC clone F27H5
 C:Genetics:
 A:Gene: ATSP:F27H5.30
 A:Map position: 3
 A:Introns: 455/3; 1370/2; 1435/2; 1523/1; 1529/1; 1558/3; 1586/2

Query Match 3.4%; Score 99.5; DB 2; Length 1606;
 Best Local Similarity 20.5%; Pred. No. 44;
 Matches 119; Conservative 71; Mismatches 217; Indels 173; Gaps 29;

QY 20 ASGLSSTRSRESQTLASSTSGNPRQANTMKTFRMLTLHHOSGIYVDLGGDK----- 75
 DB 310 SSDSTSSVARRAQNVMSAL--PVNAKVSVK-----PQVSEKLGSPKDRSH 355
 QY 76 -EVDGTLVREPAGLCIPMGKHIETLQDP-----DRLPYRNPLEVDVPEKEKXOG 124
 DB 356 GEVNIISLQKNVACGLSSS---QQPKSPFVSGVNSAPKASVEVEPLAKSVEIV 411
 QY 125 NPLPGGFNLNFPVPS-----GQRISFPFMELEKNSNIAKSTDLGCAEF 169
 DB 412 PPVKSSEVETAPVTTTETIRRAEMVSESISVEDQCTKVEPHNLNTEGQTPMDPLVSDPE 471
 QY 170 AKRTVAMDKNKATKTRYPVVDYSKRLCHILYVSNQMEGKKYCVKKEPRLTYCYCK 229
 DB 472 A--TVAAKEN-----LSLPATNGFRKQLKV-----STSDAPTSDSVDTS 510
 QY 230 PRKSVTENHLLYGSAYVGENPDAPISKPCNALRGVREGVWKKGRCLDYTELDT----- 285
 DB 511 IDKSTEGSSHA--SSEISGSSPEKDLKCDNR-----ASDKLDRSVISDAKHET 559
 QY 286 ---VIERVESKAQ-----CMV--KTFENDGVASDQH--TYPLTQASQWMDWPLHOSDOP 334
 DB 560 LSGVLEKAQNEVDGATDVCPSSEKLAVTDDTSDLSPLSHSTVLSSSTV-----PLGHS--ET 612
 QY 335 HSGGVGRNNGFYVDTTGEGKCALSDQVPCLVSDAANSYTAAGSLSE--EPENFIIP- 391
 DB 613 HNSAVETN--TRRNSTYKGGKKIKELQKADAGTSDLYMYKKEPEEKSSNVVHDV 669
 QY 392 SNPSVPTPETALQCTADKFP-----DSFGACDVQACRQKTSQVGGIOSTSVYDCTA 445
 DB 670 SNONLPAIPQ-AVEAIVDTEPVKNEBEDMEDADADVSTPLCTERA-----DNSVNAKR 720
 QY 446 DEONEGCSN-----TALTAGLAV-----GGVLLALLGGGCTPAKR 481
 DB 721 GSSDEVDNINCINTEKKYSRDFLLKFDALCTALPEGFDVSPDIANALIVYMG----- 772
 QY 482 LDRNKGVQAHHHEHQ-----SDR---GAR--KKRPSDL 511
 DB 773 -----ASHHEHDSYPTPGKVMRQASGARLDRRPSNV 804

RESULT 31

S44054
 genome polyprotein - Marburg virus (strain Popp)
 N:Alternate names: structural protein L
 N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
 C:Species: Marburg virus.
 A:Virus: strain Popp
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
 C:Accession: S44054; S32776
 R:Bukreyev, A.A.; Volchok, V.E.; Blinov, V.M.; Dryga, S.A.; Netesov, S.V.
 submitted to the EMBL Data Library, January 1994
 A:Description: Full-length nucleotide sequence of Marburg virus Popp strain: The compari
 A:Reference number: S44049
 A:Accession: S44054

A:Molecule type: genomic RNA
 A:Residues: 1-2331 <BUK>
 A:Cross-references: EMBL:Z29337; NID:g450908; PIDN:CAA82542.1; PID:g450915
 A:Experimental source: strain Popp
 R:Bukreyev, A.A.; Netesov, S.V.
 submitted to the EMBL Data Library, September 1992
 A:Description: The partial nucleotide sequence of Marburg virus genome.
 A:Reference number: S32775
 A:Accession: S32776
 A:Molecule type: genomic RNA
 A:Residues: 1-2331 <BUK>
 A:Cross-references: EMBL:X68494; NID:g296962; PIDN:CAA48508.1; PID:g296963
 A:Experimental source: strain Popp
 C:Genetics:
 A:Gene: L
 C:Superfamily: paramyxo-like virus RNA-directed RNA polymerase
 C:Keywords: ATP; nucleotidyltransferase

Query Match 3.4%; Score 99; DB 2; Length 2331;
 Best Local Similarity 22.8%; Pred. No. 83;
 Matches 68; Conservative 31; Mismatches 101; Indels 98; Gaps 14;

QY 4 VGVQVLLVADCTIFASGLSSTRSRESQTLASSTG-----NPRQANTEM--- 50
 DB 176 IGTDLFGLIADFIIFK--VPVKTIIRNAVSLSQSKPGLRWYRQNTPLYLCDDEFIVS 233
 QY 51 -----KTFMERFNL-----THHQSGIYVDLQDQKVDGDTLVREPAGLCPI 91
 DB 234 VASVYECFTIMKDVLEFRNVTWEICARAWLEDSDGADYPL---DVLGLYNO----- 282
 QY 92 WCKHIELOQDRLPYRNPLEVDVPEKEKYGSGNPLPGGFNL-----NFW 136
 DB 283 -GDQIIAM-----YLED-----GFLIKHLEPLCVSCIOTHGF 315
 QY 137 TP-----SGQRISPPFMELEKNSNIAKSTDLGRCFAEFAKTAMDKNKATKRYPPVY 191
 DB 316 TFGKXWFGSQRIEYEEELCSLWKFKISGNKACQAFIKITII---OGKLTPOQYCELF 372
 QY 192 DSKKRLCH--ILYVSNQMEGKKYC--SVKGEPPDLTWYCEKPRK--SVTENHLLYGSAY 246
 DB 373 SLQKMGHPVLIVDALDKVKKQASVILKPKVMFETFCVFKITVAKNHYSQGSWY 430

RESULT 32

E65203
 probable dehydrogenase (EC 1.8.1.-) udha - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C:Accession: E65203; S21563
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Persing, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: E65203
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-444 <BLAT>
 A:Cross-references: GB:AE000470; GB:U00096; NID:g2367332; PIDN:AACT6944.1; PID:g1790400;
 A:Experimental source: strain K-12, substrain MG1655

R:Gustafsson, C.
 Submitted to the ENBL Data Library, May 1992
 A:Reference number: S21563
 A:Accession: S21563
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-41, 'L', '43-95, 'L', '97-324 <GUS>
 A:Cross-references: EMBL:X66026; NID:943236; PIDN:CAA46822.1; PID:943237
 C:Genetics:
 A:Gene: udhA
 C:superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
 C:Keywords: oxidoreductase

Query Match 3.4%; Score 98; DB 2; Length 444;
 Best Local Similarity 20.3%; Pred. No. 9.3;
 Matches 87; Conservative 53; Mismatches 137; Indels 152; Gaps 21;

```

QY 150 LLEKSNIKASTDLRCACFAFKTV---AMDKNKATKRYRPFYVDSKKRLCHIL----- 201
DB 41 IIEFNQNP-PLYSDHRLRSPADILNHADNVINQOTMRQGFY---ERNHCEILQGNAR 96
QY 202 YV-----SMOLMEGKKYCSVKGEPP-----DLTWYCFKPKRSVTENHH----- 239
DB 97 FVDHTTLALDCPDGSEVETLAEKFIACGSRPHPTVDFTPHRIYDSDSLMSHEPRH 156
QY 240 -LIYGSAYVG-----ENPDAFISKCPNOLRGYRFGWKKGRCLD 278
DB 157 VLIYAGVIGCYASIFRGMVDYKVDLINTRDLRLAFLOQEMSDSL-SYHF--MNSGVVIR 213
QY 279 YTE-----LDTYIERVES---KAQCWV-----KTEPDGVASDQPHYPL 316
DB 214 HNEVEYKEICGDDGVIMHKKSGKRLKADCLLYANGRTGNTSLAQNLGTDSRGOLKV 273
QY 317 TSQASWMDWMPHOSDOPHSGVGGRNNGFYVDYTG--EGKALSDDQVPDCLVSDSAVS 374
DB 274 NS-----MYQAOHPHYAVAGDVIGYPSIASAAYQGR-----IAQALVK 313
QY 375 YTAAGLSSEETPN--FIIPSNPSVTPPTPETALQCTADKFPDSFGACDVQACKROKTSKV 432
DB 314 GEATNHLLEDIPGTGYTIPETISSV--GKTEQQLTANKVPYEVGRAPFKHLAR----- 363
QY 433 GGQIOSTVCTCADEQNEGSGNTALLIAGLVGVLIL-----ALLGGCCYFAKRLDRNK 486
DB 364 -----AQIVGMNVGTLKILFRERKYLGIHCF----- 391
QY 487 GVQAAHHEH 495
DB 392 GERAAEITH 400

```

RESULT 33

Internalin like protein (LpXtG) [imported] - *Listeria innocua* (strain Clijp11262)
 A:Accession: AF1525
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AC1525
 R:Glaser, P.; Fraenkel, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karsic, U.
 Science 294, 849-852, 2001
 A:Authors: Krell, J.; Kuhn, M.; Kuntz, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schuener, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genome of *Listeria species*.
 A:Reference number: AB1077; MUID:21537279; PMID:11679666
 A:Accession: AC1525
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-521 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CA95971.1; PID:916413191; GSPDB:GN00178
 A:Experimental source: strain Clijp11262
 C:Genetics:
 A:Gene: lin0739

Query Match 3.4%; Score 98; DB 2; Length 521;
 Best Local Similarity 19.7%; Pred. No. 12;
 Matches 78; Conservative 57; Mismatches 133; Indels 128; Gaps 21;

```

QY 67 IYVDGDKKVDGTLREPAALCPINGHITLQOPDLRYNNFLEDV--PREKEKQSGN 125
DB 196 VYIYLAADKXID-----ISPLAKSFPQ-----QLTLNNEISDISPSKMTLYSED 241
QY 126 PLPGGFNLNFTYPSGQRISPPMELLENKSNIIKASTDLRCACFAFKVANDKN--NKAT 183
DB 242 PLADDF--YIDISNNHISDI-----SSLK-NADGKLDYF-----FAEDQSIVNPK 285
QY 184 KYRYPFYVDSK-KRLCHILVYSQMLMEGKKYCSVKGEPPDLTW-----YCFKPRK 232
DB 286 AFSTNFTLENKVNQINGTLVPRKNISNGSYSNM-----ILSWQLPSFVANDYGFSE-- 338
QY 233 SVTENHLLIYGSAYVGENPDPAFISKCPNOLRGYRFGWKKGRCLDYLDTYIERVES 292
DB 339 -----TTIGRSTGEFSGKVTQSLVGY-----TV----- 363
QY 293 KAQCWVTFENDV-----ASDQPHYPLTSQASWMDWMPHOSDOPHSGVGGRNNGFY 346
DB 364 -----TFDNEGTLSTRTPASDELVEPA-----KESKTGFYFT--GWY 399
QY 347 YVDITGEKCALSDQVPDCLVSDSAVSYTAAGLSSEETPNFIIPSNPSVTPPTPETALQ 406
DB 400 DAKTGKKKNPATDKMP-----ANNMTLYAQYEGTTPVPDPASP--VAPTKPTDPVK 450
QY 407 CTADKFPDSFGACDVQACKROKTSVGGQIOSTVSD 442
DB 451 --PDEIVSSSESGDME-1KGEQSGTIAASENATSID 483

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RESULT 34

alkaline amylopullulanase, probable [imported] - *Streptococcus pneumoniae* (strain TIGR4)
 A:Accession: B95031
 C:Species: *Streptococcus pneumoniae*
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
 C:Accession: B95031
 R:Teteljin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple, nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: B95031
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1280 <KUR>
 A:Cross-references: GB:AE005672; PIDN:AAK74446.1; PID:914971739; GSPDB:GN00164; TIGR:SP4
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP0268

Query Match 3.3%; Score 97.5; DB 2; Length 1280;
 Best Local Similarity 18.3%; Pred. No. 46;
 Matches 90; Conservative 68; Mismatches 146; Indels 189; Gaps 24;

```

QY 28 RSRSQRTLSASTSGNPQANVEMKTFMERFNLTRHHQSGIYVDLGQDKVDTLYREBAG 87
DB 923 RLRLGNLMVLTAQSTPF-----IHSGQ-----EYGRTKQ-----FRDPAY 957
QY 88 LCPFWGKHIEIQDRLPYRNPFLEDVPTKEVYQSGNPPLBGSNNLNFVTPSGQRISFPF 147
DB 958 KTPV-----ABDKVPNNKSHLLRD-----KDGNPFDYPIYHDSYDSDAVNKF 1001
QY 148 MLEKSNIKASTDLRCACFAFKTVAMDKNKATKRYRPFYVDSKKRLCHILVYSQQL 207
DB 1002 W---TKATDGAAYENKSKSDYMKGLIALRQSTBA--FRKSLQDIDRIV-HLITV----- 1051
QY 208 MEGKKYCSVKGEPPDLTWYCFKPKRSVTENHLLIYGSAYVGENPDPAF--ISKCPNOLRGY 266

```

Db 1052 -----PGANGVEKEDVVIQYQTAPNGDIYAFVNADEKAEF 1089
QY 267 RFGVM-----KKGRCLDYTE-----LTDVIERVSKAOC 296
Db 1090 NLGTFAPHLRNAVLADENQAGPVGIANKPG--LEWTEKGLKLNALTAFLV-RVSONGT- 1145
QY 297 WVKTFENGVASDOPHTYPLTSQASWMDWPLHOSQPHSGVGNRYVYDTTGEGKC 356
Db 1146 -----SHESTAEKFDSTFSK-----PHQNEASHPA-----HDDPAPEAR- 1181
QY 357 ALSDVPDCLVSDSAVSYTAGSLSEETPNFTIPSNPSVTPPTBETALQCTADKFPDSF 416
Db 1182 -PDSTKPKADKVD-----AENKFS-----QATADSOAE-- 1208
QY 417 GACDVQACRKQKTSVCGQIOSTSV-----CTADQNEC-----GSTALIAAGLA 462
Db 1209 -----QPAQEAQASSKVAENVESENSENENIPATPKQABLPTGTINKENKLLFAGIS 1263
QY 463 VGVLLALLGGG 475
Db 1264 ----LLALLGLG 1271

RESULT 35

A55624
fibrillin-1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 02-Aug-2002
C:Accession: A55624
R.Yin, W.; Smilley, E.; Germiller, J.; Sangiulietti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995
A:Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene
A:Reference number: A55624; MID:95130561; PMID:7829516
A:Accession: A55624
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2871 <YIN>
A:Cross-references: GB:L29454; NID:9575509; PIDN:AAA56840.1; PID:9575510
C:Gene: Fbn-1
A:Superfamily: fibrillin 1; EGF homology
F:1201-1236/Domain: EGF homology <EGF>

Query Match 3.3%; Score 97.5; DB 2; Length 2871;
Best Local Similarity 22.6%; Pred. No. 1.5e+02;
Matches 93; Conservative 51; Mismatches 139; Indels 129; Gaps 29;

QY 124 GNPLPGGFNLN-----FVTPSGORISPPMELLEKNNSIKASTDLGRCAEFAKTVAMDKX 179
Db 2173 GNPCGNGTCKNVIGSECTCEBFEFGPMWTC-----DINCAQ-----N 2213
QY 180 NKATKRYPPVYDSKRLCHILYVSMQLEGGKYGVKGPDLTWYCKRPR---KSVTE 236
Db 2214 PLTCAFRCVNTGVSYECKCPGVYV---LREDRMCKDEBCAEGKHDCTEKQWCKNLLG 2270
QY 237 NNHLIYGSAYVGENPAPAFISKCNQALRGYRFGWKKGCLD-----YT-ELTD-----T 285
Db 2271 TYMCTIGGPGV-QRRPG--EGCLDENECOTKPGICENGRCLNLTGTYTCECNDGFASPT 2327
QY 286 VIERVESK-AQCWKTFEN---DGVASDOPHTYPLTSQAS--WMDWPLHOSQPHSGV 339
Db 2328 QDECLDNREGYCESEVFENMCOIGSSNRNPVT---KSECCCVGGRMGHLCETCPREGTV 2384
QY 340 -----GRNYGF-----YYVDTGEGKCALSDQVPD-----CLVSDSAV 373
Db 2385 AVYKLCPPHR--GFMTNGADVDECKYIHVCYRNGEC-----VNDRSYHCICKTGYTPI 2437
QY 374 SYTAASLSB--ETP---NFIISNPSVTPPTBETALQCTADKFPDSF-----GAC-DY 421
Db 2438 TGTSCVDLNECNQAPKCNFTCKNT-----EGSYQSC--PAGYIIQEDGRCKDL 2486
QY 422 QACKRKQKTS-----VGG-----QIOSTSV-----CTADQNEGS 453

Db 2487 DECATKQNCQFLCVNTIGFTCKCPBGTQHTACTIDNNECTSD-INLCSG 2537

RESULT 36

B40228
neurexin I-beta precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Dec-2002
C:Accession: B40228; S27885
R.Ushakov, Y.A.; Petrenko, A.G.; Geppert, M.; Suehof, T.C.
Science 257, 50-56, 1992
A:Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recep
A:Reference number: B40228; MID:92320296; PMID:1621094
A:Accession: B40228
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-468 <USH>
A:Cross-references: GB:M96375; NID:9205712; PIDN:AAA41705.1; PID:9205713
C:Superfamily: neurexin; EGF homology
C:Keywords: alternative splicing; transmembrane protein
F:1-47/Domain: signal sequence #status predicted <SIG>
F:48-468/Product: neurexin I-beta #status predicted <MAT>

Query Match 3.3%; Score 97; DB 2; Length 468;
Best Local Similarity 22.3%; Pred. No. 12;
Matches 52; Conservative 38; Mismatches 103; Indels 40; Gaps 11;

QY 330 QSDPHSGCGVGRNYFY-----VDTTSE-----GKCALSQVPPCLVSDSAVSYT 376
Db 249 ECGQPFQQLS---GLYNGKLVMAAENDANIAIVGNVRLVGEVPSMTSTATAMQ 305
QY 377 A-AGSLSEETPNFTIPSNPSVTPPTBETALQCTADKFPDSFGAC-----DVQACKROKT 429
Db 306 SEMSISIMETTTTATATARKGKPTKPIQOTTDILVAS-ABEPSDEIDPEEPS- 363
QY 430 SCVGQIOSTSV-----DCTADQNEGSGNTALIAVGVLALLGGGCTPAKRLD 483
Db 364 ---GGLANPTRYGVREPYGSAEVIRESSTTGWVGVIAAAAILLLVAMY--KYRN 418
QY 484 RNKGVQAHHHEHREPSDGRARKKRPDLMQAEPSFMEARENIE-ODGETHV 535
Db 419 RDEG---SYHDESRNYISNSAQSGAVVKEKQPSAKSNKKKKKKEITYV 468

RESULT 37

F97279
TPR-repeat-containing protein, Cell-adhesion domain [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: F97279
R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.V.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MID:21359325; PMID:21359325
A:Accession: F97279
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-694 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK01025.1; PID:915026149; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3085

Query Match 3.3%; Score 97; DB 2; Length 694;
Best Local Similarity 18.1%; Pred. No. 21;
Matches 102; Conservative 59; Mismatches 205; Indels 196; Gaps 23;

QY 36 SASSTGNPQANVEKKTIFERENLT-HHHQSIYVDL-----GQKEVDGTLYRBPAGLC 89
Db 18 SFTTTNNVASDPTTTPASTPQDLTVTPNBSGYNVDLKKMNSGASQDYSYKLY----- 70
QY 90 PIWKGHIELQCPDRLPYRNPFLEDPVTEKEYKQSGNPLPGGF---NLNFPVPSGO---RI 143

Db 71 ---SKSDTDTQFQTLPCKGTNTDKIHVLNIYFDLGNLKGWMTSNTDINDYGGKIIKV 127
Oy 144 SPFMELEKSNINIAST-----DUGRAEAF 171
Db 128 DEIPSTNSPNINIKDSNGNEVDYIMLSGWSNNSBGLNATSEAVESPIKSGKVLFGH 187
Oy 172 KTVAMDKNNKATKYRYPFVYDSKKRLCHILYVSMQMEGKXYCVKGEPPDLT----- 224
Db 188 DSINQVNSLNDLVANVAKFPSPDAK-----LYTGAIVGGRITLSPGSTTSLITTKTGLL 241
Oy 225 ---WYCKPRK-STENHHLIYGSAVYGENPDAFISKCPNALGNYFGWKGRCLDY 279
Db 242 VNFPRKIGNNLSVPYTHNSOISYGP-----TWRFTHKSY 276
Oy 280 TELDTVIERVESKAQCVKTPENDY-----ASDQP-----HTYPLTQAS 321
Db 277 T--ADDMT---NPNFYLSTWNTNNGVLTQTHSGOATSDKGLANTLFLYLAQVTDQTS 330
Oy 322 WNDWVPLHQS---DQP-----HSGGVGRNYGF-----YVVDITGB----- 353
Db 331 WDD---HKGDVDAPSKPVINSYNDTFKQDISLNTSGSTNGSYDYVVEATGKNDGTX 386
Oy 354 -----GKCALSDQVPCLVSD---SAVSYT-----AA 378
Db 387 VDSDTKCTVTTGIAVGIWVDQNSDTIPSNITTTSTNYTLNLSYKNDFYVHIAIDKA 446
Oy 379 GSLSEETNFIIPSNPSVTPPTPEFALQCTADKFPDSGACDVQACRQKSNVSGVGOQS 438
Db 447 GNISVTTQKQSVNDAT-----NIALNKTDTNL--TVGANDTLTATITPTDAVDKNVTW 498
Oy 439 TSVDTCTADEQNECGSNTALLAG 460
Db 499 TSSDPSIATVDSAGKITAVKPG 520

RESULT 38
A40228
neurexin I - alpha precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Dec-2002
C:Accession: A40228; S27884
R:Uenikayov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.
Science 257, 50-56, 1992
A:Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recep
A:Reference number: A40228; MUID:92320296; PMID:1621094
A:Accession: A40228
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1507 <USH>
A:Cross-references: GB:M6374; NID:9205710; PIDN:AA41704.1; PID:9205711
C:Superfamily: neurexin; EGF homology
C:Keywords: alternative splicing; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-1507/Product: neurexin I-alpha #status predicted <MAT>
F:680-712/Domain: EGF homology <EGF>
F:1087-1119/Domain: EGF homology <EGF1>

Query Match 3.3%; Score 97; DB 2; Length 1507;
Best Local Similarity 22.3%; Pred. No. 64;
Matches 52; Conservative 38; Mismatches 103; Indels 40; Gaps 11;
Oy 330 QSDPHSGVGRNYGFY-----VDITGE-----GKCALSDQVPCLVSDSAVSYT 376
Db 1288 EGGDPFGQOLS---GLYNGKLKVLMAAENDANAIYVNVRLVGVSPSSMTSTATAIMQ 1344
Oy 377 A--AGSLSEETNFIIPSNPSVTPPTPEFALQCTADKFPDSFGAC-----DVQACRQKT 429
Db 1345 SEMSTSIWETTTLATSTARBGKPTKPEISQTTDDILVAS--AEPSDEDDIDPEPSS- 1402
Oy 430 SCVGOIQISTVY-----DCTADEQNECGSNTALLAGLVGVLLALLGGCCTFAKLD 483
Db 1403 ---GGLANPRTVGREYPGSAEAVIRESSSTTGWVGIVAAALCILITLILAMY--KYRN 1457

Oy 484 ENKGVQAAHHEFEQSDRGAKRRPSDLMQAEPSFMDEAENIE-ODGETHV 535
Db 1458 RDEG---SYHDESRNYSNSAQSGNAVVEKQFSSAKSNKKNKNDKEXYV 1507

RESULT 39
B86414
hypocholesteric protein P28N24.14 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: B86414
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltli, R.; Matzfall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B86414
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1020 <STO>
A:Cross-references: GB:A805172; NID:95502422; PIDN:AA88121.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 3.3%; Score 96; DB 2; Length 1020;
Best Local Similarity 20.8%; Pred. No. 44;
Matches 78; Conservative 45; Mismatches 130; Indels 122; Gaps 19;

Oy 223 LTWYCFKPKRSVTENHHLIYGSAVYGENPDAFISKCPNOLRG-----YRFGWKGR 275
Db 102 LEWH---PRIPITON-HLIYDDL-----PHIMDPYECRCGPRLHLTDKPFINGPS 150
Oy 276 CLD-YTELTPVIERVES-----KAQCVKTPFENDVGAASDPHYPLTQASW 322
Db 151 CLKRYSD--PYFPRASSNLSQGNKKFKQDKKCKMKKKKSSSRDWSRLASLANQAR 208
Oy 323 NDWVPLHQSDDPHS-----GCVGRNYGFY-----YVDTGSEKCALSDQVPCLVSDS 370
Db 209 KTPASPSFGSTSTKTTSTSDMKRYDFQHNHRSFESRSGSG-----YNECL---S 258
Oy 371 AAVSYTAAGSLSEETNFIIPSNPSVTPPTPEFALQCTADKFPDSFGACDVQACRQ 427
Db 259 TATSSLKTG---BRPKGVFVSS--SLTPGSCITIASVSECTEDAHDFGSPGQGAAR 313
Oy 428 KTSCY-----GGQIQSTVDTCTADEQNECGSNTALLAGLVGVLL 468
Db 314 GSSCVSDEKAEIVESLGLQTDASEVNEVANSVVDITDEKSYDEG----- 359
Oy 469 LALLGGCVFPAKRLDRNKGVAHHEFEQSDRGAKRRPSDLMQ-----AEPSFW 520
Db 360 ---IGVDVHSHKDNENDK-----SESLRKRAAGIDEVREIKNGEIVGER-- 402
Oy 521 DEAEENIEODGETHV 535
Db 403 -DSEGETESBECECV 416

RESULT 40
G97902
alpha-amylase (EC 3.2.1.1) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: G97902
R:Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001
A: Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
A: Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A: Reference number: A97872; MUID: 21429245; PMID: 11544234
A: Accession: G97902
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-1256 <KUR>
A: Cross-References: GB: AE007317, PDB: 1AAK9051.1, PDB: 1G5457796; GSPDB: GN00174
C: Genes:
A: Gene: Pula
C: Keywords: glycosidase; hydrolase

Query Match 3.3%; Score 96; DB 2; Length 1256;
Best Local Similarity 18.5%; Pred. No. 59;
Matches 91; Conservative 64; Mismatches 140; Indels 198; Gaps 24;

QY 28 RRESQTLSTASGNGPQANVEKTEMERFNLTHHSGIYVDLGQDKEVDGLYREPAQ 87
DB 908 RLRLGNLWLVLTQGTFF-----IHSQ-----EYGRTKQ-----FRDPAY 942
QY 88 LCPIMGKHLLEQPPRLPYRNPNLEDPTEKEYKOSGNPLPGGFNLNFTVPSGORISPP 147
DB 943 KTFV-----AEDKVPNKSHLRD-----KDNPFDPYFYHDSYDSSDAVNKFD 986
QY 148 MELLEKNSTKASTDLGRCAEFKTVANDKNNKATKRYRYPFYDSEKRLCHILYVSMQL 207
DB 987 W---TATGDKAYPEVVKSRDYWKGLIALRQSTDA--FRLKSLQDIXDRV-HLTV---- 1036
QY 208 MEGKKYCSYKGEPPDLTWYCFKPKKSVTENHHLIYSAVGENPDAF-ISKCPNQLRGY 266
DB 1037 -----PGQNGVEKEDVIGYQITAPRGDIYAVFNVADEKAREF 1074
QY 267 REGW-----KKGRCLDYTE-----LTDVIERVESKAQC 296
DB 1075 NLGTAFAHLRNAEVLADENQAGSVGIANPKG--LEWTEKGLKLNALTAATVL-RVSONGT- 1130
QY 297 WYKTFENDGVASDQPTTYPLTSGASWMDWPLHOSDQPHSGVGRNYGFIYVDTTGEKC 356
DB 1131 -----SHESTAEKPDSTPSK-----PEHQDPAPFA-----RPDST----- 1161
QY 357 ALSDQVPDCLVSDSAVSYTAAGSLSEETPNFIIPSNPSVTPTPETALQCTADKFPDSF 416
DB 1162 -----KPDAKVAD-----AENKPS-----QATDSQAE--- 1184
QY 417 GACDVQACKRKQKTSYVGGQIQSTSV-----CTADEQNEC-----GSNTALYAGLA 462
DB 1185 -----QPAQBAQASVKEAVQNESVENS SKNIPATPRQAE LPTGINKMENLTFAGIS 1239
QY 463 VGGVLLALLGCG 475
DB 1240 -----LLALLGLG 1247

Search completed: October 2, 2003, 15:52:26
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 2, 2003, 15:39:29 ; Search time 25 Seconds

(without alignments)
1017.658 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 2322
Sequence: 1 MGLVGVVLVLVADCTIFA.....EAEENIRQGETHWVEGDY 541

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	447	15.3	562 1	AMAI_PLAFR
2	431	14.8	622 1	AMAI_PLAFR
3	431	14.8	622 1	AMAI_PLAFR
4	423.5	14.5	563 1	PK66_PLAFU
5	412	14.1	622 1	AMAI_PLAFR
6	412	14.1	622 1	AMAI_PLAFR
7	410	14.0	622 1	AMAI_PLAFR
8	398.5	13.6	558 1	MAPB_PLACH
9	127	4.3	2459 1	MAPB_PLACH
10	120	4.1	2464 1	MAPB_MOUSE
11	118	4.0	2468 1	MAPB_MOUSE
12	117	4.0	697 1	SM2A_SCHGR
13	113	3.9	765 1	DRP4_FELCA
14	111.5	3.8	1592 1	SORL_CHICK
15	107.5	3.7	376 1	CATW_HUMAN
16	107.5	3.7	1104 1	NFX1_HUMAN
17	106	3.6	415 1	LMP2_MOUSE
18	104	3.6	1207 1	RPOC_MOUSE
19	104	3.6	1213 1	RPOC_MOUSE
20	104	3.6	1255 1	ERB2_HUMAN
21	102	3.5	2871 1	FN1_HUMAN
22	101.5	3.5	120 1	CYF_WHEAT
23	100	3.4	1213 1	RPOC_MOUSE
24	99	3.4	2331 1	RPL_MABVP
25	98.5	3.4	572 1	SVR_PYRPU
26	98.5	3.4	732 1	ACPH_PIG
27	98	3.4	465 1	STHA_ECOLI
28	98	3.4	2842 1	APC_RAT
29	97.5	3.3	2871 1	FN1_MOUSE
30	97	3.3	468 1	FN1_MOUSE
31	97	3.3	484 1	LEN2_PIG
32	97	3.3	529 1	NX1A_MOUSE
33	97	3.3	906 1	AD22_HUMAN

34	97	3.3	1514 1	NX1A_RAT	063372 ratnus novy
35	95.5	3.3	320 1	CYF_ATRBE	0688w4 atropa bell
36	95.5	3.3	320 1	CYF_ORYZA	P07888 oryza sativ
37	95.5	3.3	583 1	C166_MOUSE	061490 mus musculu
38	95	3.3	357 1	MYCM_HUMAN	P12525 homo sapien
39	95	3.3	2845 1	APC_MOUSE	061315 mus musculu
40	94.5	3.2	320 1	CYF_SPIOL	P16013 spinacia ol
41	94.5	3.2	320 1	CYF_TOBAC	P06449 nicotiana t
42	94.5	3.2	468 1	T10A_HUMAN	000220 homo sapien
43	94.5	3.2	705 1	SM2A_DROME	024323 drosophila
44	94	3.2	982 1	ENV_VITV	P03379 viana lenti
45	94	3.2	989 1	ENV_VITV	P23422 viana lenti

ALIGNMENTS

RESULT 1	AMAI_PLAFR	STANDARD	PRT	562 AA.
AC	P22622:			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Apical membrane antigen 1 precursor (Merozoite surface antigen).			
GN	AMA-1, OR AG352.			
OS	Plasmodium fragile.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
NC	NCBI_TaxID=5657;			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE=90205978; PubMed=2181309;			
RA	Peterson M.G., Nguyen-Dinh P., Marshall V.M., Elliott J.F.,			
RA	Collins W.E., Anders R.F., Kemp D.J.;			
RT	"Apical membrane antigen of Plasmodium fragile.";			
RL	Mol. Biochem. Parasitol. 39:279-284(1990).			
CC	-1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FALCIPARUM, AND			
CC	TO PK66 FROM P.KNOXLEST.			
CC	-----			
CC	EMBL: M29898; AAA29474.1; -			
DR	PIR: A44944;			
DR	InterPro: IPR003298; Apmem_Agl.			
DR	Pfam: PF02430; AMA-1; 1.			
DR	PRINTS: PRO1361; MER020175A.			
KW	Malaria; Signal; Transmembrane; Antigen; Glycoprotein.			
FT	SIGNAL 1 21			POTENTIAL.
FT	CHAIN 22 562			APICAL MEMBRANE ANTIGEN 1.
FT	DOMAIN 22 484			EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 485 507			POTENTIAL.
FT	DOMAIN 508 562			CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 84 84			N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 176 176			N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 226 226			N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 405 405			N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 441 441			N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 441 441			N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE 562 AA.; 64488 MW; 9EAB72DA37EA7164 CRC64;			
Query Match	15.3%; Score 447; DB 1; Length 562;			
Best Local Similarity	25.9%; Pred. No. 1,1e-26;			
Matches 159; Conservativity 91; Mismatches 231; Indels 132; Gaps 26;				
6 VOVLVLVADCTIF-----ASGLSSSTRS---RESQTLASTSGNPFQANVEMKT 52				

```
DB 4 IYCIILFSLAQCLVHMGKCEPNQPSRLTRFSAKVLLQEOPWVERSTRMSNPW-----KA 57
QY 53 FMERNLTHHOSGIVYDGLGDKXVDGTLTYRPPAGLCPIWGHILQOPDRPLRYNNLTLE 112
DB 58 FMEXYDIKHTSSSGIRVLDGEDAEVGNSSYRIPACKCPVFGGIYIUNSE-----VSFLT 112
QY 113 DVPT-EKEYKQSGNDLPQGFNLNFTVPSGORISPPFM-----ELKSNISIKASTDLGCA 167
DB 113 PVATNGNQLKDGGFAP-----QANDHISPSIKRLRRYKENDPLMLCNDLALCK 163
QY 168 EFAFTV-AMDKNKATKYRYPYVDYDQSKRLCHILVSMQMEGKKYCSVKGEPPDLTWY 226
DB 164 THAASFVEMDKN-----SSYRHPAVYDDEDKICMYLTLSPQEWGPRYCSKDAENKD-AMF 219
QY 227 CFKPKKSTENHLLYGSAYGEN-PDAFISKCPNOLRGYFGVWKGRCLDYELDT 285
DB 220 CFKPKKSTENHLLYGSAYGEN-PDAFISKCPNOLRGYFGVWKGRCLDYELDT 285
QY 286 VIERVESKACQVWTFENDGVASDQPHYPLTSQASWMDWPLHOSDQPHSGV----- 339
DB 275 ---QAKDLRECNRIYFE--ASASDQPTQY---EELDYQKIQGFRONDDGMKSAFL 325
QY 340 -----GRNYGFYVDTTGEK-CALSDQVPCLVSDSAVSYTAAG---SLG 382
DB 326 PVGAFNSDNFKSGKGYWNAFDT--ENKCYLTFNAKPTCLINDKNFIATLALSHQEVYD 383
QY 383 EETPFITIPSN-----PSVTPFPFETALQCTAKKFPDSRGA 418
DB 384 NEFPISYDEMERERKESRMSLYNDKARIVLPRIFISNDKOSLKCPCAPEHITNST 443
QY 419 CDVQACKROKTSV---GGQIOSTSVDTADE-----QNECGSNTALIALAGVGL 468
DB 444 CNFYVC-----NCEKRAETIKENNEVAITEERKQDYQVAGSSKQMLIIIGITGVYV 498
QY 469 IALLGGCGYFAKRLDRNKGVAHHEHFEQSDRGARKRPSDLQEAEPFWEAEENIE 528
DB 499 VA-LASMFYFRKKAHNDK-----YDKMEQADQYKPTRKDEMIDPEASFGEER--R 548
QY 529 QDGETHWVWEGDY 541
DB 549 ASHTTPVLMKEY 561

RESULT 2
AAAI_PLAIF STANDARD; PRT; 622 AA.
ID AAI_PLAIF
AC P22621;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apical membrane antigen 1 precursor (Mercozote surface antigen).
GN AHA-1 OR P783.
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5837;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89384584; PubMed=2701947;
RA Peterson M.G., Marshall V.M., Smythe J.A., Crewther P.E., Lew A.,
RA Silva A., Anders R.F., Kemp D.J.;
RT "Integral membrane protein located in the apical complex of
RT Plasmodium falciparum."
RL Mol. Cell. Biol. 9:3151-3154(1989).
CC -1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: STRONG TO AHA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO
CC PK66 FROM P.KOMLESI.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC entries requires a license agreement (see http://www.fab-sib.ch/announce/
CC or send an email to license@fab-sib.ch).
CC -----
DB 53 EMBL; M27133; AAA29475.1; -
DB 58 EMBL; M27957; AAA29476.1; -
DB PIR; A08267; CAA00764.1; -
DB PIR; A32499; A32499.
DB InterPro; IPR003298; Apmem_Agt.
DB Pfam; PF02430; AHA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
KW Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
FT SIGNAL 1 24
FT CHAIN 1 25
FT DOMAIN 25 546
FT TRANSMEM 547 567
FT DOMAIN 568 622
FT CARBOHYD 162 162
FT CARBOHYD 286 286
FT CARBOHYD 371 371
FT CARBOHYD 421 421
FT CARBOHYD 422 422
FT CARBOHYD 499 499
FT CONFLICT 308 308
FT CONFLICT 332 332
FT CONFLICT 407 407
FT CONFLICT 439 439
FT CONFLICT 496 496
FT CONFLICT 503 503
SQ SEQUENCE 622 AA; 72009 MW; 7D41335E249FA18F CRC64;

Query Match 14.8%; Score 431; DB 1; Length 622;
Best Local Similarity 26.2%; Pred. No. 2,2e-25;
Matches 149; Conservative 86; Mismatches 212; Indels 122; Gaps 24;

QY 41 GNPFOANYEMKTFMERENLTHHOSGIVYDGLGDKXVDGTLTYRPPAGLCPIWGHILQ 100
DB 107 GNPW-----TEYAKYDIEVHSGIRVLDGEDAEVAGTQYRRLPSGCKPVFGKIILEN 160
QY 101 PDRLPYRNNFLQEDVPTKEYKQSGNPLPGGFNLNFTVPSGORISPPFM-----LLEKSN 156
DB 161 SN-----TTFPLVATGNQYLDK-----GGFAF--PPTPLMBMTLDERHRFKDNKY 207
QY 157 IKASTDLGRCAEFKTVAMDKNKATKYRYPFYDYSKRLCHILVSMQMEGKKYCSV 216
DB 208 VKNDELTLGSRHAGNM--PDNDKSNYKYPAYVDKDKCHILYIAQNGNPGRYCN- 264
QY 217 KGEPPDLTWYCKPKKSTENHLLYGSAYGEN-PDAFISKCPNOLRGYFGVWKGR 275
DB 265 KDESRENMFQFRPAKDISFQNY-----TYLSKVVDWMEKVCPRKNLQNAKFFGLWVGN 319
QY 276 CLDYELTD-VYIERVESKACQVWTFENDGVASDQPHYPLTSQASWMDWMP----- 327
DB 320 CEDITHAVEFSAIDLFE-----CNKLVEFLS--ASDQPYQCHLTDYKIEGFGKRNAS 373
QY 328 -----LHOSDQPHSGGVNRYGYVDTTGEKCALSDQVPCLVSDSAVSYTA 377
DB 374 MIKSAFLPTGAFKDRYKSHGKGYWGNVNETQ--KCEIFNVYPTCLINNNSYIATTA 430
QY 378 AGSLSEETPNFIIPSN-----PSVTPFPFETAL 405
DB 431 LSHPLEVHNF--PCLYKNEIMKEIERESKRILKNDNDGNKKIILPRIFISDDKSL 488
QY 406 OCTADKFPDSFGACQVQACKROKTSVGVGQIOSTSVDTA-----DEQNEGSGN----- 454
DB 469 KCPCPPEIVSSTCNCFYCK-----CVERRAEVTSSNNEVVYKKEKDYADIPKPKPYD 543
QY 455 --TALIAGAVGVYLLALLGGCGYFAKRLDRNKGVAHHEHFEQSDRGARKRPSDLM 512
DB 544 KKKIILASAAVAVALITLM---VLYKR-----KQNAKRYQMDPQYKGSNSR-NDNM 595
QY 513 QEAEPSPWDEAEENIEQDGETHWVWEGDY 541
DB 596 LDPEASFWEGER--RASHTTPVLMKEY 621
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RESULT 3
AMAL_PLAFLH STANDARD; PRT; 622 AA.
ID AMAL_PLAFLH STANDARD; PRT; 622 AA.
AC P50491;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apical membrane antigen 1 precursor (Merozoite surface antigen).
GN AMA-1 OR PF83.
OS Plasmodium falciparum (isolate chn / Thailand).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=70151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101665; PubMed=2270110;
RA Thomas A.W., Waters A.P., Carr D.;
RT "Analysis of variation in PF83, an erythrocytic merozoite vaccine
  candidate antigen of Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 42:285-287(1990).
CC 1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
CC 1- SUBCELLULAR LOCATION: Type I membrane protein.
CC 1- SIMILARITY: STRONG TO AMA-1 FROM P. CHABAUDI AND P. FRAGILE, AND TO
  PK66 FROM P. KNOWLESI.
CC -----
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CC or send an email to license@isb.sib.ch).
CC -----
DR EMBL; M58547; AAA29720.1; -.
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITE3A.
DR Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
KM SIGNAL 1 24
FT CHAIN 25 622 APTICAL MEMBRANE ANTIGEN 1.
FT DOMAIN 25 546 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 547 567 POTENTIAL.
FT DOMAIN 568 622 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 422 422 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 622 AA; 71989 MW; 1DFA53593C9AC5 CRC64;
Query Match 14.8%; Score 431; DB 1; Length 622;
Best Local Similarity 26.7%; Pred. No. 2,2e-25;
Matches 153; Conservative 81; Mismatches 209; Indels 130; Gaps 25;
Db 41 GNPEQANEMKTFEMRNFLTHHSGIYVDIGDKEVDGTLTYREBAGLCPIIMGKHIEIQ 100
107 GNFW-----TEYMAKVIDEKHSGIRYVDJEDAEVAGTOYRLSGKCPVFGKIIEN 160
QY 101 PDRLEYYRNNFLFEDVTE-KEYKQSGNPLPGGFNLNLFVPSGORTISPPFME-----LLEKNS 155
Db 161 S-----KTFPLTPVATENODLKDGFAFP-----PTBELISPMTLDOQRHLKYONE 206
QY 156 NIKASTDGRCAEFKTVADDKNNKARKYRPFPYDSKRLCHILLYSMQIMSEKYYCS 215
Db 207 YVKNLDELTLSSRHAAGN--KNPDNDKSNYKPAYVYDEDDKCHILLYLAADENNGPRVCN 264
QY 216 VKGEBPDLTWYCFEKRRK-SVTENHLLIGSAVGEN-PPAFISKCPNALRGYRFGVWK 273
Db 265 -KDESKRSMVCFRAKOKLPENT-----TYSKNVVDNNEVEYPRKYLENAKGLAVD 317
QY 274 GRCLDYELTLDTYIERVESKACQCVKTEINDGVASDQHTTP--LTSQASNDWMP----- 327

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Db 318 GNCEDIPIRVNFE---SANDLEPCNKVLIVPELS--ASDQKQYQBNHUTDYEKIKKEGRKNNKA 372
Qy 328 -----LHOSDOPHSGCGVRNGCFYYVDVTGTEBCKALSDOVPCQLVSDSAVAASVT 376
Db 373 SMKSAFLPTAPAFAPADRYKSRGKGGMGNVNTETO---KCEIFNVKPYCLLINSSYIATV 429
Qy 377 AAGLSSEETPNFIIPSN-----PSVTPPTPEETA 404
Db 430 ALSHPNEVENPN--PCSLYKDEIKKEIERESKRITKLDNDDEGNKKITAPRIFTISDDXS 487
Qy 405 LQCTADKEPFDSFGACDVQACRKOKTS CVGQIOGTS-----VDCTAD--EQNECG 452
Db 488 LKCCDDEPVSNSNCNPFVCK-----CYEKRAEYTSNNEVVYKEBYKDEYADIPHKPT 542
Qy 453 SNTALI---AGLAVGVLLALILAGGCGFYAKRLDRNKGVQAAAHNEHEFQSDRGARRKRP 508
Db 543 DNMKIIIISSAAVAVLATILVV-----YLYKR---KGNAEKYDKMDEPDQYKSTSR- 591
Qy 509 SDLMQEAEPSPFMDAEENIIBEDDGTTHVVEBDY 541
Db 592 NDEMLDPFASFWGSEK--RASHTTPVLMEKPY 621

RESULT 4
PR66_PLAKU
AC P21303;
ID PK66_PLAKU STANDARD; PRT; 563 AA.
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 19, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Merozoite receptor PK66 precursor (66 kDa protective minor surface antigen).
GN PK66.
OS Plasmodium knowlesi (strain nur1).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
CX NCBI_TaxID=5852;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=Line W1;
RX MEDLINE=91089268; PubMed=2211675;
RA Waters A.P., Thomas A.W., Deans J.A., Mitchell G.H., Hudson D.E., Miller L.H., McCutchan T.F., Cohen S.;
RT "A merozoite receptor protein from Plasmodium knowlesi is highly conserved and distributed throughout Plasmodium."
RL J. Biol. Chem. 265:17974-17979 (1990).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN=NURI;
RX MEDLINE=91187058; PubMed=2011149;
RA Waters A.P., Thomas A.W., Mitchell G.H., McCutchan T.F.;
RT "Intra-genetic conservation and limited inter-strain variation in a protective minor surface antigen of Plasmodium knowlesi merozoites."
RL Mol. Biochem. Parasitol. 44:141-144 (1991).
RN [3].
RP FUNCTION: MEROZOITE RECEPTOR PK66 IS A SURFACE ANTIGEN INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CONCENTRATED AT THE APICAL END PRIOR TO RUPTURE, FOLLOWING WHICH IT CAN DISTRIBUTE ITSELF ENTIRELY ACROSS THE SURFACE OF THE FREE MEROZOITE. DURING INVASION PK66 IS EXCLUDED FROM THE ERYTHROCYTE AT, AND BEHIND, THE INVASION INTERFACE.
CC - MISCELLANEOUS: PK66 EXPRESSED IN MATURE SCHIZONTS IS RAPIDLY PROCESSED AS THE SCHIZONT RUPTURES, YIELDING A 42/44 kDa DOUBLET ASSOCIATED WITH THE SURFACE MEROZOITE.
CC - SIMILARITY: STRONG TO AMA-1/Pf83 OF P.FALCIPARUM, P.CHABAUDI, AND P.FRAGILE.
CC -----
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CC -----
DR EMBL: M58317; AAA63444.1; -
DR EMBL: M61057; AAA29728.1; -
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam: PF02430; AMA-1; 1.
DR PRINTS: PR01361; MEROZOITESA.
KW Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
FT SIGNAL 1 13
FT CHAIN 1 13
FT DOMAIN 14 563
FT TRANSMEM 14 487
FT DOMAIN 488 508
FT CARBOHYD 509 563
FT CARBOHYD 36 36
FT CARBOHYD 107 107
FT CARBOHYD 176 176
FT CARBOHYD 189 189
FT CARBOHYD 238 238
FT CARBOHYD 441 441
FT VARIANT 228 228
SQ SEQUENCE 563 AA; 64680 MM; 9EP0620264AA5CCF CRC64;

Query Match 14.5%; Score 423.5; DB 1; Length 563;
Best Local Similarity 24.9%; Pred. No. 7, 2e-25;
Matches 150; Conservative 94; Mismatches 249; Indels 109; Gaps 25;

6 VQVLVLVADCTIFASGL---SSSTSRSSQTLSTSGNPNPQANEM---KTPMEREN 58
4 IYIIFLSHOCVHMGCERNOKTYTLTSANNASLEKPIIERSTRMSNPMKAFMEKTD 63
59 LTHHNSGIVYDVGQDKEVDGLTYREBAGLCPIWGHIELOOBDRLPYENNFLEDPVPT-E 117
64 LERAHNSGIRIDGEDAEVGSNRYRIPACKCPVFGGIYIENSN-----VSFLTPVATGA 118
118 KEYKSGNPLPGGFNLNFTVPSGQRISSPPM---ELLEKSNITKASTLGRCAEAFKT 173
119 QRLKEGGFAFPN-----ADHISPTITANLKERYEKNADIMLNDIALCKTHAASF 169
174 VAMDKNKATKRYRPVYDSKSKLCHILVYVSMOMEGSKYCSXKGGPDLTWCFPRKS 233
170 VIAEDGN--TSYRHPAVYDEKNTCYMLYSAOENMGPRICSPDSQNKD-AMFCFPPDKX 226
234 VTEN--HHLIYGSAYVGENPDAPISKCPNOLRGYRFGVWKKGKCLDYTELTDVIERVES 292
227 --ENFNLVYLSGNVND---WENKCPKRLGNAGKGLWVDNGCEI-----PYVNEVEA 276
293 KA--QCVKTFENDVGAADQPHTY--PLTSGASWDMWPLHOSDQPHSG----- 337
277 RSLRECNRIIVFE--ASASDQPRQYEELTDYEKIOEGFRONNDMIKSAFLPYGAFNSDN 334
338 --GCVGNNGFYVYDTTGECKALSDQVPCLVSDSAVSTAG---SLSEETPNFIIS 392
335 FSKSGKGYWMPFDSV--NNKCYIFNKPTCLINDKNPFATLASHPOEVNNEPFCISYDQ 393
393 N-----PSVTPRPETALQCTADKRPDSFGACDVQACKROK 428
394 EIERETIKKOSRNMLYSDVKERTVLPRIISTDKESIKCPEBEHISNSTCNRYVC----- 449
429 TSCV--GGQIQSTS-----VDCTADQNECGSN--TALLAGLAVGVLLALLGGCCTYA 479
450 --NCVEKRAEIKENNEVILIKEEFKEDYENPDGKHKKMLLIIIVTAVCVVAASLFYR 508
480 KRLDRKGYQOAAHNEHFOSDGRARKKRPEDLMQEAERPFMDAEENIEDGSETHVMVG 539
509 KKAQDDK-----YDKMDQAEAYGKTANTRKDEMLDRBASFWGSDK--RASHTTPLYMEX 560
540 DY 541
561 PY 562

RESULT 5
AMAL_PLAF8 STANDARD; PRT; 622 AA.
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AC P50492;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apical membrane antigen 1 precursor (Merozoite surface antigen).
GN AMA-1 OR PF83.
OS Plasmodium falciparum (isolate 768).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_Taxid=57266;
RX MEDLINE=9110165; Pubmed=2270110;
RA Thomas A.W., Waters A.P., Carr D.;
RT "Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum."
RL Mol. Biochem. Parasitol. 42:285-287(1990).
CC -1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: STRONG TO AMA-1 FROM P. CHABAUDI AND P. FRAGILE, AND TO PK66 FROM P. KNOWLESI.
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CC -----
DR EMBL: M58548; AAA29721.1; -
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam: PF02430; AMA-1; 1.
DR PRINTS: PR01361; MEROZOITESA.
KW Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
FT SIGNAL 1 24
FT CHAIN 25 622
FT DOMAIN 25 546
FT TRANSMEM 547 567
FT DOMAIN 568 622
FT CARBOHYD 162 162
FT CARBOHYD 286 286
FT CARBOHYD 371 371
FT CARBOHYD 421 421
FT CARBOHYD 422 422
FT CARBOHYD 489 489
SQ SEQUENCE 622 AA; 71990 MM; 1C9C8715BDE2915F CRC64;

Query Match 14.1%; Score 412; DB 1; Length 622;
Best Local Similarity 25.8%; Pred. No. 6, 3e-24;
Matches 147; Conservative 81; Mismatches 219; Indels 122; Gaps 23;

41 GNPFOANVEMKTFMRPNLTHHNSGIVYDVGQDKEVDGLTYREBAGLCPIWGHIELOQ 100
107 GNPW-----TEYMKYDIKEVHSGIRVDLGEDEAVAGTORLPSGKCPVFGKGIILEN 160
101 PRLPLRYNNFLEDPVT-EKEVYKSGNPLPGGFNLNFTVPSGQRISSPPM---ELLEKNS 155
161 SN-----TTFLEKPAVATGNQDLKDGFAFP-----PTNPLISPMWLDHMRDYYKNE 206
156 NIKASTDLGRCAEFAKTVANDKNKATKRYRPVYDSKSKLCHILVYVSMOMEGSKYCS 215
207 YKNDLDELTLCSRHAGN--MNPNDNKNNSYKRAYADVNDKCHILYIAOENMGPRYCN 264
216 VAGPERDLTYVCFKRSKSTENHHLIYGSAYVGEN--PDAFISKCPNOLRGYRFGVWKKG 274
265 -KDESKRNSMFCFRPAKDKSFQNY-----TYLSKVVVDWMEKVCPKRLNNAKFGWLVDG 318
275 RCLDYTELTDVIERVESKAOQVKTENDVGAADQPHTYP--LTSQASWDMWMP----- 327
319 NCEDLPHVNEF---SANDLFECKNLVFEIS--ASDPKQYBQHLTDYEKIKSGFKNKXAS 373
328 -----LHQSQPHSGGVGRNRYGYVYDTTGECKALSDQVPCLVSDSAVSYTA 377
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Db 374 MIKSAFLPTGAFKADRYKSGKGYMGNVNRKTQ--KCEIFNVKPTCLINSSYIATTA 430
 Qy 378 AGSLSEETPNFIIPSN-----PSVTPPTPETAL 405
 Db 431 LSHPRVEVHN--PCSLYKDEIKKEIERESKRITLNDNDGCKKIAPRIFISDDISL 488
 Qy 406 OCTADKPPDSFGACDVQACRKQKTS CVGQIQSTSVDTA-----DEONECGS----- 454
 Db 489 KCPDPEWNSNTRCFVCK-----CVERAEVTSNNEVVEKYDEYADIPEKPTPD 543
 Qy 455 --TALIAGLAVGVLLALLGGCGCFARLDRNKGVOAAHHEHRSQDGRGAKRPPSLM 512
 Db 544 NMKIITASSAAVAVATILM--VLYKR--KGNAEKYDMODPODYGKSNR-NDNM 595
 Qy 513 OEAEPSFWEAEENIEODETHWVEGDY 541
 Db 596 LDPEASFWGEER--RASHTTPVLMEXRY 621

RESULT 6

AMAL_PLAFG STANDARD; PRT; 622 AA.
 ID AMAL_PLAFG
 AC P50459;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apical membrane antigen 1 precursor (Merozoite surface antigen).
 GN AMA-1 OR PF83.
 OS Plasmodium falciparum (isolate Camp / Malaysia).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 ON NCBI_TaxID=5835;
 RX MEDLINE=91101665; PubMed=2270110;
 RA Thomas A.W., Waters A.P., Carr D.;
 RT "Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum."
 RL Mol. Biochem. Parasitol. 42:285-287(1990).
 CC -1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO PK6 FROM P.KNOWLESI.

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 CC -----
 CC EMBL; M58545; AAA29718.1; -
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PRO1361; MEROZOITESA.
 KM Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
 FT SIGNAL 1 24
 FT CHAIN 1 24
 FT DOMAIN 25 622
 FT TRANSMEM 25 546
 FT DOMAIN 547 567
 FT TRANSMEM 568 622
 FT CARBOHYD 162 162
 FT CARBOHYD 286 286
 FT CARBOHYD 371 371
 FT CARBOHYD 421 421
 FT CARBOHYD 422 422
 FT CARBOHYD 499 499
 SQ SEQUENCE 622 AA; 71943 MW; 26CE8CF76D07C637 CRC64;

Query Match 14.1%; Score 412; DB 1; Length 622;
 Best Local Similarity 26.2%; Pred. No. 6.3e-24;
 Matches 150; Conservative 80; Mismatches 214; Indels 128; Gaps 25;

Qy 41 GNPRQAVNEMKTFMERFNLTHHOSGIYVDLGQDEKVDGLTYREBAGLCPIWKGHILEQ 100
 Db 107 GNPW-----TEWAKVDEEVHSGIRVDDGEAEVAGTQYRLPSGKCPVFGKILLEN 160
 Qy 101 PDRLPYRNNLEEDVPT-EKEYKSGNPLPGGFNLNFTPSQRISSPFM---ELLEKNS 155
 Db 161 SN-----TFLKRPVATGQDLKDGFAFP-----FTBPLISPMTLGMGRPFYKNE 206
 Qy 156 NIKASTDGRCAEFAFKVANDKNNKATKYAPPVYOSKRLCHLYVSNOLMGKKYS 215
 Db 207 YKALDELTLCSRRH-GNNPDKDEN-SNYKTPAVYDDKCKCHLYIAAENNGPRYCN 264
 Qy 216 VKGEPDLYTWYCFPRKSVTEHHILYGSAYVGEN-PDAFISKCPNQLRGYRFGWKKG 274
 Db 265 -KDSKNSMCFPRPAKDSFGN-----TLSKNVVDNWKVCEPRKYLENAKGLWVDG 318
 Qy 275 RCLDYTELDTVIERVESKACQWKTENDVASDQPTYP-LTQASNDWMP----- 327
 Db 319 NCEDIPIVNEF---SANDLFECKNLVEELS--ASDQPKYRQHLTDYEKIKEGFNKNAS 373
 Qy 328 -----LHSDQPHSGGVGRNRYVDYDTGEGCALSDQVPOCLVSDSAVSTTA 377
 Db 374 MIKSAFLPTGAFKADRYKSGKGYMGNVNRKT--HKCEIFNVKPTCLINSSYIATTA 430
 Qy 378 AGSLSEETPNFIIPSN-----PSVTPPTPETAL 405
 Db 431 LSHPRVEVHN--PCSLYKDEIKKEIERESKRITLNDNDGCKKIAPRIFISDDISL 488
 Qy 406 OCTADKPPDSFGACDVQACRKQKTS CVGQIQSTSVDTA-----VDCTAD-EONECGS 453
 Db 489 KCPDPEWNSNTRCFVCK-----CVERAEVTSNNEVVEKYDEYADIPEKPTPD 543
 Qy 454 NTALI-----AGLAVGVLLALLGGCGCFARLDRNKGVOAAHHEHRSQDGRGAKRPPS 509
 Db 544 NMKIITASSAAVAVATILM--VLYKR--KGNAEKYDMODPODYGKSNR-N 592
 Qy 510 DLMOAEPSFWEAEENIEODETHWVEGDY 541
 Db 593 DEMLDPEASFWGEER--RASHTTPVLMEXRY 621

RESULT 7

AMAL_PLAFG STANDARD; PRT; 622 AA.
 ID AMAL_PLAFG
 AC P50459;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apical membrane antigen 1 precursor (Merozoite surface antigen).
 GN AMA-1 OR PF83.
 OS Plasmodium falciparum (isolate FCR-3 / Gambia).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 ON NCBI_TaxID=5835;
 RX MEDLINE=91101665; PubMed=2270110;
 RA Thomas A.W., Waters A.P., Carr D.;
 RT "Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum."
 RL Mol. Biochem. Parasitol. 42:285-287(1990).
 CC -1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO PK6 FROM P.KNOWLESI.

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 CC -----

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DR EMBL: M58546: AAA29719.1; -
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam: PF02430; AMA-1; 1.
DR PRINTS: PR01361; MEROZOITESA.
KM Malaria: Signal; Transmembrane; Antigen; Glycoprotein.
FT SIGNAL 1 24
FT CHAIN 25 622
FT DOMAIN 25 622
FT TRANSMEM 547 567
FT DOMAIN 568 622
FT CARBOHYD 162 162
FT CARBOHYD 286 286
FT CARBOHYD 371 371
FT CARBOHYD 421 421
FT CARBOHYD 422 422
FT CARBOHYD 499 499
SQ SEQUENCE 622 AA; 71967 MW; 089336BE0464695C CRC64;

Query Match 14.0%; Score 410; DB 1; Length 622;
Best Local Similarity 26.0%; Pred. No. 8,9e-24;
Matches 149; Conservative 80; Mismatches 214; Indels 130; Gaps 25;

QY 41 GNPQANVEMKTFMERFNLTHHOSGIYVDLGQDKXVDGTLRBPAGLCPINGKHIELQO 100
DB 107 GNPW-----TEYMAKYDIEVHAGSIRVDLGEADAVACTOYRLPSGKCPVFGKIIIE 160
QY 101 PRLRYNNFLIEDVPT-EKEYKQSGNPLDGGFNLNFTVPSGORISFPFV---ELLEKNS 155
DB 161 SN-----TFLKPVATAGNODLKDGGFAPF-----PTNPLISPMITNGKRDYKXNE 206
QY 156 NIKASTDLGRCAEFAPKVTAMQKNKATKYRYPFVYDYSKKRLCHILYVSMQMEGKYCS 215
DB 207 YKNKLDLTLGSRHSHN--MNPNDKNSNYKTPAVTDYDKCHILYIAQENNGERYCN 264
QY 216 VKGEPPDLTWYCFKPKPK-SVTENHLLIYSAYVGEN-PPAFISKCPNALRGYRQGVWK 273
DB 265 -KQSGKRNMFQCRPAKOKLFENY-----TYSKXVVDNWBEVCPKRLLENAKFGLAVD 317
QY 274 GRCLDYTELTVIVIEVESKACQWKTFFENDVYASQPHYTP--LTSQASNDWMP----- 327
DB 318 GNCEDIPIHYNEF---SANDLFECKNLVFELS--ASQPKQYEOHLDYERIKIEGFQKNKA 372
QY 328 -----LHSDQPHSGGVGRNYGFYVDVTGEGKALSDQVDDCLVSDSAVAVYT 376
DB 373 SMITKAFLLTGAFAKADRYKSHGKGYMGNVNNETO--KCEIFNVVPTCLINNSYIAT 429
QY 377 AAGSLSEETPNFIIPSN-----PSVTPPTPETA 404
DB 430 ALSHPLEVEHNF--PCSLYKDEIKKEIERESKRIKLDNDDEGNKKIAPRIFISDKDS 487
QY 405 LOCTADKFPDSFGACVQACROKTCVGGQIOTS-----VDCIAD--EQNEGC 452
DB 488 LKCPDCEPWNSTCRPFVCK-----CVERRAVTSNNEVYVKEBYKDEYADIPKRPY 542
QY 453 SNTALI-----AGLAAGVGLLLALLGGCYFAKRLDNKGQVQAHHHEFQSDRGAKKRP 508
DB 543 DNKKITIIASSAAVAVALTILMV-----YLYKR-----KG-MEKYKMDOPQHYGKSTR 591
QY 509 SDLMQAEPSFWMDEAEENIEQDGETHVVEGDY 541
DB 592 NDEMIDPEASFWEERK---RASHTTVIMEKPY 621

RESULT 8
AMAL PLACH STANDARD; PRT; 558 AA.
AC P16445;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apical membrane antigen 1 precursor (merozoite surface antigen).
GN AMA-1.
OS Plasmodium chabaudi.

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DS;
RX MEDLINE=90114335; PubMed=2608101;
RA Marshall V.M., Peterson M.G., Lew A.M., Kemp D.J.;
RT "Structure of the apical membrane antigen 1 (AMA-1) of Plasmodium
RT chabaudi.";
RL Mol. Biochem. Parasitol. 37:281-284(1989).
RN [2]
RP SEQUENCE OF 38-377 FROM N.A.
RC STRAIN=DK;
RX MEDLINE=96333375; PubMed=875769;
RA Crewether P.E., Matthew M.L., Flegg R.H., Anders R.F.;
RT "Protective immune responses to apical membrane antigen 1 of
RT Plasmodium chabaudi involve recognition of strain-specific
RT epitopes.";
RL Infect. Immun. 64:3310-3317(1996).
CC -I- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: STRONG TO AMA-1/PP83 FROM P.FALCIPARUM, P.FAGILE AND
CC TO PK66 FROM P.KNOWLEST.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M25248; AAA90929.1; -
DR EMBL: A08270; CAH00765.1; -
DR EMBL: U49745; AAB36511.1; -
DR PIR: A44964; A44964.
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam: PF02430; AMA-1; 1.
DR PRINTS: PR01361; MEROZOITESA.
KM Malaria: Signal; Transmembrane; Antigen; Glycoprotein.
FT SIGNAL 1 21
FT CHAIN 22 558
FT DOMAIN 22 480
FT TRANSMEM 481 503
FT DOMAIN 504 558
FT CARBOHYD 20 20
FT CARBOHYD 189 189
FT CARBOHYD 231 231
FT CARBOHYD 249 249
FT CARBOHYD 276 276
FT CARBOHYD 288 288
FT CARBOHYD 412 412
SQ SEQUENCE 558 AA; 63973 MW; 9773F3E6439A972 CRC64;

Query Match 13.6%; Score 398.5; DB 1; Length 558;
Best Local Similarity 25.8%; Pred. No. 5,9e-23;
Matches 147; Conservative 86; Mismatches 202; Indels 135; Gaps 24;

QY 42 NFPQANVEMKTFMERFNLTHHOSGIYVDLGQDKXVDGTLRBPAGLCPINGKHIELQO 101
DB 53 NFWP-----KMEKXDIKXVSGSIRVDLGEADAVENODRIRPSGKCPVMGKGIITONS 106
QY 102 DRLPYNNFLIEDVPT-EKEYKQSGNPLDGGFNLNFTVPSGORISFPFV---ELLEKNS 156
DB 107 -----KVSFELTRVATAGNOKVREGGLAPF-----OTDVNISPTITDNLKMTKDKHE 152
QY 157 IKASTDLGRCAEFAPKVTAMQKNKATKYRYPFVYDYSKKRLCHILYVSMQMEGKYCSV 216
DB 153 ILALNDMSLCAGHA--SFVYPTGTNTVTAIRHAYVDKSNKCYILYVAQENMGPRYCS- 209
QY 217 KGEPPDLTWYCFKPKPKSVTENHLLIYSAYVGENDAIISKCPNALRGYRQGVKKGRG 276
DB 210 NEDNENQPFCTPPEKK--DEYKNSLYLTKNRED---WETSCPNSKIONAKRGVWVDYGC 265

```

QY 277 LDY---TELDTVIERVESKACQWKTENDVASDOPHTY----- 314
 Db 266 SEYKKEVHN-----KTLKCNQIVNES---ASDQPPQYKEHLEDTAKIRGIVDRNGK 318
 QY 315 -----PLTSQASNDWMPHOSDQPHSGVGVRNGFYVDTTGEKCALSDQVDCLV 367
 Db 319 LIGBALPITGS-----YRADQVSKSGKGVWANYDKTK---KCYIFNKKPFTCLI 365
 QY 368 SDSAAVSTAGSLSEETFNFIIPSN-----PSVTPPT 400
 Db 366 NDKQVATTAALSSL-EEGPOESPEDDIYKKIAEIKVMNVNRNNGNDITKPIPIFISD 424
 QY 401 PETALQCTADKPPSPFCACDVQAC-----KROKTSQVGGQIOSTSVCTADEQNECGS--- 453
 Db 425 DKSELANCCEPTQLQSTCKFCVNCVCKRQFIS-----ENVEIYDEKSEYESPIN 478
 QY 454 --NTALLAGLAVGVLLIALIGGCGYPAKRLDRNKQVAHHEHEFGSDRQARKRPSDL 511
 Db 479 QRMILIIILITATGAILASLLI---FYFPR---SNK---PGDDYDKMGQADTYGKAQSRKDE 530
 QY 512 MQEAPSPFDEAEENIBODGETHWVVEGDY 541
 Db 531 MLDPVSWFGSDK---RASHTTPVLMEXPY 557

RESULT 9

MAPB_RAT STANDARD; PRT: 2459 AA.
 AC P15205; Q62958; Q9ER21; Q9GM92;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1
 DE Light chain LC11].
 GN MAP1B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE OF 1-142 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=96257242; PubMed=866295;
 RA Liu D., Fischer I.;
 RT "Isolation and sequencing of the 5' end of the rat microtubule-
 RT associated protein (MAP1B)-encoding cDNA.";
 RL Gene 172:307-308(1996).
 RN [2]
 RP SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Gli1al tumor;
 RX MEDLINE=92347374; PubMed=1639092;
 RA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;
 RT "Identification of two distinct microtubule binding domains on
 RT recombinant rat MAP 1B.";
 RL Eur. J. Cell Biol. 57:66-74(1992).
 RN [3]
 RP SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Spinal cord;
 RX MEDLINE=90059871; PubMed=255150;
 RA Rientz A., Gremmling J., Hermans-Borgmeyer I., Kitzsch J.,
 RA Litzner U.Z., Prior P., Gundelfinger B.D., Schmitt B., Betz H.;
 RT "Neuraxin, a novel putative structural protein of the rat central
 RT nervous system that is immunologically related to microtubule-
 RT associated protein 5.";
 RL EMBO J. 8:2879-2888(1989).
 RN [4]
 RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.
 RX MEDLINE=97405699; PubMed=9260743;
 RA Ma D., Nothias F., Boyne L.J., Fischer I.;
 RT "Differential regulation of microtubule-associated protein 1B (MAP1B)
 RT in rat CNS and PNS during development.";
 RL J. Neurosci. Res. 49:319-332(1997).

CC -1- FUNCTION: The function of brain MAPs is essentially unknown.
 CC Phosphorylated MAP1B may play a role in the cytoskeletal changes
 CC that accompany neurite extension. Possibly MAP1B binds to at least
 CC two tubulin subunits in the polymer, and this bridging of subunits
 CC might be involved in nucleating microtubule polymerization and in
 CC stabilizing microtubules.
 CC -1- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
 CC with MAP1A and MAP1B proteins.
 CC -1- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,
 CC cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
 CC heart or muscle.
 CC -1- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
 CC nerve levels are high early in development but decrease during
 CC postnatal development and are low in adults. In dorsal root
 CC ganglia levels remain high throughout development.
 CC -1- INDUCTION: By nerve growth factor.
 CC -1- DOMAIN: Has a highly basic region with many copies of the sequence
 CC KEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC -1- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
 CC from MAP1B by proteolytic processing. It is free to associate with
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region
 CC of MAP1B (by similarity).
 CC -1- PTM: Phosphorylated.
 CC -1- SIMILARITY: TO MAP1A.
 CC -1- CAUTION: A C-terminal fragment of this protein (residues 1597 to
 CC 2459) was originally described as neuraxin in Ref.3.
 CC -----
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 CC or send an email to license@isb-eb.ch).
 CC -----
 CC EMBL; U52950; AAB17068.1; -
 CC DR EMBL; X60370; CAC16162.1; -
 CC DR EMBL; X16623; CAA34620.1; ALT_SEQ.
 CC DR PIR; A56577; A56577.
 CC DR InterPro; IPR00102; MAP1B neuraxin.
 CC DR Pfam; PF00414; MAP1B neuraxin; 10.
 CC DR PROSITE; PS00230; MAP1B NEURAXIN; 8.
 CC KW Microtubules; Repeat; Phosphorylation.
 CC FT CHAIN ? 2459
 CC FT REPEAT 1869 1885 MAP1B 1.
 CC FT REPEAT 1886 1902 MAP1B 2.
 CC FT REPEAT 1903 1919 MAP1B 3.
 CC FT REPEAT 1920 1936 MAP1B 4.
 CC FT REPEAT 1937 1953 MAP1B 5.
 CC FT REPEAT 1954 1970 MAP1B 6.
 CC FT REPEAT 1988 2004 MAP1B 7.
 CC FT REPEAT 2005 2021 MAP1B 8.
 CC FT REPEAT 2022 2038 MAP1B 9.
 CC FT REPEAT 2039 2055 MAP1B 10.
 CC FT DOMAIN 559 1035 GLU-RICH.
 CC FT DOMAIN 588 786 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
 CC KEE AND KKEI/V REPEATS).
 CC FT DOMAIN 2224 2312 LYS-RICH.
 CC FT CONFLICT 127 127 M -> V (IN REF. 1).
 CC FT CONFLICT 140 140 T -> S (IN REF. 1).
 CC FT CONFLICT 2112 2112 R -> K (IN REF. 3).
 CC FT CONFLICT 2169 2169 L -> I (IN REF. 3).
 CC SO SEQUENCE 2459 AA; 269497 MW; 283F6872DDB8BA2 CRC64;
 CC -----
 CC Query Match 4.3%; Score 127; DB 1; Length 2459;
 CC Best Local Similarity 19.4%; Pred. No. 0.27;
 CC Matches 97; Conservative 55; Mismatches 101; Indels 168; Gaps 21;
 CC -----
 CC QY 15 DCTIFAGGLSSSTRSSQTLASSTSGNPFQANVEMTFPERF--NLTTHHQSITVYDLG 72
 CC Db 1749 DMSLYASLAEKVOQLSEGLKLSPKSDISPLTPRESSPTVSPGFSSTGAKESTYAAVQTS 1808

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QY 73 ODKVDGLTYREPAQ-----LCPIWGHIELOQDPRLPYRNNLEDPTEKEKOSGNPL 127
DB 1809 SSPIDAAA-ABEYFRRSMLEPTMOHIALSR-----DLTTSVEKONGKGT 1855
QY 128 PGCFNLNFVTPSGORISP-----FPMI 149
DB 1856 PGDFVYAVQKPESTTESPEEDYDYESHKEKTIQADHVGYYEKEKERTIKSPCDGYSYE 1915
QY 150 LLEKSNIKASTDLGRCAEFAPKTV-----AMDKNNKATK-----YRPFYDYSK 195
DB 1916 TLEKTT--KTPEDGGVCEITETKTRTPREGGYSEISEKTRTPESGYTEKTERSR 1973
QY 196 RL-----CHILYVSMQL-----EGKY-----CSVKGPEPDLTWYCF 228
DB 1974 LLDJISNGYDDEGHTLGDOSYETETKTSPPESSESYETTTKTRPDTSAICY 2033
QY 229 KERKSVTENHLYGSAYVGENPDAFISKCPNALRGVFRGWKKGRCIDYELTDYIE 288
DB 2034 ETMEKITKTPQ--ASTVGETSD-----RC--YTPERKSPSE 2066
QY 288 RVESRAQCVKTFENDGVASDOPHYPLTSQASWN--DWM-----PLHOSDOP--HSGVYG 340
DB 2067 AAQVDYLCIVSSCE-----FKHPTKELSPSFINPNPLEWFAGEEPTESEERLTSQGGAP 2121
QY 341 RNYGFFYVDTTGEKCALSDOVPDCLVSDA-----AVSYTAAGSLSEETP 386
DB 2122 PPSG-----GKQGRQCDERTPPTSVSBSAQSQDSQVPPETEBPSITADANLSEDE 2174
QY 387 NFIFSPNSVT-----PPTP 401
DB 2175 SETIPDKVTYKHMPPAP 2195

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RESULT 10
MAPB MOUSE STANDARD; PRT; 2464 AA.

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AC ID MAPB MOUSE STANDARD; PRT; 2464 AA.
AC P14873;
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
DE [Contains: MAP1 light chain LC1].
DE GN MAP1B OR MTAP1B OR MTAP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND DOMAIN.
RC STRAIN=Swiss Webster; TISSUE=Brain;
RX MEDLINE=90094539; PubMed=2480963;
RA Noble M., Lewis S.A., Cowan N.U.;
RT "The microtubule binding domain of microtubule-associated protein
RT MAP1B contains a repeated sequence motif unrelated to that of MAP2
RT and tau."
RT J. Cell Biol. 109:3367-3376(1989).
RL
CC -I- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
CC PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
CC THAT ACCOMPANY NEURITE EXTENSION. POSSIBLE MAP1B BINDS TO AT LEAST
CC TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDING OF SUBUNITS
CC MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
CC STABILIZING MICROTUBULES.
CC -I- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE
CC WITH MAP1A AND MAP1B PROTEINS.
CC -I- DOMAIN: Has a highly basic region with many copies of the sequence
CC KKEE and KKEIV, repeated but not at fixed intervals, which is
CC responsible for the binding of MAP1B to microtubules.
CC -I- PTM: LC1 IS COEXPRESSED WITH MAP1B. IT IS A POLYPEPTIDE GENERATED
CC FROM MAP1B BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH
CC BOTH MAP1A AND MAP1B. IT INTERACTS WITH THE AMINO-TERMINAL REGION
CC OF MAP1B.
CC -I- SIMILARITY: TO MAP1A.

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DR EMBL, X51396; CA35761.1; -.
DR PIR, S07549; QRMSP1.
DR MGJ, MGJ:1306778; Map1b.
DR GO, GO:0016358; P: dendrite morphogenesis; IMP.
DR GO, GO:0001578; P: microtubule bundling; IMP.
DR InterPro, IPR000102; MAP1B neuraxin.
DR Pfam, PF00414; MAP1B neuraxin; 10.
DR PROSITE, PS00230; MAP1B_NURAXIN; 7.
KW Microtubules; Repeat; Phosphorylation.
FT CHAIN ? 2464 MAP1 LIGHT CHAIN LC1.
FT REPEAT 1874 1890 MAP1B 1.
FT REPEAT 1891 1907 MAP1B 2.
FT REPEAT 1908 1924 MAP1B 3.
FT REPEAT 1925 1941 MAP1B 4.
FT REPEAT 1942 1958 MAP1B 5.
FT REPEAT 1959 1975 MAP1B 6.
FT REPEAT 1993 2009 MAP1B 7.
FT REPEAT 2010 2026 MAP1B 8.
FT REPEAT 2027 2043 MAP1B 9.
FT REPEAT 2044 2060 MAP1B 10.
FT DOMAIN 589 787 MAP1B 10. (HIGHLY BASIC, CONTAINS MANY
FT LYS-RICH (KKEE AND KKEIV) REPEATS).
SQ SEQUENCE 2464 AA; 270408 MW; FBD3DD99CFDDBA87 CRC64;

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Query Match 4.1%; Score 120; DB 1; Length 2464;

Best Local Similarity 19.3%; Pred. No. 0.92; Indels 184; Gaps 22;
Matches 98; Conservative 53; Mismatches 174;

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QY 15 DCTIFASGLSSSTRSRESQTLASTSGNPQANVEMKTFMERFN-----LTHNQ 64
DB 1754 EMSLYASLASAKRYGSEKXLSKSDISPLRPRESSPLYSFGSSTAAKETAHQAAS 1813
QY 65 SGIYVLDQDVEVDGLTYREPAQ-----LCPIWGHIELOQDPRLPYRNNLEDPTEKE 119
DB 1814 SSPIDAAAT-----ABEYFRRSMLEPTMOHIALNR-----DLTTSV 1852
QY 120 YKQGNPLPGGFNLNFVTPSGORISP----- 145
DB 1853 EKDSGKTPGDENAVQKPENAAGSPDEEDYDYESQETKTRTHDVRYYEKERTISIP 1912
QY 146 ----FPMELLEKSNIKASTDLGRCAEFAPKTV-----AMDKNNKATK-----YRY 187
DB 1913 CDGSGSYETIEKTT--KTPEDGGYCEITETKTRTPREGGYSEISEKTRTPESGYTY 1970
QY 188 PFVYDSKRL-----CHILYVSMQL-----EGKY-----CSVK--GEP 220
DB 1971 EKTERTSRRLDDISNGYDDEGHTLGDOSYETETKTSPPESSESYETSTKTRTS 2030
QY 221 PDLTWYCKRKRKSVTENHLYGSAYVGENPDAFISKCPNALRGVFRGWKKGRCIDYT 280
DB 2031 PPTSAYCYETMEKITKTPQ--ASTVGETSD-----RC--YT 2063
QY 281 ELTDVIRRVSKAQCVKTFENDGVASDOPHYPLTSQASWN--DWM-----PLHOSDOP 334
DB 2064 TEKSPSEARQVDVCLVSSCE-----FKHPTKELSPSFINPNPLEWFAGEEPTESEK 2118
QY 335 --HSGVGRNAGFYVDTTGEKCALSDOVPDCLVSDA-----AVSYTA 378
DB 2119 LTQSGGAPPSG-----GKQGRQCDERTPPTSVSBSAQSQDSQVPPETEBPSITAD 2171
QY 379 GSLSEETNFIFSPNSVT-----PPTP 401
DB 2172 ANIDSEDESETIPDKVTYKHMPPAP 2200

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RESULT 11
 MAPB_HUMAN STANDARD; PRT; 2468 AA.
 AC P46821;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Microtubule-associated protein 1B (MAP1B) [Contains: MAP1 light chain LCL1].
 GN MAP1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=95104835; PubMed=7806212;
 RA Lien L.V., Feener C., Fischbach N., Kunkel L.M.;
 RT "Cloning of human microtubule-associated protein 1B and the identification of a related gene on chromosome 15.";
 RL Genomics 22:273-280(1994).
 CC -1- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
 CC PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN STABILIZING MICROTUBULES.
 CC -1- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LCL1, LCL2 AND LCL3, CAN ASSOCIATE WITH MAP1A AND MAP1B PROTEINS.
 CC -1- DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAP1B to microtubules.
 CC -1- PTM: LCL1 is coexpressed with MAP1B. It is a polypeptide generated from MAP1B by proteolytic processing. It is free to associate with both MAP1A and MAP1B. It interacts with the amino-terminal region of MAP1B (by similarity).
 CC -1- SIMILARITY: TO MAP1A.
 CC -----
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 CC -----
 CC EMBL; L06237; AAA18904.1; -
 CC Genew; HGNC:6836; MAP1B.
 DR MIM; 157129; -
 DR GO; GO:0005875; C:Microtubule associated complex; TAS.
 DR InterPro; IPR00102; MAP1B_neuraxin.
 DR Pfam; PF00414; MAP1B_neuraxin; 10.
 DR ProSITE; PS00230; MAP1B_NEURAXIN; 6.
 DR Microtubules; Repeat; Phosphorylation.
 FT CHAIN ? 2468 MAP1 LIGHT CHAIN LCL1.
 FT REPEAT 1878 1894 MAP1B 1.
 FT REPEAT 1895 1911 MAP1B 2.
 FT REPEAT 1912 1928 MAP1B 3.
 FT REPEAT 1929 1945 MAP1B 4.
 FT REPEAT 1946 1962 MAP1B 5.
 FT REPEAT 1963 1979 MAP1B 6.
 FT REPEAT 1987 2013 MAP1B 7.
 FT REPEAT 2014 2030 MAP1B 8.
 FT REPEAT 2031 2047 MAP1B 9.
 FT REPEAT 2048 2064 MAP1B 10.
 FT DOMAIN 589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).
 SO SEQUENCE 2468 AA; 270618 MW; 540839CDBF09D461 CRC64;
 Query Match 4.0%; Score 118; DB 1; Length 2468;
 Best Local Similarity 19.4%; Pred. No. 1.3;
 Matches 129; Conservative 66; Mismatches 222; Indels 248; Gaps 28;

QY 15 DCTIFASGLSSSTRSRESQTLASSTSGNPFOANVEMKFMERFNLTHHSGIYVDLGD 74
 DB 1758 DMSLYASLTSEKQVSLBEKSLSPKSDISP-----LTPRESSPLVSPETSD 1802
 QY 75 -----KEYDGLY-----REPAG-----LCPIWGHILEQOPDRLPYRNFLPD 113
 DB 1803 STSAVKEKATACHSSSSPPIDAASAEFGFASVLFDTMQLHALNR-----D 1850
 QY 114 VPTKEVKGSGNPJPGFNLNPTVPSGORISP-----FMELLEKNS----- 155
 DB 1851 LSTPELEKDSGAKTPGDSVAYQKPEETTRSPDEEDVYESYEKTRTSVGYEYKIE 1910
 QY 156 -NIRASTDLGRCAEFAFKTV-----AMDKNKATK----- 184
 DB 1911 RTTSPSDSGSYETIGKTTTPEDGDVSYIEKTTTPREGGYSYISKETSPPRVS 1970
 QY 185 -YRPPFV-----YDSKRLCHIL-----YVSQLMGSKY-CSVK 217
 DB 1971 GYSYEKTERSHRLLDISNGYDSEDDGHTLGDPSYSYETTEKITSPESEGGYSYETSTK 2030
 QY 218 -GEPPDLTWGCFKPKRKYSTENHHLIYGSAVYGENPDARISCPNALRGYFGWKKGR 276
 DB 2031 TTRTPDITSTCYETAETKTRTPQ--ASTSYETSD----- 2063
 QY 277 LDYTELDTVIERVESKACQWVTFENDGVASDQPHYPLT--SQASWN-----DMW----- 326
 DB 2064 LCTYAEKSPBEAODVCLVSSCE-----YKPKTELSPSFNPPLFVFASEE 2114
 QY 327 PLHOSDOP--HSGVGRNYGYVDTTGEKCALSDQVDCLVSDA----- 371
 DB 2115 FTSESEKVLTOGSGAPPPG-----GKQGRCCDETPRVSBSAPSDQDVPPETE 2167
 QY 372 -AVSTYAGSGSEETPNITLPSNPSVT-----PPPEALDCTADKFPDSCGACDVQC- 424
 DB 2168 ECPSTADANIDSESEETITPDTVTYVKHMDPPAPVQDPSPRHMD-VSMVPEALA 2226
 QY 425 -----KROKTCVCGIOISTVDTCADEQNEGCSNTALJAGLAVGVLLA 470
 DB 2227 IEQNLGKALKKDLKERTTKRPGTKTKSSSVYKSD-----GKSPFLAASRKPAGL----- 2277
 QY 471 LLGGCYFAKRLDRNKGVQAHHHEHFEQSDRGARKRPSDLMQEAEPFWE--AEENIE 528
 DB 2278 -----KSSDPKSVSVASPKKESYEKAKPPTTPEVKARGE 2315
 QY 529 QDGET 533
 DB 2316 KDEET 2320
 RESULT 12
 SW2A_SCHGR STANDARD; PRT; 697 AA.
 AC Q9XZC8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 2A precursor (Sema 2A) (Sema II).
 GN SEMA-2A.
 OS Schistocerca gregaria (Desert locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
 OX NCBI_TaxID=7010;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=99203450; PubMed=10101134;
 RA Iabister C.M., Teal A.A., Wong S.T., Kolodkin A.L., O'Connor T.P.;
 RT "Discrete roles for secreted and transmembrane semaphorins in neuronal growth cone guidance in vivo.";
 RL Development 126:2007-2019(1999).
 CC -1- FUNCTION: ACTS AS CHEMOREPULSIVE GUIDANCE MOLECULE CRITICAL FOR

CC AXON FASCICULATION AND FOR DETERMINING BOTH THE INITIAL DIRECTION
 CC AND SUBSEQUENT PATHFINDING EVENTS OF THE TI AXON PROJECTION.
 CC -1- SUBCELLULAR LOCATION: Secreted (potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT IN THE DEVELOPING LIMB
 CC BUD EPITHELIUM DURING TI PIONEER AXON OUTGROWTH.
 CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
 CC -1- SIMILARITY: Contains 1 Sema domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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 CC -----
 CC DR EMBL: AF134904; AAD30114.1; -.
 CC DR InterPro: IPR007110; Ig-like.
 CC DR InterPro: IPR003559; Ig.
 CC DR InterPro: IPR01627; Sema.
 CC DR Pfam: PF01403; Sema; 1.
 CC DR SMART: SM00630; Ig; 1.
 CC DR SMART: SM00630; Sema; 1.
 CC DR PROSITE: PS50835; IG_LIKE; 1.
 CC KM Signal; Immunoglobulin domain; Neurogenesis; Developmental protein;
 KW Glycoprotein. 1 20
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 697 SEMAPHORIN 2A.
 FT DOMAIN 231 515 SEWA.
 FT DOMAIN 526 634 IG-LIKE C2-TYPE.
 FT DISULFID 618 654 BY SIMILARITY.
 FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 369 369 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 697 AA; 78673 MW; 7FESSAB4965E1E4 CRC64;
 Query Match 4.0%; Score 117; DB 1; Length 697;
 Best Local Similarity 19.6%; Pred. No. 0.29; Indels 184; Gaps 26;
 Matches 106; Conservative 63; Mismatches 187;
 QY 21 SGLSTRRESQTLASTSGNPFQANVEKTFMERFNLTHHQSGIYVDLGQDEVDGT 80
 DB 65 TNISLSDCERDSTLTLEPTNI-----ANCYSKSGSADPDCNHNIRVOPMGDSRLYICGT 119
 QY 81 LYREPAGLCPIWKGKHELQOPRLPYRNNFLEDPTEKE-----YKQSGNP-LFG--- 129
 DB 120 NAHSPKDWV-VYENLHLQHEHYVPGVIGVIAKCPDPEDDSYPAVVENGNPFDLGLYS 178
 QY 130 GFLNANV-----TPSGQRISPPMELLE-----KSNIKASPTDLGRCAEPAF 171
 DB 179 GTVAEFTKADTVIFRTDLYNLITGRREYSFKRTLYKDSKMLDPNPNVSGDFVEYVLFEP 238
 QY 172 KTVAMKNNKATKYRPFYVDKSKRLC-----HIIYVS-MQMGKKKCVSKGSEPPDL 223
 DB 239 RETAVREYINGKGS-----VSRARVCKKQVGGKNIISQWMAFLAKRLNCSLPGFEP-- 291
 QY 224 TWYCFKPKRSV-----TENHLLIYGSAYVS-----ENPAFISKCPNQALRGY 266
 DB 292 --FYFNEIQGVYKMPNTDKFVGFSVTSVLTGSAICSPFLTKDIOEFVSGKFKQATSS- 348
 QY 267 RRGVW-----KKGKCLDYTE-LTDVTVERVESKQGVKVFENDGVASDQPHY 314
 DB 349 --SAMLVPLPSRVPDPPEGCVDTELLPDTVLNFRSH-----VGRN--YGFYYVD 385
 QY 315 PLTSQASWMDWPLHOSDQPHSGG-----VGRN--YGFYYVD 349

DB 386 -----PLMDGAVSHGEGKPYFKADVLFTQVLVDKLKYNLWGNMEYIVVYAG 433
 QY 350 TTGECKALSDQVDPCLVSDSAAYSITAGSLSETPFIIISNPSVTPPETALQCTA 409
 DB 434 TS-----TSQV-----XKVQWYDSSGL-----PQSLVDFDVTPEPVQALHLSK 475
 QY 410 DKFPDSFGACD-----VOACKRKQKTSVCGQIQISTSVDTAD-----EONECGSNT 455
 DB 476 E-YKSLVNASDNIYRQIQLFWNCHRYNSC-----LQCARDPYCGMDSDNSCKSYT 525
 RESULT 13
 ID DPP4_FELCA STANDARD; PRT; 765 AA.
 AC 09N217;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Dipeptidyl peptidase IV (EC.3.4.14.5) (DPP IV) (T-cell activation
 DE antigen CD26).
 GN DPP4 OR CD26.
 OS Fells silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=peripheral blood;
 RX MEDLINE=20094000; PubMed=10630304;
 RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
 RA Mikami T., Takahashi E.;
 RT "Molecular cloning and sequencing of a cDNA encoding the feline T-cell
 RT activation antigen CD26 homologue.";
 RL Immunogenetics 50:366-368(1999).
 CC -1- FUNCTION: Removes N-terminal dipeptides sequentially from the
 CC polypeptides having unsubstituted N-termini provided that the
 CC penultimate residue is proline (By similarity).
 CC -1- CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Xbb-|-
 CC Xcc, from a polypeptide, preferentially when Xbb is Pro, provided
 CC Xcc is neither Pro nor hydroxyproline.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists in
 CC a soluble form (By similarity).
 CC -1- PTM: The soluble form (SDPP) derives from the membrane form (MDPP)
 CC by proteolytic processing (By similarity).
 CC -1- SIMILARITY: Belongs to peptidase family S9b.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL: AB023952; BAA92344.1; -.
 DR MEROPS: S09.003; -.
 DR InterPro: IPR002469; DPP4V_N-term.
 DR InterPro: IPR001375; Peptidase_S9.
 DR InterPro: IPR002471; Prol_endopep_ser.
 DR InterPro: IPR000379; Ser_catr_site.
 DR Pfam: PF00930; DPP4V_N-term; 1.
 DR Pfam: PF00326; Peptidase_S9; 1.
 DR PROSITE: PS00708; PRO_ENDOPEP_SER; 1.
 KW Hydroxylase; Aminopeptidase; Dipeptidase; Serine protease;
 KW Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 765 DIPEPTIDYL PEPTIDASE IV MEMBRANE FORM
 FT CHAIN 1 765 (MDPP).
 FT CHAIN 38 765 DIPEPTIDYL PEPTIDASE IV SOLUBLE FORM
 FT DOMAIN 1 6 (SDPP) (BY SIMILARITY).
 FT TRANSMEM 7 29 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL 7 29 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).

FT	DOMAIN	933	979	EGF-LIKE.
FT	DOMAIN	983	1021	LDL-RECEPTOR CLASS A 1.
FT	DOMAIN	1022	1062	LDL-RECEPTOR CLASS A 2.
FT	DOMAIN	1063	1100	LDL-RECEPTOR CLASS A 3.
FT	DOMAIN	1103	1143	LDL-RECEPTOR CLASS A 4.
FT	DOMAIN	1143	1180	LDL-RECEPTOR CLASS A 5.
FT	DOMAIN	1180	1224	LDL-RECEPTOR CLASS A 6.
FT	DOMAIN	1230	1268	LDL-RECEPTOR CLASS A 7.
FT	DOMAIN	1273	1312	LDL-RECEPTOR CLASS A 8.
FT	DOMAIN	1324	1362	LDL-RECEPTOR CLASS A 9.
FT	DOMAIN	1376	1415	LDL-RECEPTOR CLASS A 10.
FT	DOMAIN	1419	1457	LDL-RECEPTOR CLASS A 11.
FT	DOMAIN	1462	1551	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	1559	>1592	FIBRONECTIN TYPE-III 2.
FT	DISULFID	985	997	BY SIMILARITY.
FT	DISULFID	992	1010	BY SIMILARITY.
FT	DISULFID	1004	1019	BY SIMILARITY.
FT	DISULFID	1024	1038	BY SIMILARITY.
FT	DISULFID	1032	1051	BY SIMILARITY.
FT	DISULFID	1045	1060	BY SIMILARITY.
FT	DISULFID	1065	1077	BY SIMILARITY.
FT	DISULFID	1072	1090	BY SIMILARITY.
FT	DISULFID	1084	1099	BY SIMILARITY.
FT	DISULFID	1105	1117	BY SIMILARITY.
FT	DISULFID	1112	1130	BY SIMILARITY.
FT	DISULFID	1124	1141	BY SIMILARITY.
FT	DISULFID	1145	1155	BY SIMILARITY.
FT	DISULFID	1150	1168	BY SIMILARITY.
FT	DISULFID	1162	1222	BY SIMILARITY.
FT	DISULFID	1232	1244	BY SIMILARITY.
FT	DISULFID	1239	1257	BY SIMILARITY.
FT	DISULFID	1251	1266	BY SIMILARITY.
FT	DISULFID	1275	1288	BY SIMILARITY.
FT	DISULFID	1283	1301	BY SIMILARITY.
FT	DISULFID	1295	1310	BY SIMILARITY.
FT	DISULFID	1333	1351	BY SIMILARITY.
FT	DISULFID	1345	1360	BY SIMILARITY.
FT	CARBOHYD	6	6	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	65	65	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	275	275	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	523	523	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	581	581	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	725	725	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	778	778	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	975	975	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1098	1098	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1152	1152	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1366	1366	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1454	1454	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1514	1514	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1552	1552	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	1592	1592	AA; 178409 MW; 24EDANA5EA231B203 CRC64;

Query Match	3.8%	Score 11.5	DB 1	Length 1592
Beet Local Similarity	22.2%	Pred. No. 2.3		
Matches	46	Conservative 24	Mismatches 88	Indels 49
				Gaps 9
Qy	271	WKKGRLD-----YT	ELDTVIERESKQ	CKWTFKENDGASDOPHTYPLT--SQASW 322
Db	829	WPNGISVDHWTYMT	EAYMDRIERVDNG-----LQ	RSVIDLSLPHPAIVAFKNEIYW 882
Qy	323	NDWWPLHOSDQ	HSGC-----VGRNYG-----	FYYVDTEEGCALSDQYPRDLVNS 370
Db	883	NMWSQSLIFRASKNS	GRMELTVGRYIGYIMDKIFRGKTTQ	ONACIAHPCLCLPMSN 942
Qy	371	AAVSYTAGSLSEET	ENFIIPNSPVTP	PETALQCTADKPPDSFACDVOACKOKTS 430
Db	943	NGRSKCCEPGVS-----	STVLSGSEVKDC-----	PHGYSMGN-NTCYAEENT 984
Qy	431	CVGGQIGQTSVDC-----	TADEONECG 452	
Db	985	CLPNQYRCFENGNC	INSIWOCDDNNDCG 1011	

ID	CATW	HUMAN	STANDARD	PRT	376	AA
AC	01-NOV-1997	(Rel. 35, Created)				
DT	01-NOV-1997	(Rel. 35, Last sequence update)				
DT	28-FEB-2003	(Rel. 41, Last annotation update)				
DE	Cathepsin W precursor	(EC 3.4.22.-) (Lymphopain)				
DE	CTSM					
OC	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
FX	MEDLINE=99039559; PubMed=9823953;					
RA	Brown J., Matutes E., Singleton A., Price C., Molgaard H., Buttle D.,					
RA	Enver T.;					
RT	"Lymphoblast, a cytotoxic T and natural killer cell-associated					
RL	cyteine proteinase.";					
RL	Leukemia 12:1771-1781(1998).					
RM	[2]					
RP	SEQUENCE FROM N.A.					
FX	MEDLINE=97261865; PubMed=9108299;					
RA	Limheers C., Smeekens S.P., Broemme D.;					
RA	"Human cathepsin W, a putative cysteine protease predominantly					
RT	expressed in CD8+ T-lymphocytes.";					
RL	FEBS Lett. 405:253-259(1997).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
FX	MEDLINE=98342076; PubMed=9675123;					
RA	Wex T., Levy B., Smeekens S.P., Ansgore S., Desnick R.J., Broome D.;					
RA	"Genomic structure, chromosomal localization, and expression of human					
RT	cathepsin W.";					
RL	Biochem. Biophys. Res. Commun. 248:255-261(1998).					
CC	-1- FUNCTION: MAY HAVE A SPECIFIC FUNCTION IN THE MECHANISM OR					
CC	REGULATION OF T-CELL CYTOLYTIC ACTIVITY.					
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN NATURAL KILLER AND CYTOTOXIC T					
CC	CELLS.					
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.					
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -					
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CC	use by non-profit institutions as long as its content is in no way					
CC	modified and this statement is not removed. Usage by and for commercial					
CC	or send an email to license@ibw-sib.ch).					
DR	EMBL, AF013611; AAB82449.1; -					
DR	EMBL, AF015954; AAB82457.1; -					
DR	EMBL, AF055903; AAC32181.1; -					
DR	HSSP, P14080; IYAL.					
DR	MEROPS, C01.037; -					
DR	Genew; HGNC:2546; CTSM.					
DR	MIM, 602364; -					
DR	GO, GO:0008234; F:cysteine-type peptidase activity; TAS.					
DR	GO, GO:0006955; F:immune response; TAS.					
DR	InterPro, IPR000668; Peptidase C1.					
DR	InterPro, IPR000169; SHProt_acsite.					
DR	Pfam, PF00112; Peptidase_C1; 1.					
DR	PRINTS, PR000705; PAPA1N_C1; 1.					
DR	ProDom, P000158; Peptidase_C1; 1.					
DR	SMART, SM00645; Pept_C1; 1.					
DR	PROSITE, PS00139; THIOI_PROTEASE_CYS; FALSE_NEG.					
DR	PROSITE, PS00639; THIOI_PROTEASE_HIS; 1.					
DR	PROSITE, PS00640; THIOI_PROTEASE_ASN; 1.					
KW	Hydrolase; Thiol protease; Glycoprotein; Signal; Zymogen.					
FT	SIGNAL	1	21	POTENTIAL.		
FT	PROPEP	22	127	POTENTIAL.		
FT	CHAIN	128	376	CATHEPSIN W.		


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FT ACT_SITE 153 153 BY SIMILARITY.
FT ACT_SITE 231 231 BY SIMILARITY.
FT ACT_SITE 331 331 BY SIMILARITY.
FT DISULFID 150 191 BY SIMILARITY.
FT DISULFID 184 226 BY SIMILARITY.
FT DISULFID 284 352 BY SIMILARITY.
FT CAROHXD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHXD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 376 AA; 42099 MW; 718DB8478916FB0 CRC64;

Query Match
Best Local Similarity 21.7%; Score 107.5; DB 1; Length 376;
Matches 92; Conservative 50; Mismatches 150; Indels 131; Gaps 23;

OY 8 VLVVLVADCTTFASGLSTRSRESQTLASSTGNPQNMKTFMERFNTL-----H 61
DB 10 LVALVAG---LAQIRGLRAQD-----LGPPLELKEAFKLFQIQFNSTVSPREH 59
OY 62 HHQSGIVY-----DLGQ-----DKEVDGTL--YREPAGLCPWGXHI 96
DB 60 AHRLDIFAHNLAAQARLOBEDLGTAEFGVTPSPDLTEEFQQLYGRRAAGVPSMGREI 119
OY 97 ELQOPDLRYRNNFLIEDVPTKEVYQSG---NPLGCGFNLN---FVTSQGRISFPNEL 150
DB 120 RSEEP-----ESVPSGDMRWKVAAGALSPIDOKKNCMMAMAAAGN-----IET 164
OY 151 LEKNS-----NIKASTDLGRCAE-----FAFKTVAMDKNNKATRYRPFYVSKK 195
DB 165 LWRISFMDPVDSVHLLDCCGCGGCGHGFWDVAFITV--LNSGLASEKDYPPGKRA 223
OY 196 RLCHILYVSMQMEKRYCYSVKGEPPDLTWYCFERKRSVTENHLI-----YGSAYVE 249
DB 224 HRCH-----PKYQKV-----AM--IQPIMQNNHRIAGVLAATYGPITVTI 264
OY 250 NPDAISKPNQALRGYRFGWKKRCIDYELTPTVI-----EYESKACQWVTFEND 304
DB 265 N-----MKPLDLYRKGVIKATPTTCDPLVHSHVILVGFSGVKEBEGIMATVSSQ 315
OY 305 GVASDQPTVPL--TSQASNDWMPHQSODPHSGGVNRYVDYDTGEGKCALSDOV-- 362
DB 316 S-QPPPHPTPYWILKNSGMAQMGKGYFRLHRS-----NTGCIITYPLTARVQ 364
OY 363 -PD 364
DB 365 KPD 367

RESULT 16
NFX1_HUMAN STANDARD; PRT; 1104 AA.
ID NFX1_HUMAN
AC Q12986;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transcriptional repressor NF-X1 (EC 6.3.2.-) (Nuclear transcription
factor, X box-binding, 1).
GN NFX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95053707; PubMed=7964459;
RA Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.;
RT "A novel cysteine-rich sequence-specific DNA-binding protein
RT interacts with the conserved X-box motif of the human major
RT histocompatibility complex class II gene via a heptanucleotide
RT domain and functions as a transcriptional repressor."
RL J. Exp. Med. 180:1763-1774(1994).
RP [2]
RP FUNCTION AS A E2-DEPENDENT UBIQUITIN LIGASE.
RP MEDLINE=99432238; PubMed=10500182;

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RA Lortick K.L., Jensen J.P., Pang S., Ong A.M., Hatakeyama S.,
RA Weisman A.M.;
RA "RING fingers mediate ubiquitin-conjugating enzyme (E2)-dependent
RA ubiquitination."
RL Proc Natl Acad Sci U S A. 96:11364-11369(1999).
CC -1- FUNCTION: Repressor of HLA-DRA transcription. Binds to the X-box
CC motif of MHC class II genes. May play an important role in
CC regulating the duration of an inflammatory response by limiting
CC the period in which MHC class II molecules are induced by
CC interferon gamma. Mediates E2-dependent ubiquitination.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- INDUCTION: By interferon gamma.
CC -1- DOMAIN: The RING-type zinc finger domain interacts with an
CC ubiquitin-conjugating enzyme (E2) and facilitates ubiquitination.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- SIMILARITY: Contains 1 R3H domain.
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CC EMBL; U15306; AAA69517.1; -.
CC PIR; I38869; I38869.
CC TRASNPAAC; T01694; -.
CC Genew; HGNC; 7803; NFX1.
CC MIM; 603255; -.
CC GO; GO:0003700; F:transcription factor activity; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0001032; P:negative regulation of transcription from P. . .; TAS.
CC GO; GO:0006356; P:transcription from pol II promoter; TAS.
CC InterPro; IPR001374; R3H.
CC InterPro; IPR000967; Znf_NFX1.
CC InterPro; IPR001965; Znf_PHD.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF01424; R3H; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC Pfam; PF01422; zf-NFX1; 8.
CC SMART; SM00393; R3H; 1.
CC SMART; SM00184; RING; 1.
CC SMART; SM00438; ZNF_NFX; 9.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS50089; ZF_RING_2; 1.
CC Ubl conjugation pathway; Ligase; Transcription regulation; Repressor;
CC DNA-binding; Nuclear protein; Repeat; Zinc-finger.
CC ZN_RING 342 393
FT DOMAIN 424 876
FT REPEAT 424 463
FT REPEAT 480 517
FT REPEAT 541 580
FT REPEAT 606 647
FT REPEAT 695 734
FT REPEAT 806 842
FT REPEAT 843 876
FT DOMAIN 992 1041
FT DOMAIN 1068 1073
SQ SEQUENCE 1104 AA; 123149 MW; 36FECA292F78130C CRC64;

Query Match
Best Local Similarity 19.7%; Score 107.5; DB 1; Length 1104;
Matches 103; Conservative 61; Mismatches 159; Indels 199; Gaps 29;

OY 85 PAGLCPIWKGKIELOQDRLEPYRNNPLEDVPTKEVYKQSGNPLPGFNLNFTVPSGORIS 144
DB 579 PCGGTPL-SQLBELGSSS-----RTKMDPVPSG--KVCGKPLPG--SLDFIHCEKLC 630
OY 145 PFMELLEKNKSNIKASTDLGRCAEFAPKTYAMD---KNNKATYRYPFYVD---SKRL 197
DB 631 EGDGPGVSRSTVISC-----RC---SPRTKELPCTSLKSDAT-----FMCDKRCNKKRL 677

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Query Match          3.6%; Score 106; DB 1; Length 415;
Best Local Similarity 21.1%; Pred. No. 1;
Matches 71; Conservative 24; Mismatches 91; Indels 150; Gaps 15;

OY 277 LDYELDTVIERVSKACQVKTFFENGVASD-----QHTYPLTQASAMNMPWPHQ 330
DB 112 LSYTSDSTVPPGAAKVHTVKPKNRPVLDYIFKCNVLTNLTPLVV--QKRWGHL 169
OY 331 SDQSGVSGVGNRYGYVDTTGECKALSDQVPCDCLVSDSAVSTAAGSLSETPNFI 390
DB 170 QAFQNGVNSKRN-----EVCYCE-EDQTPPTV---APIHTTPS-----TTTLT 210
OY 391 P-SNPSVTP-PPEETA-----LQCTADKFPDSF-----GAC 419
DB 211 PTSTPTPTPTPTPTVGNYSINGNTTCLATWGQLNITEKVPPIFINPATTFGTSC 270
OY 420 DVQA----- 423
DB 271 QPQSAQLRLNNSQIKYLDLIPAVNKKRFLKEVNVVYLANGSAFNISNKLSPWAPL 330
OY 424 -----CKRQKTSVCGQIQ-----STVDCATDEQNEGSGNTALAG 460
DB 331 GSSITWCKEQLVLSRAFOINTFNKQVPTNKTQVSTADQCSADEBNFL--VPIAVG 387
OY 461 LAVGCVLLALLGGCCYFAKRLDRNKGVQAAMHEHE 496
DB 388 AALGCVLITLVL---AYFI-----GLKRRHTGYE 413

RESULT 18
RPOC STRP3 STANDARD; PRT; 1207 AA.
ID RPOC STRP3
AC Q8K6W2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC OR SPY3 0076 OR SPS0077.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Betes S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RT Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RL (12)
RN SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurikawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes: a comparative analysis
RT of S. pyogenes SSI-1, SP370 and MGAS8232."
RT Submitted (May-2002) to the EMBL/Genbank/DBPST databases.
RL (1)
RN FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
RN OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
RN SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA] (N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

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CC
DB EMBL; AB014137; AAM78683.1;
DB EMBL; AP005141; BAC63172.1; ALT_INIT.
DB InterPro; IPR00722; RNA_pol_A.
DB InterPro; IPR006592; RNA_pol_A_N.
DB Pfam; PF04997; RNA_pol_Rp1_1; 1.
DB Pfam; PF00623; RNA_pol_Rp1_2; 1.
DB Pfam; PF04983; RNA_pol_Rp1_3; 1.
DB Pfam; PF05000; RNA_pol_Rp1_4; 1.
DB Pfam; PF04998; RNA_pol_Rp1_5; 1.
DB SMART; SM00663; RPOLA_N; 1.
DB Transferrase; DNA-directed RNA polymerase; Transcription;
KW Complete proteome.
FT CONFLICT 602 D -> N (IN REF. 2).
SO SEQUENCE 1207 AA; 134695 MW; 9672B98E0AA8745 CRC64;

Query Match          3.6%; Score 104; DB 1; Length 1207;
Best Local Similarity 19.3%; Pred. No. 6;
Matches 91; Conservative 54; Mismatches 166; Indels 160; Gaps 22;

OY 115 PTEKEYQSGNPLBGGNLFVTSPGQISFPFM-ELLEKN--SNIA----- 159
DB 349 PTLKMY-QCGVPRMAIEL-----FRFVREIYAEYAGVNAKRMVERGDRI 398
OY 160 -----STDIGRCABFAFKVAMDKNKKATKYRPV-----YDSKK 195
DB 399 WDILEYIKHPVLNAPTLHRGIDAFPEVLID--GKALRL-HPLVCEAYNADFPBGDQ 455
OY 196 RLCHILVSNQLMGCKKYCSVKGPPDLTYWCFKPKS---VTENHLLIYGSAVV----- 247
DB 456 MAIHV-PLSEBAQAEARLLMLAE-----HILNPKDGKPVPTSQMVVLCNYVLTWEDA 508
OY 248 GENDDAITISKCPNOLAGYRPGVKKGRCLDYTLTDTVIERVSKACQVKTFFENGVASD 307
DB 509 GREBEGMIFKDXKDAVNAVYRG-----YAHLSRV-----GIA 541
OY 308 SDQHTVPLTQASAMNMPWPHLQSDPHSGGVGNRYGYVDTTGECKALSDQVPCDCLV 367
DB 542 VDSMPNKP-----WKD-----SQRK-----IMTVVGKILFNDIMP----- 573
OY 368 SDSAAVSYTAAGSLSEETPNFIIPSNPSVTPPEETAQLQCTADKFPDSFGACDVQACKRQ 427
DB 574 -----EDLPYIQEBNNANLTGFTDKYFLERQGIQEVIDGLDINVPEKK 618
OY 428 KTSCVCG-----QISTVSDCTADQNEGSGNTALAGVGVLLALLGGCCYFAK 480
DB 619 KN--LGIINIAETFRKFTTETSAFLDKLDGYHSTAGITVGIADIPV----- 667
OY 481 RLDRNKG--VOAAHHEHFEFOSDRGARKKRPDSLQGBAEPSPWDAEENIEQ 529
DB 668 ---DNKALIIDAAHRYEINIKAFRRGLMTDDDRYVAVTTTWRAKALEK 715

RESULT 19
RPOC STRP3 STANDARD; PRT; 1213 AA.
ID RPOC STRP3
AC P95816;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC OR SPY0099.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

```

Query Match	Best Local Similarity	3.6%	Score 104	DB 1	Length 1213
Matches	91	Conservative	55	Mismatches	165
				Indels	160
				Gaps	22

QY	111	PREPEKSGNSGLPGGFNLFVTFPGQGISFPPV-ELLEKN--SNIA	159
Db	349	PLTKMT-QCCVREMAIEL-----FKPPVREIYAAKEAGNVAAARMVERGERI	398
QY	160	-----STDLCRCAEFAKTVAMDKNKIKTKRYFPV-----YDSKK	195
Db	399	WDILEEVIKEHPVLNRAPTLHRIGIQAFEPVLID--GKALRL-HPLVCEAYNADFDGQ	455
QY	196	RLCHILIVYMQLMEGKTKCSVKGEPPDLTWCFPRKS---VTENHHLIYSAYV-----	247
Db	456	MAIIV-PLSEEAQAEARLMLAAE-----HILNPKGKGPVYPSQDMVLGNVYLTWEDA	508
QY	248	GENPDAFISCKNOALRGYRFGVKKGCRLDYETLTDTVIERVESKAQCWTKFENDGVA	307
Db	509	GREGEEMTKKDKDEAVMAYRNG-----YALHLSRV-----GIA	541
QY	308	SDQPHTYPLTSQASNMWMLPHQSDOPHSGGVGRNGFYVDITGEGKALSQVDPCLV	367
Db	542	VDSEMPKP-----WKD-----NQRRK-----IMVTYVKGILFNDIMP-----	573
QY	368	SDSAVSYTAAGSLSEETPNFIIPSNESVTPPTETALQCTADKFPSPFACDYQACKRQ	427
Db	574	-----EDLPYLOEPPNNAMLTGTDPKFLEPGQDIOEVIDRLDINVPFKK	618
QY	428	KTSCVGG-----QIGTSVDCTADEQNEGSGNTALAGVAGVLLALLGSGCVFAK	480
Db	619	KN--LGNIIAETFPKPRRTTETSAPFLDKIDGYHSTLAGITLVIIADIPVI-----	667
QY	481	RLDRNGK--VQAAHHEHESFOSDRGARKRPPDLMOEAEPSPWDEAEENIEQ	529
Db	668	---DNKAELIIDAHHRVEIINKAPFRGLMTDDRYVAVTTTWBRKALKLEK	715
RESULT 20			
ERB2_HUMAN			
ID	ERB2_HUMAN	STANDARD;	PRT; 1255 AA.
AC	P046Z6;		
DT	13-AUG-1987	(Rel. 05, Created)	
DT	13-AUG-1987	(Rel. 05, Last sequence update)	
DT	15-SEP-2003	(Rel. 42, Last annotation update)	
DE	Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)		
DE	(p185erbB2) (NBU proto-oncogene) (C-erbB-2) (Tyrosine kinase-type cell		
DE	surface receptor HER2) (MEN 19).		
GN	ERBB2 OR HER2 OR NGL OR NEU.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=6118663; PubMed=3003577;		
RA	Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,		
RA	Saito T., Toyoshima K.;		
RT	"Similarity of protein encoded by the human c-erb-B-2 gene to		
RL	epidermal growth factor receptor."		
RL	Nature 319:230-234(1986).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=66070181; PubMed=2999974;		
RA	Cousens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A.,		
RA	McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J.,		
RA	Finckle U., Levinson A., Ullrich A.;		
RT	"Tyrosine kinase receptor with extensive homology to EGF receptor		
RL	shares chromosomal location with neu oncogene."		
RL	Science 230:1132-1139(1985).		
RN	[3]		
RP	SEQUENCE OF 737-1031 FROM N.A.		
RX	MEDLINE=66016729; PubMed=2955967;		
RA	Semba K., Kamata N., Toyoshima K., Yamamoto T.;		
RT	"A v-erbB-related protooncogene, c-erbB-2, is distinct from the		
RL	c-erbB-1/epidermal growth factor-receptor gene and is amplified in a		
RL	human salivary gland adenocarcinoma."		
RL	Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).		

[4]
 RP VARIANTS VAL-654 AND VAL-655.
 RX MEDLINE=93194196; PubMed=8095488;
 RA Ehsani A., Low J., Wallace R.B., Wu A.M.;
 RT "Characterization of a new allele of the human ERBB2 gene by allele-
 RT specific competition hybridization.";
 RL Genomics 15:426-429(1993).
 CC -1 FUNCTION: Essential component of a neuoregulin-receptor complex,
 CC although neuregulins do not interact with it alone. GP30 is a
 CC potential ligand for this receptor. Not activated by EGF, TGF-
 CC alpha and amphiregulin.
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1 SUBUNIT: Heterodimer with each of the other ERBB receptors
 CC (Potential). Interacts with PRKCAP (By similarity).
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 PTM: Ligand-binding increases phosphorylation on tyrosine
 CC residues (By similarity).
 CC -1 POLYMORPHISM: There are four alleles due to the variations in
 CC positions 654 and 655. Allele B1 (654-Ile-Ile-655) has a frequency
 CC of 0.782; allele B2 (654-Ile-Val-655) has a frequency of 0.206;
 CC allele B3 (654-Val-Val-655) has a frequency of 0.012.
 CC -1 SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CC -----
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 CC -----
 DR EMBL, M11767; AAA35808.1; JOINED.
 DR EMBL, M11761; AAA35808.1; JOINED.
 DR EMBL, M11762; AAA35808.1; JOINED.
 DR EMBL, M11763; AAA35808.1; JOINED.
 DR EMBL, M11764; AAA35808.1; JOINED.
 DR EMBL, M11765; AAA35808.1; JOINED.
 DR EMBL, M11766; AAA35808.1; JOINED.
 DR EMBL, M11730; AAA35493.1; JOINED.
 DR EMBL, M12036; AAA35978.1; JOINED.
 DR EMBL, X03363; CAA27060.1; JOINED.
 DR PIR, A24571; A24571.
 DR PDB, 1N82; 18-FEB-03.
 DR PDB, 1QR1; 01-JAN-00.
 DR Gene: HGNC:3430; ERBB2.
 DR MIM, 164870; ERBB2.
 DR GO, GO:0005012; F:Neu/ErbB-2 receptor activity; TAS.
 DR GO, GO:0004716; F:receptor signaling protein tyrosine kinase . . ; TAS.
 DR GO, GO:0008283; P:cell proliferation; TAS.
 DR GO, GO:0007048; P:oncogenesis; TAS.
 DR GO, GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR GO, GO:0006469; P:protein amino acid phosphorylation; TAS.
 DR InterPro: IPR000494; EGFR_L_domain.
 DR InterPro: IPR006211; Furin-like.
 DR InterPro: IPR006212; Furin repeat.
 DR InterPro: IPR000719; Prot Kinase.
 DR InterPro: IPR001245; Tyr_Kinase.
 DR InterPro: IPR004019; YLP_motif.
 DR Pfam, PF00757; Furin-like; 1.
 DR Pfam, PF00069; pkinase; 1.
 DR Pfam, PF02757; Recep_L_domain; 2.
 DR Pfam, PF02757; YLP; 2.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD000001; Prot_Kinase; 1.
 DR SMART, SM00261; FU; 4.
 DR SMART, SM00219; TYRKIN; 1.
 DR PROSITE, PS0107; PROTEIN KINASE ATP; 1.
 DR PROSITE, PS0109; PROTEIN KINASE TYR; 1.
 DR PROSITE, PS0011; PROTEIN KINASE DOM; 1.
 KW Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
 KW transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Polymorphism; 3D-structure.

FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	1255	RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
FT	DOMAIN	22	1255	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	653	675	POTENTIAL.
FT	DOMAIN	676	1255	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	720	987	PROTEIN KINASE.
FT	NP_BIND	726	734	ATP (BY SIMILARITY).
FT	BINDING	753	753	ATP (BY SIMILARITY).
FT	ACT_SITE	845	845	BY SIMILARITY.
FT	DISULFID	195	204	BY SIMILARITY.
FT	DISULFID	199	212	BY SIMILARITY.
FT	DISULFID	220	227	BY SIMILARITY.
FT	DISULFID	224	235	BY SIMILARITY.
FT	DISULFID	236	244	BY SIMILARITY.
FT	DISULFID	240	252	BY SIMILARITY.
FT	DISULFID	255	264	BY SIMILARITY.
FT	DISULFID	268	295	BY SIMILARITY.
FT	DISULFID	299	311	BY SIMILARITY.
FT	DISULFID	315	331	BY SIMILARITY.
FT	DISULFID	334	338	BY SIMILARITY.
FT	DISULFID	511	520	BY SIMILARITY.
FT	DISULFID	515	528	BY SIMILARITY.
FT	DISULFID	531	540	BY SIMILARITY.
FT	DISULFID	544	560	BY SIMILARITY.
FT	DISULFID	563	576	BY SIMILARITY.
FT	DISULFID	567	584	BY SIMILARITY.
FT	DISULFID	587	596	BY SIMILARITY.
FT	DISULFID	600	623	BY SIMILARITY.
FT	DISULFID	626	634	BY SIMILARITY.
FT	DISULFID	630	642	BY SIMILARITY.
FT	MOD_RES	1139	1139	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	1248	1248	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CARBOHYD	68	68	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	124	124	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	187	187	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	259	259	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	530	530	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	571	571	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	629	629	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	VARIANT	654	654	I -> V (IN DBSNP:1801201).
FT	VARIANT	655	655	/FTID=VAR_004077.
FT	VARIANT	655	655	I -> V (IN DBSNP:1801200).
FT	CONFLICT	1170	1170	/FTID=VAR_004078.
FT	CONFLICT	1170	1170	P -> A (IN REF. 2).
FT	SEQUENCE	1255 AA; 137909 MW; 3959DPA04DC962 CRC64;		

Query Match 3.6%; Score 104; DB 1; Length 1255;
 Best local similarity 22.5%; Pred. No. 6.3;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

QY	81	LYRPPAGLCPIWGHIELOQDRLPYRNNFIEDVPTKEYQSGNPLPG--FNLNPFVT	137
DB	256	LHFNHSGIC-----ELHCPALVTYNTDFESMPN-----PEGYTFGASCVT	297
QY	138	PSGORISPPFMWELKSNINIKASTDLGRCAEFA---FKTVAMDKNKATRYRPFVYDS	193
DB	298	AC-----PYNVL-----STDVSGCTLVGLVHNOGYVAEGTGRCEKSCFCA---	339
QY	194	KGRLLCH-----ILYVSKQLMEKKYTC-----SYKEPPDLTWYCFKPRK	232
DB	340	--RVCYGIGMEHLEKRVAVTSANIOEFAGCKIFGSLAFLPESPDGPASNTAALOPEQL	397
QY	233	SVTEHHLLIYGSAVVGSPDAF--ISKCPN-QALRG-----YRQGV-WKRGRC	276
DB	398	QVFETLEITGYLYTISMPDLSPLSVQNIQVIRGILHNAGAYSLTLOGIGISWLGIRS	457
QY	277	LDYTELTDVTLERVESKACQVKTFFENDGVAADQ---PHTYPLTSQASWMDWMLHOSD	332
DB	458	L--RELDSGLALIHNNHLCFVHT-----VPWDLFPNPH-----QAL-----LITAN	498
QY	333	QPHSGGVGRNRYGVYVDTEE-----GKCALSDQ-----VPDLVSSAASVYPAAG	379
DB	499	RFDECEVGEGLACHQLCARGHCMGPGPTQCVNCSQFLRGQCEVCECHVLOGLPREYVNAR	558

QY 380 SLSEETPNFIPNSVTPTPTALQCTAD-----KF 412
 DB 559 HCLPCHPE-COPONSGVTCFGE-ADQCACAHYKDPFCVACRCPGKVPDLSTYPIWKF 616
 QY 413 PDSEACVQACKQKTKSCVGGQIGSTSVDCADSEONGSNTALAGLAVGVLLALL 472
 DB 617 PDSEAC--QPC---PINCTHSCVLDLDDKXCPAEOR--ASPLTSLIS--AVVGILLVVL 667
 QY 473 G 473
 DB 668 G 668
 RESULT 21
 FBN1 HUMAN
 ID FBN1 HUMAN STANDARD; . PRT; 2871 AA.
 AC P35555;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrillin 1 precursor.
 GN FBN1 OR FBN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=placenta;
 RX MEDLINE=93372860; PubMed=8364578;
 RA Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,
 RA Panglilhan T., Bonadio J.,
 RT "Genomic organization of the sequence coding for fibrillin, the
 RT defective gene product in Marfan syndrome.";
 RL Hum. Mol. Genet. 2:961-968(1993).
 RN (2)
 RP SEQUENCE OF 1-932 FROM N.A.
 RC TISSUE=fibroblast, and Placenta;
 RX MEDLINE=94010947; PubMed=7691719;
 RA Corson G.M., Chalberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.,
 RT "Fibrillin binds calcium and is coded by CDNA's that reveal a
 RT multidomain structure and alternatively spliced exons at the 5'
 RT end.";
 RL Genomics 17:476-484(1993).
 RN (3)
 RP SEQUENCE OF 899-2871 FROM N.A.
 RX MEDLINE=91304568; PubMed=1852207;
 RA Maslen C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.,
 RT "Partial sequence of a candidate gene for the Marfan syndrome.";
 RL Nature 352:334-337(1991).
 RN (4)
 RP SEQUENCE OF 813-1313 FROM N.A.
 RX MEDLINE=91304567; PubMed=1852206;
 RA Lee B., Godfrey M., Vitale E., Horl H., Mattei M.-G., Sarfarazi M.,
 RA Tsipouras P., Ramirez F., Hollister D.W.,
 RT "Linkage of Marfan syndrome and a phenotypically related disorder to
 RT two different fibrillin genes.";
 RL Nature 352:330-334(1991).
 RN (5)
 RP CHARACTERIZATION.
 RX MEDLINE=91317849; PubMed=1860873;
 RA Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.P.,
 RT "Purification and partial characterization of fibrillin, a cysteine-
 RT rich structural component of connective tissue microfibrils.";
 RL J. Biol. Chem. 266:14763-14770(1991).
 RN (6)
 RP STRUCTURE BY NMR OF 2054-2125.
 RX MEDLINE=98031893; PubMed=9362480;
 RA Yuan X., Downing A.K., Knott V., Handford P.A.,
 RT "Solution structure of the transforming growth factor beta-binding
 RT protein-like module, a domain associated with matrix fibrils.";
 RL EMBO J. 16:6659-6666(1997).

RN (7)
 RP STRUCTURE BY NMR OF 2124-2205.
 RX MEDLINE=96144829; PubMed=856869;
 RA Knott V., Downing A.K., Cardy C.M., Handford P.A.,
 RT "Calcium binding properties of an epidermal growth factor-like domain
 RT from human fibrillin-1.";
 RL J. Mol. Biol. 255:22-27(1996).
 RN (8)
 RP STRUCTURE BY NMR OF 2124-2205.
 RX MEDLINE=96222301; PubMed=8653794;
 RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,
 RA Handford P.A.,
 RT "Solution structure of a pair of calcium-binding epidermal growth
 RT factor-like domains: implications for the Marfan syndrome and other
 RT genetic disorders.";
 RL Cell 85:597-605(1996).
 RN (9)
 RP REVIEW ON MPS VARIANTS.
 RX MEDLINE=96174615; PubMed=8594563;
 RA Colod G., Beroud C., Soueisi T., Junten C., Boileau C.,
 RT "Software and database for the analysis of mutations in the human
 RT FBN1 gene.";
 RL Nucleic Acids Res. 24:137-141(1996).
 RN (10)
 RP REVIEW ON MPS VARIANTS.
 RX MEDLINE=97169383; PubMed=9016526;
 RA Colod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,
 RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,
 RA Richards R.I., Wang W., Junten C., Boileau C.,
 RT "Marfan Database (second edition): software and database for the
 RT analysis of mutations in the human FBN1 gene.";
 RL Nucleic Acids Res. 25:147-150(1997).
 RN (11)
 RP REVIEW ON VARIANTS.
 RX MEDLINE=96062175; PubMed=9401003;
 RA Hayward C., Brock D.J.H.,
 RT "Fibrillin-1 mutations in Marfan syndrome and other type-1
 RT fibrillinopathies.";
 RL Hum. Mutat. 10:415-423(1997).
 RN (12)
 RP VARIANT MPS PRO-1137.
 RX MEDLINE=91304569; PubMed=1852208;
 RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,
 RA Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,
 RA Christen S.M., Stetten G., Meyers D.A., Francomano C.A.,
 RT "Marfan syndrome caused by a recurrent de novo missense mutation in
 RT the fibrillin gene.";
 RL Nature 352:337-339(1991).
 RN (13)
 RP VARIANTS MPS SER-1249; ARG-1663; SER-2221 AND SER-2307.
 RX MEDLINE=93250834; PubMed=1301946;
 RA Dietz H.C., Saraiva J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.,
 RT "Clustering of fibrillin (FBN1) missense mutations in Marfan syndrome
 RT patients at cysteine residues in EGF-like domains.";
 RL Hum. Mutat. 1:366-374(1992).
 RN (14)
 RP VARIANT MPS SER-2307.
 RX MEDLINE=92235290; PubMed=1569206;
 RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J. Jr.,
 RA Corson G.M., Maslen C.L., Sakai L.Y., Francomano C.A., Cutting G.R.,
 RT "Marfan phenotype variability in a family segregating a missense
 RT mutation in the epidermal growth factor-like motif of the fibrillin
 RT gene.";
 RL J. Clin. Invest. 89:1674-1680(1992).
 RN (15)
 RP VARIANTS MPS ILB-548 AND ALA-723.
 RX MEDLINE=94010946; PubMed=8406497;
 RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chalberg S.C.,
 RA Pyeritz R.E., Francomano C.A.,
 RT "Four novel FBN1 mutations: significance for mutant transcript level
 RT and EGF-like domain calcium binding in the pathogenesis of Marfan
 RT syndrome.";
 RL Genomics 17:468-475(1993).

RN [16]
 RP VARIANTS MFS SER-2144.
 RA MEDLINE=93278402; PubMed=8504310;
 RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;
 RT "A novel fibrillin mutation in the Marfan syndrome which could
 RT disrupt calcium binding of the epidermal growth factor-like module."
 RL Hum. Mol. Genet. 2:475-477(1993).
 RN [17]
 RP VARIANTS MFS ARG-862; TYR-1117; PRO-1137 AND PHE-1589, AND VARIANT
 RP ALA-1148.
 RX MEDLINE=94108431; PubMed=8281141;
 RA Tyman K., Comau K., Pearson M., Milgenbus P., Levitt D., Gaesner C.,
 RA Berg M.A., Miller D.C., Francke U.;
 RT "Mutation screening of complete fibrillin-1 coding sequence: report
 RT of five new mutations, including two in 8-cysteine domains."
 RL Hum. Mol. Genet. 2:1813-1821(1993).
 RN [18]
 RP VARIANTS MFS GLY-217 AND ARG-2627.
 RX MEDLINE=95067970; PubMed=7977366;
 RA Karttunen L., Raghunath M., Loengqvist L., Peltonen L.;
 RT "A compound-heterozygous Marfan patient: two defective fibrillin
 RT alleles result in a lethal phenotype."
 RL Am. J. Hum. Genet. 55:1083-1091(1994).
 RN [19]
 RP VARIANT EL LYS-2447.
 RX MEDLINE=94245249; PubMed=8188302;
 RA Longqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,
 RA Peltonen L.;
 RT "A novel mutation of the fibrillin gene causing ectopia lentis."
 RL Genomics 19:573-576(1994).
 RN [20]
 RP VARIANT MFS CYS-627.
 RX MEDLINE=94272487; PubMed=8004112;
 RA Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;
 RT "Two novel mutations and a neutral polymorphism in EGR-1-like domains
 RT of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan
 RT syndrome patients."
 RL Hum. Mol. Genet. 3:373-375(1994).
 RN [21]
 RP VARIANT MFS CYS-122.
 RX MEDLINE=94314977; PubMed=8040326;
 RA Stahl-Hallengren C., Ukkonen T., Kainulainen K., Kristofersson U.,
 RA Saxne T., Tornqvist K., Peltonen L.;
 RT "An extra cysteine in one of the non-calcium-binding epidermal growth
 RT factor-like motifs of the FBN1 polypeptide is connected to a novel
 RT variant of Marfan syndrome."
 RL J. Clin. Invest. 94:709-713(1994).
 RN [22]
 RP VARIANT MFS TYR-1223.
 RX MEDLINE=94351682; PubMed=8071963;
 RA Hewett D.R., Lynch J.R., Child A., Sykes B.C.;
 RT "A new missense mutation of fibrillin in a patient with Marfan
 RT syndrome."
 RL J. Med. Genet. 31:338-339(1994).
 RN [23]
 RP VARIANT MFS HIS-1170.
 RX MEDLINE=95174777; PubMed=7870075;
 RA Hayward C., Porteous M.E.M., Brock D.J.H.;
 RT "A novel mutation in the fibrillin gene (FBN1) in familial
 RT aortic dissection."
 RL Mol. Cell. Biol. 13:325-327(1994).
 RN [24]
 RP VARIANTS MFS GLY-217; ASN-1023; ARG-1074; TYR-1242; ARG-1513;
 RP GLU-2127; TRP-2151; LYS-2447 AND ARG-2511.
 RX MEDLINE=94184368; PubMed=8136887;
 RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.;
 RT "Mutations in the fibrillin gene responsible for dominant ectopia
 RT lentis and neonatal Marfan syndrome."
 RL Nat. Genet. 6:64-69(1994).
 RN [25]

Query Match 3.5%; Score 102; DB 1; Length 2871;
 Best Local Similarity 21.9%; Pred. No. 27;

Matches 114; Conservative 61; Mismatches 212; Indels 134; Gaps 32;
 QY 19 PASGLSSSTR--ESOTLASTSGNPQAVNEMKTFM--ERFNLTHHGGIYVDLQD 74
 DB 2065 FEGGKCSSPKRNRNSKDECCALKGEGMDPCELCPTEPDDAFROICRYGGIIVG-PDD 2123
 QY 75 KEVDGTLVREPAGLCPIWKGHIELQPD-----RLPYRNNFLVDYPTREKXKQSGNPLPG 129
 DB 2124 SAVDMECKEP-DVC-----KHGCCINTGYSRCPECFYTLAGNECVDTDCSGVNCPCGN 2178
 QY 130 GPNNL---FVTPSGQRISPPMELLENKSNIKASTDGRCAEFAFKVAADKNNKATKY 185
 DB 219 GTCRNVIGSFECTCEGEPBPMTCE-----DINECAQ-----NPLCAF 2219
 QY 186 RYFPYDSEKRLCHLYVSMQMEGKKYCSYKGEPPDITWCFKPR---KSVTEHHILY 242
 DB 2220 RCVNTGYSCEKCPVGYV---LREDRRCKDEDECEBKADCTEKQMECKNLIGYMCIC 2276
 QY 243 GSAYVGNPDFAFISCPNQLRGYRFGVKKGRCLD---YT-ELTDTVI-----ERVE 291
 DB 2277 GPQY-QRRPDG--EGCVDENECQTKPGICENGRCINTRGSYTCENDDFTASPNQDECLD 2333
 QY 292 SK-AQCWVKTEN--DGVASDQHTYPLTSQASNNMWPJHSDQPHSGV----- 339
 DB 2334 NREGYCFTEVLQNMCOIGSSNRNPVTSECCCDGGRGWP-HCEICPQGTVAFAKGLCPH 2392
 QY 340 GRNGF-----YVDTGEGKALSQVDP-----CLVDSAAVSYTAAGSL 381
 DB 2393 GR-GFMTNGADIDCKYIHVCNNGEC-----VNDKSGHYICCTGYTPIPTIGSCVDL 2445
 QY 382 SE-ETP---NFILPSNPSTVTPPETALQCTADK---PPDSFGACDVQACKRQKTSK- 431
 DB 2446 NECNQAPKPCNFICNT-----EGSYQSCSKGYVILQSDGSKCLDLCATKQKQNCQ 2497
 QY 432 -----VGG-----QIQTSTVD---CTADEQNEGCS 453
 DB 2498 FLCVNTIGFTCKCPGFTQHTSCIDNNECTSD-INLCSG 2537
 RESULT 22
 CYP_WHEAT STANDARD; PRT; 320 AA.
 AC P05151;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apocytochrome f precursor.
 GN PETA.
 OS Triticum aestivum (Wheat).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Willey D.L., Howe C.J., Aufret A.D., Bowman C.M., Dyer T.A.,
 RA Gray J.C.;
 RT "Location and nucleotide sequence of the gene for cytochrome f in
 RT wheat chloroplast DNA."
 RL Mol. Gen. Genet. 194:416-422(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN:cv. Chinese Spring;
 RA Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shina T.,
 RA Terachi T., Utsumi S., Murata M., Mori N., Takumi S., Ikeo K.,
 RA Gotohori T., Murai R., Murai K., Matsuoaka Y., Ohnishi Y., Tajiri H.,
 RA Tanuawaki K.;
 RT "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
 RT complete sequence and contig clones."
 RL Plant Mol. Biol. Rep. 18:243-253(2000).
 CC -I- FUNCTION: Translocates protons across the thylakoid membrane and
 CC transfers electrons from photosystem II to photosystem I. It


```

CC receives electrons from the Rieske iron-sulfur protein and passes
CC them to plastocyanin.
CC -1- SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
CC protein (by similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-
CC anchored (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome c family.
CC -----
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CC -----
CC EMBL, X00538; CA25213.1; -.
CC EMBL, AB042240; BAB47046.1; -.
CC PIR, S07296; S07296.
CC HSP, P36438; 1HCZ.
CC HAMAP, MF_00610; -.
CC InterPro: IPR002325; Apocyt_F.
CC InterPro: IPR000345; Cyt c heme bind.
CC Pfam: PF01333; Apocytochrome F; 1.
CC PRINTS: PR00610; CYTOCHROME_F.
CC PROSITE: PS00190; CYTOCHROME_C; 1.
CC Electrophoretic transfer; Heme; Chloroplast; Thylakoid; Photosynthesis;
CC Photosystem I; Photosystem II; Transmembrane; Signal.
CC SIGNAL 1 35
CC CHAIN 36 320
CC TRANSMEM 286 305
CC METAL 36 36
CC BINDING 56 56
CC METAL 59 59
CC METAL 60 60
CC CONFLICT 291 294
CC CONFLICT 303 307
CC SEQUENCE 320 AA; 35363 MW; 721D2B3188552289 CRC64;

```

Query Match 3.5%; Score 101.5; DB 1; Length 320;
 Best Local Similarity 21.8%; Pred. No. 1.6;
 Matches 69; Conservative 37; Mismatches 91; Indels 119; Gaps 19;

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QY 83 REPAGL-----CPWGHHELOQDPDLPRNNFLD-----VTEKEYKO-SCNPRL 128
DB 48 REATGRIVCANMCHASKRPVDIEVPOAV-----LPDTEVAVLRIEYDMLQKVLANGKK 101
QY 129 GGNLNL--FVTPSG-----QRISPPMELLEKNINIKASTDLCRAEFAFKTVANDKNN 180
DB 102 GGLNVAQVLLPFGFELAPPRDRISP---ELKEKIGNL-----AFQSYRPDKKN 146
QY 181 KATKYRYPFYVDSKELCHILVYSMOLMEGKKYCSVKGEPDLTWYCFKPRKSVTENHH 240
DB 147 -----ILVIGP---VPEKKY-----SEIVFPLSDPRTKDDAHP 178
QY 241 IYGSAYGEN-----PDAFISKCPNOLKRGYFVWKK-----GRCLDTELTLD-- 284
DB 179 LKPIPIVGGNKGQIYPPDG--SKSNNTVYATSTGIVKILKEKGGYEISITVDSOR 236
QY 285 TVIERVESKQACVWKPFPENDGVASDOPHTYPLTQSASNDWMLHOSDOPHSGGVGRNG 344
DB 237 QVIDIIPPEBELLS--EGESIKLDO---PLTS-----NNVGGFQD--- 273
QY 345 FYVVDYTGEGKCALSD 360
DB 274 -----GDAEIVLQD 282

```

RESULT 23
 RPOC_STRP8
 ID_RPOC_STRP8 STANDARD; PRT; 1213 AA.
 AC Q8P2T2;

```

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC OR SPY18 0100.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CC NCBI_TaxID=186103;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=MCA8232 / Serotype M18;
CC MEDLINE=21927593; PubMed=11917108;
CC Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
CC Sylva G.L., Scudervant D.E., Ricklefs S.M., Porcella S.F.,
CC Parkins L.D., Beyer S.B., Campbell D.S., Smith T.M., Zhang Q.,
CC Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
CC "Genome sequence and comparative microarray analysis of serotype M18
CC group A streptococcus strains associated with acute rheumatic fever
CC outbreaks.";
CC Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC -----
CC EMBL, AB009961; AAL96913.1; -.
CC InterPro: IPR000722; RNA_pol_A.
CC InterPro: IPR007080; RNA_pol_Rpb1_1.
CC InterPro: IPR007066; RNA_pol_Rpb1_3.
CC InterPro: IPR007083; RNA_pol_Rpb1_4.
CC InterPro: IPR007081; RNA_pol_Rpb1_5.
CC Pfam: PF04997; RNA_pol_Rpb1_1; 1.
CC Pfam: PF04997; RNA_pol_Rpb1_1; 1.
CC Pfam: PF04997; RNA_pol_Rpb1_2; 1.
CC Pfam: PF04983; RNA_pol_Rpb1_3; 1.
CC Pfam: PF05000; RNA_pol_Rpb1_4; 1.
CC Pfam: PF04998; RNA_pol_Rpb1_5; 1.
CC Transferrase; DNA-directed RNA polymerase; Transcription;
CC Complete proteome.
CC SEQUENCE 1213 AA; 135305 MW; 0A9462ACA37E5DA CRC64;

```

Query Match 3.4%; Score 100; DB 1; Length 1213;
 Best Local Similarity 19.1%; Pred. No. 12;
 Matches 90; Conservative 55; Mismatches 166; Indels 160; Gaps 22;

```

QY 115 PTEKEYKSGNPLPGFNLNFTVPSGORISPPM-ELLEKN--SNKA----- 159
DB 349 PTLKNV--QCGVREMAIEL-----FKPVMKEIYAKVAGNVAKAKAVERGDERI 398
QY 160 -----STDLCRAEFAFKTVAMKNNKATYRYPF-----YDSKK 195
DB 399 WDLEBEVIEKHPVLLNRAPTLARIQIAFEPLID--GKALRL--HPLVCEAVNADPFGDQ 455
QY 196 RLCHILVYSMOLMEGKKYCSVKGEPDLTWYCFKPRKS---VTENHHIYGSAYV----- 247
DB 456 MAIHV--PLSEEAQAEKRLMLAAE-----HILNPKDGKPVVTPSQDVLGNYVLTMDA 508
QY 248 GENPDAFISKCPNOLKRGYFVWKKGRCLDYTELTDTVIERVESKQACVWTFPNDGVA 307

```

Db 509 GREGGMI FKQDEAVMAYRNG-----YAHLSRV-----GIA 541
 Qy 308 SDQPTHTYLTQASWMDWMLHSDQPHSGVGRNYGYVDTTGGKALSDQVDCLV 367
 Db 542 VDSMWNK-----WKD-----SQRHK-----IMVTVGLKFLNDIMP----- 573
 Qy 368 SDSAAVSYTAGSLEETPNFIPSPVPTPEPTALQCTADKPPDSFGACDVQACKRQ 427
 Db 574 -----EDLPYLQEPNNANULTGCTPDKXFLPEPQDIQEVIDGLEINVPFKK 618
 Qy 428 KTCSCVGS-----QIQTSDVCTADQNEGCSNALLAGLAVGVLLALLGGCCYPAK 480
 Db 619 KN--LGNIIATFKKFRFTETSAFLDRKLDGYHSTLAGLVGIADIPVI----- 667
 Qy 481 RLDRNKG--VOAAHHEHEFOSDGRGARKRPSPLMGQEPSPFDEAENIEQ 529
 Db 668 ---DNKAEIIDAAHRAVEINKAFRRGLMTDDDRVAVATTTWREAKEALEK 715

RESULT 24
 RRPL_MABVP STANDARD; PRT; 2331 AA.
 ID RRPL_MABVP
 AC P35262.
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RNA-directed RNA polymerase (EC 2.7.7.48) (large structural protein)
 GN L.
 OS Marburg virus (strain Popp).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
 OC Marburg-like viruses.
 OX NCBI_TaxID=333728;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96028047; Pubmed=7487490;
 RA Butreyev A.A., Volichkov V.E., Blinov V.M., Dryga S.A., Netesov S.V.;
 RT "The complete nucleotide sequence of the Popp (1967) strain of Marburg
 virus: a comparison with the Musoke (1980) strain.";
 RL Arch. Virol. 140:1589-1600(1995)
 CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
 CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPING, AS WELL AS
 CC METHYLATION OF CAPS, AND POLY(R) SYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA) (N).
 CC -1- SIMILARITY: PRIMARILY WITH THE N-TERMINAL HALF OF THE L PROTEINS
 CC OF RHABDOVIRUSES AND PARAMYXOVIRUSES.
 CC -----
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 CC -----
 DR EMBL: X68494; CA48508.1; -
 DR EMBL: Z29337; CA82542.1; -
 DR PIR: S44054; S44054.
 DR InterPro: IPR007098; RNA_pol_monon.
 DR InterPro: IPR001016; Viral_RNA_pol_L.
 DR Pfam: PF00946; Paramyx_RNA_pol_1.
 KM Transferrase; RNA-directed RNA polymerase.
 SQ SEQUENCE 2331 AA; 26635 MW; 7ED1D61D0EEF98B CRC64;

Query Match 3.4%; Score 99; DB 1; Length 2331;
 Best Local Similarity 22.8%; Pred. No. 35;
 Matches 68; Conservative 31; Mismatches 101; Indels 98; Gaps 14;
 Qy 4 VGVGVLLVAVDCITFASGLSSSTRSRSQTLASTSG-----NPGQANVEM--- 50
 Db 176 IGTULEFGIADFTIFK--VEPKTITRNAVSLQASKPGLRVVYRDONLTPLYLCDEDFIVS 233

Qy 51 -----KTEMERENL-----THHQGIYVDLQGDKEVDGTLREBPAGLCPI 91
 Db 234 VASVECFIMIDVIERNTMEICARAWLEBDSGDADYIPL-----DIVGELYNQ----- 282
 Qy 92 WGHIEHQDPRLPYRNFLFEDVPTKEKYKOSGNPLPGEFNL-----NFV 136
 Db 283 -GDQIIM------YLED-----GFKLIGHLEPLCVSCIQTHGIF 315
 Qy 137 TP-----SGORISPFMELEKSNINIKASTDLGCAEFAFTVAMDKNKTKRYPRVY 191
 Db 316 TPQKTFQSQRIEISYEELGSLNKKFKISGKACDAQNFITITL---QGKLTPOQYCELF 372
 Qy 192 DSKRLGH-ILYVSMQMEKKYC-SVKGEPDPLTWYCFKPRK-SYENHHLIYGSAY 246
 Db 373 SLQGHMHPVLYIVDALDKYKGHQSXKILKPKMFEIFCYFKFIVAKNHHSGGSWY 430

RESULT 25
 SVE_PYRFU STANDARD; PRT; 572 AA.
 ID SVE_PYRFU
 AC Q8U064.
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glutamy1-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
 DE (GluRS).
 GN GLTX OR P1753.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamy1-tRNA(Glu).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 CC -----
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 CC -----
 DR EMBL: AB010273; AAL81877.1; ALT_INTT.
 DR HANAP; MF_00022; -; 1.
 DR InterPro: IPR004526; GluX_arch.
 DR InterPro: IPR000924; Glu_tRNA-synt_1c.
 DR Pfam: PF00749; tRNA-synt_1c; 1.
 DR Pfam: PF03950; tRNA-synt_1c; 1.
 DR PRINTS: PR00987; TRNASYNTGLU.
 DR TIGRFAMs: TIGR00463; gltx_arch; 1.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_1; FALSE NEG.
 KM Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 107 "HIGH" REGION
 SQ SEQUENCE 572 AA; 66562 MW; 5057509BC4FE9FC6 CRC64;

Query Match 3.4%; Score 98.5; DB 1; Length 572;
 Best Local Similarity 21.8%; Pred. No. 5.8;
 Matches 67; Conservative 32; Mismatches 113; Indels 95; Gaps 15;
 Qy 71 LGQDKYVDGTLREBPAGLCPIWGHIF-----LQDPDLR--YRNKFLFEDVPTKEKYK 121
 Db 32 LGENPE-----LRKKARIVPIVKNIVBEVNTLSLEQKQKLEIPEYFMEGTKEKEEK 87
 Qy 122 QSGNPLRGFNLNFTVTSQGRISPFMELEKSNINIKASTDLGCAEFAFTVAMDKNK 181

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Db      86 KQLPLPKAKKGVKVT-----RFAPNP-----DGFHIG-----NAR 119
Qy      182 AT-KRRPVYDVK-----KELCHILYVSMQMGKKYCSVKGEPPDLTWKC 227
Db      120 AAILSYEYAKMYDGFILRFDDTDPKVKR-PELIFYDMII-----EDLEWIG 165
Qy      228 FPRPSVTENHHLIYGSAYVGE---NPDAFISKCPNQAALRGVRFGWKKGRCLDYTELTD 284
Db      166 IKPDELIVASDRLEIYYKAAEELIKMGKAYVCTCPDEFKLR---DGIACPHRD--- 218
Qy      285 TVIERVESKACQCVKTFEND-----GVASDQPHLYPLTQASWMDWPLHOSDQPHS 336
Db      219 ---EPVEVGLERMKQMLNGEYREGAIVVRIKTDLNNPRAV-----RDPALRIYDEPNH 270
Qy      337 GGVGRNY 343
Db      271 PRTGMY 277

RESULT 26
ACPH_PIG STANDARD; PRT; 732 AA.
AC 01-NOV-1990 (Rel. 16, Created)
AD P19305;
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (acyl-peptide hydrolase)
DE (APh) (acylaminoacyl-peptidase).
GN APh.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90110044; PubMed=2691504;
RA Mitter M., Asada K., Uchimura Y., Kimizuka F., Kato I., Sakiyama F.,
RA Tsuruawa S.;
RT "The primary structure of porcine liver acylamino acid-releasing
RT enzyme deduced from cDNA sequences.";
RL J. Biochem. 106:548-551(1989).
CC -1- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -1- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -1- SUBUNIT: Homotrimer.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
CC
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CC EMBL; D00524; BAA00411.1; -
CC DR MEROPS; S09.004; -
CC DR InterPro; IPR001375; Peptidase_S9.
CC DR InterPro; IPR002471; Prol_endopep_ser.
CC DR InterPro; IPR000379; Ser_ester_site.
CC DR Pfam; PF00326; Peptidase_S9; 1.
CC DR PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
CC DR Hydrolase; Acetylation.
FT MOD_RES 1
FT ACT_SITE 587 587 ACETYLATION.
FT ACT_SITE 675 675 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 707 707 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 732 AA; 81243 MW; 017BD40B049A604C CRC64;

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Query Match      3.4%; Score 98.5; DB 1; Length 732;
Best Local Similarity 20.9%; Pred. No. 8.1;
Matches 96; Conservative 56; Mismatches 176; Indels 111; Gaps 25;

Qy      81 LYREBAGLCPIWKGKIELQOPDRLEPRNNPLEDVFTEKEYQSGN-----PLGGFN 132
Db      20 LSRQALSAACGLPEVTVYQGR--YRTVHTE--WTQDLERMENIRFCROYLVPHDGS 75
Qy      133 LNFVTPSGQRISPPFMELEKNSN-----IKASTDGRCAEFAFKVANDKNNKARY 185
Db      76 VFAGPAGNSVET-REGELLSRESPEGTWKAVLRKAGTGTAEEKQFLEV-WEKNNKLSF 133
Qy      186 -----RYPFVYDSKRLC-----HILYVSMQMGKKYCSVKGEPPDLTWKCFKPR 231
Db      134 NLSALEKGPVYEDDCFGCLSKSHETHLVYA-----DKK-----RPK 172
Qy      232 KSVTENHHLIYGSAYVGENPDPAFISKCPNQAALRGVRFGWKKGRCLDYTELTVIER-- 289
Db      173 ---ASFQTKALDVTGSDDEWARTKKPDQAIKDPQ-----LFYEDGEMNWSKST 221
Qy      290 -----VESKACQCVKTFEN--DGVASDQPHLYPLTQASWMDWPLHOSDQPHSGV- 339
Db      222 PVLCLVDIESGN---ISVLEGVPESVSPGAFWAGDTGVFVGW-----HEPRLDGR 273
Qy      340 ---GRNYGPPYVDTGEGKCALSDQVLSDAVSYTAGSLSETPNFIIPSNPV 396
Db      274 FCTNRKSLIYVDLTG-GKEL-----LDSEVAIV---SPRLSPQOCRIVLRPFL 322
Qy      397 TEPPEPETAQC-----TADKPPDSFGACDVQA--CKRQKTCVSGQIOST 439
Db      323 VPHQ-----QCGQLCLDYMTYRTVSVDVIVPRLGE--DFSGIYCSLPLCGWSADSORV 376
Qy      440 SVDCTADEQ-----NECGNTALNAGLVILL 471
Db      377 VFDSPQSRQDLFAVDTQMGSVTSLTAGSGGSKWLT 415

RESULT 27
STHA_ECOLI
ID STHA_ECOLI STANDARD; PRT; 465 AA.
AC P27306;
AD 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Soluble pyridine nucleotide transhydrogenase (EC 1.6.1.1) (STH)
DE (NAD(P) (+) transhydrogenase [B-specific]).
GN STHA OR STH OR UDHA OR B3962.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 1-26, AND CHARACTERIZATION.
RX MEDLINE=99121046; PubMed=9922271;
RA Boonstra B., French C.E., Wainwright I., Bruce N.C.;
RT "The udha gene of Escherichia coli encodes a soluble pyridine
RT nucleotide transhydrogenase.";
RL J. Bacteriol. 181:1030-1034(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.U.;
RT "Analyses of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes.";
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [3]
RP REVISIONS.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

```

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.,
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474 (1997).
 RN [4]
 RP SEQUENCE OF 1-345 FROM N.A.
 RC STRAIN=K12;
 RA MEDLINE=93077482; PubMed=1447162;
 RX Guetafason C., Marne S.R.,
 RT "Physical map of the oxyR-lrma region (minute 89.3) of the
 RT *Escherichia coli* chromosome";
 RL J. Bacteriol. 174:7878-7879 (1992).
 RN [5]
 RP SEQUENCE OF 346-465 FROM N.A.
 RX MEDLINE=90066338; PubMed=2511419;
 RA Tao K., Makino K., Yonei S., Nakata A., Shinagawa H.,
 RT "Molecular cloning and nucleotide sequencing of oxyR, the positive
 RT regulatory gene of a regulon for an adaptive response to oxidative
 RT stress in *Escherichia coli*: homologues between OxyR protein and a
 RT family of bacterial activator proteins";
 RL Mol. Gen. Genet. 218:371-376 (1989).
 CC -1- FUNCTION: Conversion of NADPH, generated by peripheral catabolic
 CC pathways, to NADH, which can enter the respiratory chain for
 CC energy generation.
 CC -1- CATALYTIC ACTIVITY: NADPH + NAD(+) = NADP(+) + NADH.
 CC -1- COFACTOR: Binds 1 FAD per subunit.
 CC -1- SUBUNIT: HOMODIGOMER; PROBABLE HOMODIGOMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
 CC OXIDOREDUCTASES CLASS-I.
 CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 CC FRAMESHIFT IN POSITION 14.
 CC -----
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 CC -----
 DR EMBL, U00006; AAC43068.1; ALT_FRAME.
 DR EMBL, AE000470; AAC76944.1; ALT_INIT.
 DR EMBL, X65026; CAA46822.1; ALT_FRAME.
 DR EMBL, X16531; NOT_ANNOTATED_CDS.
 DR HSP, P14218; ILPF.
 DR EcGene; EG1428; ssha.
 DR HAMAP; MF_00247; -; 1.
 DR InterPro; IPR000759; Adnrx_reductase.
 DR InterPro; IPR001327; FAD pyr redox.
 DR InterPro; IPR000815; Hg_reductase.
 DR InterPro; IPR000205; NAD_binding.
 DR InterPro; IPR001100; Pyr_redox.
 DR InterPro; IPR004099; Pyr_redox_dim.
 DR Pfam; PF00070; Pyr_redox; 1.
 DR Pfam; PF02852; Pyr_redox_dim; 1.
 DR PRINTS; PR004419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00945; HGRDTASE.
 DR PRINTS; PR00411; PNRDRTASE.
 DR ProDom; PD000139; FAD pyr redox; 1.
 KW Oxidoreductase; Flavoprotein; FAD; NADP; NAD; Complete proteome.
 FT INT_MET 0
 FT NP_BIND 7 37 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 300 310 FAD (FLAVIN PART) (BY SIMILARITY).
 FT CONFLICT 63 1 -> L (IN REF. 4).
 FT CONFLICT 117 117 R -> L (IN REF. 4).
 SO SEQUENCE 465 AA; 51429 MW; 18EF2770B60D3C56 CRC64;

Query Match 3.4%; Score 98; DB 1; Length 465;
 Best Local Similarity 20.3%; Pred. No. 4.8;
 Matches 87; Conservative 53; Mismatches 137; Indels 152; Gaps 21;

QY 150 LLEKNSNIKASTDLCRCFAFAKTV---AMDKNKATKRYRPFVYDSKRLCHIL----- 201
 DB 62 IIFENQ-N-PLVSDSRLLRSFADILNADVINOQPRMRGQFY---ERNHCILLQGNAR 117
 QY 202 YV-----SMQMESKRYCSVKGEPP-----DLTWCFKPKKSTENHH----- 239
 DB 118 FVDEHTLALDCPDSPVETLTAEKEFVIACGSRPHYPTVDFTPHRIYDSDSLMSHHEPRH 177
 QY 240 -LIYSAVVG-----ENPAFISKCPNOALRGYRFGVWKGRCLD 278
 DB 178 VLIYAGVYIGCEYASIFRGMDVKVDLINTDRLLAFIDQEMSDSL-SYHF--MNSGVIR 234
 QY 279 YTE-----LTDVIERVES---KAQCWV-----KTFENDGVASDOPHTYPL 316
 DB 235 HNEVEKEEGDDGVIMHLNKSCKRLKADCLLYANGRTGNTSLALQNTGLETDSCGQKLV 294
 QY 317 TSQASNDWMPFLHSDQPHSGVGRNFGFYVDTTG--EGKCALSDOVPCDLVSDSAVS 374
 DB 295 NS-----MYOTAOPHYVAVGDVIGPISLAAYDQGR-----IAQALVK 334
 QY 375 YTAGSLSEERN--FIIPSNPSVTPPTPERALQCTADKFPDPSGACDVQAKCKQKTSV 432
 DB 335 GEATPAHLIEDIPGTIYTPETISV---GKTEQQLTAKVPEYVGRQFKLAR----- 384
 QY 433 GGOIGSTSVDCDAEONECGSNTALLIAGVGLL-----ALLGGCYFAKRLDRNK 486
 DB 385 -----AOYGMNVGTILKLFHRTKEILGHC----- 412
 QY 487 GVQAHHHEH 495
 DB 413 GERAAEIIH 421

RESULT 28
 APC RAT
 ID APC RAT STANDARD; PRT; 2842 AA.
 AC P70478;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Adenomatous polyposis coli protein (APC protein).
 GN APC.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer 344/N; TISSUE=Brain;
 RX MEDLINE=96116966; PubMed=8563176;
 RA Toyota M., Ushijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A.,
 RT "cDNA cloning of the rat APC gene and assignment to chromosome 18.";
 RL Mamm. Genome 6:746-748 (1995).
 RN [2]
 RP MUTAGENESIS.
 RC STRAIN=Sprague-Dawley, and Fischer 344/N;
 RX MEDLINE=95148647; PubMed=7846077;
 RA Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K.,
 RT Welsbuerger J.H., Sugimura T., Nagao M.,
 RT "Specific 5'-GGGA-3'--5'-GGA-3' mutation of the APC gene in rat colon
 RT tumors induced by 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:910-914 (1995).
 CC -1- FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1
 CC and participates in Wnt signaling. APC activity is correlated with
 CC its phosphorylation state (By similarity).
 CC -1- SUBUNIT: Forms homooligomers. Associates with catenins. Binds
 CC actin (By similarity).
 CC -1- PM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
 CC -1- SIMILARITY: Contains 7 ARM repeats.
 CC -----
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DR EMBL: D38629; BAA07609.1; -
 DR HSSP: Q02248; 3BCT.
 DR InterPro: IPR000225; Armadillo.
 DR Pfam: PF00514; Armadillo_seg; 4.
 DR SMART: SM00185; ARM; 5.
 DR PROSITE: PS00176; ARM_REPEAT; 1.
 KW Mut signaling pathway; Anti-oncogene; Phosphorylation; Coiled coil;
 KM Repeat.
 FT DOMAIN 1 728 LEU-RICH
 FT DOMAIN 1 62 COILED COIL (POTENTIAL).
 FT DOMAIN 125 260 COILED COIL (POTENTIAL).
 FT REPEAT 451 493 ARM 1.
 FT REPEAT 503 545 ARM 2.
 FT REPEAT 546 589 ARM 3.
 FT REPEAT 590 636 ARM 4.
 FT REPEAT 637 681 ARM 5.
 FT REPEAT 682 723 ARM 6.
 FT REPEAT 724 765 ARM 7.
 FT REPEAT 739 781 SER-RICH.
 FT DOMAIN 1130 1155 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 1864 1891 HIGHLY CHARGED.
 FT MUTAGEN 523 C->R; IN AN IQ-INDUCED COLON TUMOR.
 SQ SEQUENCE 2842 AA; 310530 MW; 3CB82E8A348F47 CRC64;

Query Match 3.4%; Score 98; DB 1; Length 2842;
 Best Local Similarity 19.4%; Pred. No. 54;
 Matches 110; Conservative 68; Mismatches 212; Indels 178; Gaps 25;

QY 20 ASGLSSSTRSRSSQTLASTSGNPFQANTYEMKTFMERFNL-----THHQSG-----LY 68
 DB 1652 ARLSLSLTLIESPNEIAA---GDGVASVOSGEFEKRDITPIREGRTDAQNGKSSIAI 1708
 QY 69 VDLGQDKEVDGTLVRE---PAGLCPTWGKHIELQDPRLPYRNNFLIEDVTEKEYQO 122
 DB 1709 PLLDGSKAEEGDILAEICINSALPKG-----RSHKFFRYKKIMDQVQASMTS 1755
 QY 123 SGNPLPGFNLPVFTSGQR---ISPFMEL-----LEKSNISIKS-----TDLGR 166
 DB 1756 SGT-----NKQIDTKKKKPTSPVKPMQNTERTVRKNTDTSKVNVTEETFSNKKDS 1809
 QY 167 AEFAPKTVAMDKNNK---ATKYRYPVYVDSKKRLCHILYVSMQMEGKYSVKCEPD 222
 DB 1810 KKQSLKNNKRDNDKLPDNEBRARGFTDPSPHH-----YAPIETP-- 1851
 QY 223 LTMVCKPKRSVTENHLLIYGSAVYGENPDATSKCPNALRGYRGVKKGRCLDYTEL 282
 DB 1852 ---YCFSRNDSTL-----SLIDPDDDDVDLSR-EKALRKGSKSDSEAVTCHTSP 1898
 QY 283 TDIVIRVSVSKQOCWKTFENQD---VASDQHTPLTSQASWNNMWPLHQSDQPHSG 338
 DB 1899 SSS---QOASARKQASTHPPVNRGSPSKPLQEBP-TFPQSK-----DVDRG- 1942
 QY 339 VGRNYPFYVDVTGEGKCALSDVPCLVSDSAVSTAAGLS-----EET- 385
 DB 1943 -----AATDKLQNFALIENTPVCFSSNSSLSLSVDVQENNNNEEFG 1984
 QY 386 -PNFIIIPSPSVTPPEPTALQCTADKFPDSGACVQAQCKROKTSVGGQIOSTVDC 444
 DB 1985 PVKDAEPANAQCGPKRPQ-----ASGVAPKSFVIEDTPVCFSHNS-----LSLSIDSE 2034
 QY 445 ADEQNECGSNTALIALAGAVGVLLALLGGCCYFAKRLDRNKGVQAAHHEHESQDRGAR 504
 DB 2035 DDLIREC-----ISSAMPKRRRPSRLKG-----EGEQSPKRVG 2068
 QY 505 KKRPSPDMQBAEPPFWDEAENIEDQGE 532

DB 2069 SVLAEDTLIDKDIQRPSEHGLSPDSE 2096

RESULT 29
 ID FBN1_MOUSE STANDARD; PRT; 2871 AA.
 AC 061554; 060826;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrillin 1 precursor.
 GN FBN1 OR FBN-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95130561; PubMed=7829516;
 RA Yin W., Germiller J., Sanguinetti C., Smiley E., Panglinnan T.,
 RA Pereira L., Ramirez F., Bonadio J.;
 RT "Primary structure and developmental expression of Fbn-1, the mouse
 RT fibrillin gene.";
 RL J. Biol. Chem. 270:1798-1806(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Kidney;
 RA Ota K., Kumar A., Wada U., Liu Z., Kanwar Y.S.;
 RL Submitted (Apr-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
 CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
 CC -1- LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
 CC -1- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER
 CC FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
 CC MICROFIBRILS (BY SIMILARITY).
 CC -1- SIMILARITY: Contains 47 EGF-like domains.
 CC -1- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
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DR EMBL: U29454; AAA56840.1; -
 DR EMBL: U22493; AAA64217.1; -
 DR PIR: A55624; A55624.
 DR HSSP: P35555; IABJ.
 DR MGI: MGI:95489; Fbn1.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR002212; Fibril1-aseoc.
 DR Pfam: PF00608; EGF; 46.
 DR Pfam: PF00683; TB; 9.
 DR SMART: SM00179; EGF_CA; 42.
 DR PROSITE: PS00010; ASX_HYDROXYL; 43.
 DR PROSITE: PS00022; EGF_1; 2.
 DR PROSITE: PS01186; EGF_2; 38.
 DR PROSITE: PS01187; EGF_CA; 43.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat; Signal; Multigene family.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 2871 FIBRILLIN 1.
 FT DOMAIN 81 112 EGF-LIKE 1.
 FT DOMAIN 115 146 EGF-LIKE 2.
 FT DOMAIN 147 178 EGF-LIKE 3.
 FT DOMAIN 246 287 EGF-LIKE 4.
 FT DOMAIN 288 329 EGF-LIKE 5; CALCIUM-BINDING.
 FT DOMAIN 330 401 TGFBP 1.

FT	DOMAIN	402	446	PRO-RICH.
FT	DOMAIN	449	489	EGF-LIKE 6.
FT	DOMAIN	490	529	EGF-LIKE 7, CALCIUM-BINDING.
FT	DOMAIN	530	571	EGF-LIKE 8, CALCIUM-BINDING.
FT	DOMAIN	572	612	EGF-LIKE 9, CALCIUM-BINDING.
FT	DOMAIN	613	653	EGF-LIKE 10, CALCIUM-BINDING.
FT	DOMAIN	656	721	TGFBP 2.
FT	DOMAIN	723	764	EGF-LIKE 11, CALCIUM-BINDING.
FT	DOMAIN	765	806	EGF-LIKE 12, CALCIUM-BINDING.
FT	DOMAIN	807	846	EGF-LIKE 13, CALCIUM-BINDING.
FT	DOMAIN	910	951	EGF-LIKE 14, CALCIUM-BINDING.
FT	DOMAIN	952	1018	TGFBP 3.
FT	DOMAIN	1028	1069	EGF-LIKE 15, CALCIUM-BINDING.
FT	DOMAIN	1070	1112	EGF-LIKE 16, CALCIUM-BINDING.
FT	DOMAIN	1113	1154	EGF-LIKE 17, CALCIUM-BINDING.
FT	DOMAIN	1155	1196	EGF-LIKE 18, CALCIUM-BINDING.
FT	DOMAIN	1197	1237	EGF-LIKE 19, CALCIUM-BINDING.
FT	DOMAIN	1238	1279	EGF-LIKE 20, CALCIUM-BINDING.
FT	DOMAIN	1280	1321	EGF-LIKE 21, CALCIUM-BINDING.
FT	DOMAIN	1322	1362	EGF-LIKE 22, CALCIUM-BINDING.
FT	DOMAIN	1363	1403	EGF-LIKE 23, CALCIUM-BINDING.
FT	DOMAIN	1404	1445	EGF-LIKE 24, CALCIUM-BINDING.
FT	DOMAIN	1446	1486	EGF-LIKE 25, CALCIUM-BINDING.
FT	DOMAIN	1487	1527	EGF-LIKE 26, CALCIUM-BINDING.
FT	DOMAIN	1528	1569	TGFBP 4.
FT	DOMAIN	1606	1647	EGF-LIKE 27, CALCIUM-BINDING.
FT	DOMAIN	1648	1688	EGF-LIKE 28, CALCIUM-BINDING.
FT	DOMAIN	1689	1758	TGFBP 5.
FT	DOMAIN	1766	1807	EGF-LIKE 29, CALCIUM-BINDING.
FT	DOMAIN	1808	1848	EGF-LIKE 30, CALCIUM-BINDING.
FT	DOMAIN	1849	1890	EGF-LIKE 31, CALCIUM-BINDING.
FT	DOMAIN	1891	1929	EGF-LIKE 32, CALCIUM-BINDING.
FT	DOMAIN	1930	1972	EGF-LIKE 33, CALCIUM-BINDING.
FT	DOMAIN	1973	2012	EGF-LIKE 34, CALCIUM-BINDING.
FT	DOMAIN	2013	2054	EGF-LIKE 35, CALCIUM-BINDING.
FT	DOMAIN	2055	2121	TGFBP 6.
FT	DOMAIN	2127	2165	EGF-LIKE 36, CALCIUM-BINDING.
FT	DOMAIN	2166	2205	EGF-LIKE 37, CALCIUM-BINDING.
FT	DOMAIN	2206	2246	EGF-LIKE 38, CALCIUM-BINDING.
FT	DOMAIN	2247	2290	EGF-LIKE 39, CALCIUM-BINDING.
FT	DOMAIN	2291	2332	EGF-LIKE 40, CALCIUM-BINDING.
FT	DOMAIN	2333	2400	TGFBP 7.
FT	DOMAIN	2402	2443	EGF-LIKE 41, CALCIUM-BINDING.
FT	DOMAIN	2444	2484	EGF-LIKE 42, CALCIUM-BINDING.
FT	DOMAIN	2485	2523	EGF-LIKE 43, CALCIUM-BINDING.
FT	DOMAIN	2524	2566	EGF-LIKE 44, CALCIUM-BINDING.
FT	DOMAIN	2567	2606	EGF-LIKE 45, CALCIUM-BINDING.
FT	DOMAIN	2607	2647	EGF-LIKE 46, CALCIUM-BINDING.
FT	DOMAIN	2648	2687	EGF-LIKE 47, CALCIUM-BINDING.
FT	DISULFID	85	94	BY SIMILARITY.
FT	DISULFID	89	100	BY SIMILARITY.
FT	DISULFID	102	111	BY SIMILARITY.
FT	DISULFID	119	129	BY SIMILARITY.
FT	DISULFID	123	134	BY SIMILARITY.
FT	DISULFID	136	145	BY SIMILARITY.
FT	DISULFID	150	160	BY SIMILARITY.
FT	DISULFID	154	166	BY SIMILARITY.
FT	DISULFID	168	177	BY SIMILARITY.
FT	DISULFID	250	262	BY SIMILARITY.
FT	DISULFID	257	271	BY SIMILARITY.
FT	DISULFID	273	286	BY SIMILARITY.
FT	DISULFID	292	304	BY SIMILARITY.
FT	DISULFID	299	313	BY SIMILARITY.
FT	DISULFID	315	328	BY SIMILARITY.
FT	DISULFID	453	465	BY SIMILARITY.
FT	DISULFID	460	474	BY SIMILARITY.
FT	DISULFID	476	488	BY SIMILARITY.
FT	DISULFID	494	504	BY SIMILARITY.
FT	DISULFID	499	513	BY SIMILARITY.
FT	DISULFID	515	528	BY SIMILARITY.
FT	DISULFID	534	546	BY SIMILARITY.
FT	DISULFID	541	555	BY SIMILARITY.
FT	DISULFID	557	570	BY SIMILARITY.

FT	DISULFID	576	587	BY SIMILARITY.
FT	DISULFID	582	596	BY SIMILARITY.
FT	DISULFID	598	611	BY SIMILARITY.
FT	DISULFID	617	628	BY SIMILARITY.
FT	DISULFID	623	637	BY SIMILARITY.
FT	DISULFID	639	652	BY SIMILARITY.
FT	DISULFID	727	739	BY SIMILARITY.
FT	DISULFID	734	748	BY SIMILARITY.
FT	DISULFID	750	763	BY SIMILARITY.
FT	DISULFID	769	781	BY SIMILARITY.
FT	DISULFID	776	790	BY SIMILARITY.
FT	DISULFID	792	805	BY SIMILARITY.
FT	DISULFID	811	821	BY SIMILARITY.
FT	DISULFID	816	830	BY SIMILARITY.
FT	DISULFID	832	845	BY SIMILARITY.
FT	DISULFID	914	926	BY SIMILARITY.
FT	DISULFID	921	935	BY SIMILARITY.
FT	DISULFID	937	950	BY SIMILARITY.
FT	DISULFID	1032	1044	BY SIMILARITY.
FT	DISULFID	1039	1053	BY SIMILARITY.
FT	DISULFID	1055	1068	BY SIMILARITY.
FT	DISULFID	1074	1086	BY SIMILARITY.
FT	DISULFID	1081	1095	BY SIMILARITY.
FT	DISULFID	1097	1111	BY SIMILARITY.
FT	DISULFID	1117	1129	BY SIMILARITY.
FT	DISULFID	1124	1138	BY SIMILARITY.
FT	DISULFID	1140	1153	BY SIMILARITY.
FT	DISULFID	1159	1171	BY SIMILARITY.
FT	DISULFID	1166	1180	BY SIMILARITY.
FT	DISULFID	1182	1195	BY SIMILARITY.
FT	DISULFID	1201	1212	BY SIMILARITY.
FT	DISULFID	1208	1221	BY SIMILARITY.
FT	DISULFID	1223	1236	BY SIMILARITY.
FT	DISULFID	1242	1254	BY SIMILARITY.
FT	DISULFID	1249	1263	BY SIMILARITY.
FT	DISULFID	1265	1278	BY SIMILARITY.
FT	DISULFID	1284	1296	BY SIMILARITY.
FT	DISULFID	1291	1305	BY SIMILARITY.
FT	DISULFID	1307	1320	BY SIMILARITY.
FT	DISULFID	1326	1339	BY SIMILARITY.
FT	DISULFID	1333	1348	BY SIMILARITY.
FT	DISULFID	1350	1361	BY SIMILARITY.
FT	DISULFID	1367	1380	BY SIMILARITY.
FT	DISULFID	1374	1389	BY SIMILARITY.
FT	DISULFID	1391	1402	BY SIMILARITY.
FT	DISULFID	1408	1420	BY SIMILARITY.
FT	DISULFID	1415	1429	BY SIMILARITY.
FT	DISULFID	1431	1444	BY SIMILARITY.
FT	DISULFID	1450	1461	BY SIMILARITY.
FT	DISULFID	1456	1470	BY SIMILARITY.
FT	DISULFID	1472	1485	BY SIMILARITY.
FT	DISULFID	1491	1502	BY SIMILARITY.
FT	DISULFID	1497	1511	BY SIMILARITY.
FT	DISULFID	1513	1526	BY SIMILARITY.
FT	DISULFID	1610	1622	BY SIMILARITY.
FT	DISULFID	1617	1631	BY SIMILARITY.
FT	DISULFID	1633	1646	BY SIMILARITY.
FT	DISULFID	1652	1663	BY SIMILARITY.
FT	DISULFID	1658	1672	BY SIMILARITY.
FT	DISULFID	1674	1687	BY SIMILARITY.

Query Match 3.3% Score 97.5; DB 1; Length 2871;
 Best Local Similarity 22.6% Pred. No. 60; Indels 129; Gaps 29;
 Matches 93; Conservative 51; Mismatches 139;

Qy	124	GNPLPGGFNIN----	FVTPSGQRISPPMELLEKNISIKASTDLCRCAPFAKTVMADKN	179
Db	2173	GNPCGNGTCKKVIGFECTCEGEPGMWTC-----	DINECAQ-----N	2213
Qy	180	NKAKRYPPFYDBSKKLCILLYSMOLMECKKCSYKGEPPDLTWYCFKR---	KSVTE	236
Db	2214	PLLCAFRCVNTYGSYCKCPGVV---LREDRMCKDEBCAEGKHDKCTEKOMECKNVLIG	2270	


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OY 237 NHHLYGSAVYGENDPAPISKCPNOLRGYRGWKKGRCLD-----YT-ELTD-----T 285
DB 2271 TYMCIQCGPQY-ORRDPG---EGCIDEBCOTKPGICENGLWTLGSLYCECNDGTAAPT 2327
OY 286 VIERVESK-AQCWVTFPEN---DGVASDOPHTYPLTSQAS--WMDWPLHOSDOPHSGGV 339
DB 2338 ODECDNNEGCVFSEFVEMWCGIIGSSNNRPVT---KSECCCVGGRGWLHCICFCEGTV 2384
OY 340 -----GRNYGF-----YYVDTGEGKALSQVDPD-----CLVDSAAV 373
DB 2385 AYKKLCPHGR--GFMTNGADVDECKVIHDVCRNGSC---VNDRGSYHCTCKTGYTPDI 2437
OY 374 SYTAGSUSE-ETP---NFILPSNPSVTPRPETALQCTADKFPSPF-----GAC-DV 421
DB 2438 TGTSCVDLNECQAPKPCNFCIKMT-----EGSYQSCC---PNGYILQEDGRSCKDL 2486
OY 422 QACKRQKTSK-----VGG-----QIQTSTVD---CTADEONEGGS 453
DB 2487 DECATKQHNCPFLCVNTIGTFCKCPKPRFTQHTHTACIDNNECTSD-INLCSG 2537

RESULT 30
NX1B RAT STANDARD; PRT; 468 AA.
AC 063373;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurexin 1-beta precursor (Neurexin I-beta).
GN NRXN1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
[1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=92320296; PubMed=1621094;
RA Ushakov Y.A., Petrenko A.G., Geppert M., Suedhof T.C.;
RT "Neurexins: synaptic cell surface proteins related to the alpha-
RT latrotoxin receptor and laminin.";
RL Science 257:50-56(1992).
[2]
RP SEQUENCE OF N-TERMINUS, AND O-GLYCOSYLATION.
RC TISSUE=Brain;
RX MEDLINE=94216308; PubMed=8163501;
RA Ushakov Y.A., Hata Y., Ichchenko K., Moomaw C., Afendis S.,
RA Slaughter C.A., Suedhof T.C.;
RT "Conserved domain structure of beta-neurexins. Unusual cleaved signal
RT sequences in receptor-like neuronal cell-surface proteins.";
RL J. Biol. Chem. 269:11987-11992(1994).
[3]
RP FUNCTION, AND INTERACTION WITH NEUROLIGIN 1.
RX MEDLINE=97467410; PubMed=9325340;
RA Nguyen T., Suedhof T.C.;
RT "Binding properties of neuroligin 1 and neurexin 1beta reveal function
RT as heterophilic cell adhesion molecules.";
RL J. Biol. Chem. 272:26032-26039(1997).
[4]
RP INTERACTION WITH NLGN1, NLGN2 AND NLGN3.
RX MEDLINE=96162010; PubMed=8576249;
RA Ichchenko K., Nguyen T., Suedhof T.C.;
RT "Structures, alternative splicing, and neurexin binding of multiple
RT neuroligins.";
RL J. Biol. Chem. 271:2676-2682(1996).
[5]
RP INTERACTION WITH CASK.
RX MEDLINE=96256685; PubMed=8786425;
RA Hata Y., Butz S., Suedhof T.C.;
RT "CASK: a novel dlg/PSD95 homolog with an N-terminal
RT calmodulin-dependent protein kinase domain identified by interaction
RT with neurexins.";
RL J. Neurosci. 16:2488-2494(1996).

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RN [6]
RP INTERACTION WITH ALPHA-LATROTOXIN.
RX MEDLINE=99211386; PubMed=10197529;
RA Sugita S., Khvochev M., Suedhof T.C.;
RT "Neurexins are functional alpha-latrotoxin receptors.";
RL Neuron 22:489-496(1999).
[7]
RP INTERACTION WITH ALPHA-DYSTROGLYCAN.
RX MEDLINE=21363578; PubMed=11470830;
RA Sugita S., Saito F., Tang J., Satz J., Campbell K., Suedhof T.C.;
RT "A stoichiometric complex of neurexins and dystroglycan in brain.";
RL J. Cell Biol. 154:435-445(2001).
[8]
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 47-302.
RX MEDLINE=99449307; PubMed=10520997;
RA Rudenko G., Nguyen T., Chellish Y., Suedhof T.C., Deisenhofer J.;
RT "The structure of the ligand-binding domain of neurexin Ibeta:
RT regulation of LNS domain function by alternative splicing.";
RL Cell 99:93-101(1999).
CC -1- FUNCTION: Neuronal cell surface protein that may be involved in
CC cell recognition and cell adhesion by forming intracellular
CC junctions through binding to neuroligins. May play a role in
CC formation or maintenance of synaptic junctions. May mediate
CC intracellular signaling.
CC -1- SUBUNIT: The cytoplasmic C-terminal region binds to CASK. Isoforms
CC Beta 4b bind neuroligins NLGN1, NLGN2 and NLGN3, alpha-
CC dystroglycan and alpha-latrotoxin.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative promoter;
CC Comment=A number of isoforms, alpha-type and beta-type (shown
CC here), are produced by use of alternative promoters. Beta-type
CC isoforms differ from alpha-type isoforms in their N-terminus;
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=There is a combination of two alternatively spliced
CC domains at sites 4 and 5 which are shared with alpha isoforms
CC (AC Q63372) and seem to be used independently. Experimental
CC confirmation may be lacking for some isoforms;
CC Name=1; Synonyms=Beta 4A5A;
CC IsoId=Q63373-1; Sequence=Displayed;
CC Name=2; Synonyms=Beta 4A5B;
CC IsoId=Q63373-2; Sequence=VSP_003497;
CC Name=3; Synonyms=Beta 4B5A;
CC IsoId=Q63373-3; Sequence=VSP_003496;
CC Name=4; Synonyms=Beta 4B5B;
CC IsoId=Q63373-4; Sequence=VSP_003496, VSP_003497;
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- PTM: Highly O-glycosylated and minor N-glycosylated.
CC -1- SIMILARITY: Contains 1 laminin G-like domain.
CC -1- SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, M96375; AAA1705.1; -.
CC PIR, B40228; B40228.
CC PDB, 1CAR; 28-SEP-99.
CC InterPro, IPR001791; Laminin G.
CC InterPro, IPR003585; Neurexin-like.
CC Pfam, PF00054; Laminin_G_1.
CC SMART, SM00294; 4.1m; 1.
CC DR SMART, SM00282; LamG; 1.
CC DR PROSITE, PSS0025; LAM G DOMAIN; 1.
CC Signal, Transmembrane, Cell adhesion; Glycoprotein;
CC Alternative splicing; Alternative promoter usage; 3D-structure.
CC FT SIGNAL 1 46
CC CHAIN 47 468 NEUREXIN 1-BETA.
CC DOMAIN 47 391 EXTRACELLULAR (POTENTIAL).

```


Best local similarity 22.3%; Pred. No. 6;
Matches 73; Conservative 32; Mismatches 131; Indels 92; Gaps 16;

QY 249 ENDPAFISKCPN-----QALGRF-----GVM---KKGRCLDYELDT 285
DB 185 EKPVNGVTVTQPSLPWNTTCAFECKEGFELIGPEHLQCTSSGSMQKPTCAVT--CDT 242
QY 286 V-----IERVSAQCVKVFENDGVAADDPHYVPLTSQASNMWMLPHOS 331
DB 243 VHPNGNDVSCNHSSTGEPAYASTGFTCAEGFGLQG--PAOIECTAQAGCTQAACVCA 300
QY 332 -----DQPSGCVGNNGFYVDTTGE-----GKCALSDQVDCLVSDSAVSTAAGSL 381
DB 301 VACPAVSOPKGLVVFTH-----SPRGFTYKSSCAFSCE--EGFELRGSQAQLACTISQGM 354
QY 382 SEETPNFIIPSNPSTPTPTETALQCTADKFPDPSFGACVQACRQKTSVCGQIOSTSV 441
DB 355 TQEVPSQVQVQCSLSLEVP--EINMSCSGBPV--FGAVCTFACPE-----GMMLNGSV 403
QY 442 DCTADEQNECG-----NTALLINGLVGVLALLLGGCCYFAKRLDR 484
DB 404 ALT-----CGATGHWGMLPTCEADAEBSKIPILAMGLAGVSEMTSASFLMLLKLRLK 457
QY 485 NKGVQAAHHEHFQSDRGARKKPSDLM 512
DB 456 RAKKFPVSSSSSECTLOPNGS-YQMPDLI 484

RESULT 32
ID NX1A_MOUSE STANDARD; PRT; 529 AA.
AC Q9CS84; 088722; : : : : :
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurexin 1-alpha (Neurexin I-alpha) (Fragments).
GN NRXN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RX (1)
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsumoto H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Wabito T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli U., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldo M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehima M., Mazzarelli U., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE OF 478-520 FROM N.A.

RC STRAIN=C57BL/10; TISSUE=Brain;
RA Gorecki D.C., Szklarczyk A., Lukaszuk K., Kaczmarek L., Simons J.P.,
RT "Differential seizure-induced and developmental changes of neurexin
RT expression."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Neuronal cell surface protein that may be involved in
CC cell recognition and cell adhesion. May mediate intracellular
CC signaling.
CC -1- SUBUNIT: The cytoplasmic C-terminal region binds to CASK (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q9CS84-1; Sequence=Displayed;
CC Name=2; Synonyms=Alpha-2B;
CC IsoId=Q9CS84-2; Sequence=VSP_003484;
CC Name=3; Synonyms=Alpha-2C;
CC IsoId=Q9CS84-3; Sequence=VSP_003485;
CC -1- SIMILARITY: Contains at least 2 laminin G-like domains.
CC -1- SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sb.ch).
CC -----
DR EMBL; AF387674; AAK70469.1; -;
DR EMBL; AF387674; AAK70470.1; -;
DR EMBL; AF387674; AAK70471.1; -;
DR EMBL; AK015718; BAB30815.1; -;
DR EMBL; AJ006802; CAA07257.1; -;
DR HSSP; O63373; 1CAR.
DR MGD; MGI:1096391; Nrnx1.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00054; laminin_G; 1.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS50025; LAM G DOMAIN; 1.
KW Transmembrane; Cell adhesion; Repeat; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1
FT NON_CONS 140 141
FT DOMAIN <1 453
FT TRANSMEM 474 474
FT DOMAIN 475 529
FT DOMAIN 15 140
FT DOMAIN 178 333
FT CARBOHYD 245 245
FT VARSPPLIC 90 96
FT FTID=VSP_003484.
FT Missing (in isoform 2).
FT VARSPPLIC 82 96
FT Missing (in isoform 3).
FT FTID=VSP_003485.
FT Missing (in isoform 1).
SQ SEQUENCE 529 AA; 57193 MW; 282E04A03DEBA671 CRC64;
Query Match 3.3%; Score 97; DB 1; Length 529;
Best local similarity 22.3%; Pred. No. 6.8;
Matches 52; Conservative 38; Mismatches 103; Indels 40; Gaps 11;
QY 330 QSDPHSGGVGNNGFYVDTTGE-----GKCALSDQVDCLVSDSAVSTAAGSL 376
DB 310 ECGQFQGLS---GLYVNGLVLMMAENDANIAVGVNRVLVGEVPSMTTSTATAMQ 366
QY 377 A--AGLSSEETPNFIIPSNPSTPTPTETALQCTADKFPDPSFGAC-----DVQACRQKT 429
DB 367 SEMSTSIWETTTTLATSTARCKPPTKEPISDTTDLIVAS--AECPDDEDDIDPCPPSS- 424
QY 430 SCVGGQIOSTSV-----DCTADEQNECGSNLTALINGLVGVLALLLGGCCYFAKRLDR 483

DB 425 ---GLANPTRVGGEPPYPGSAEVIRESSTTGVMVGVAAAACILILLYAMY--KTRN 479

QY 484 RNKGVOAHHEHEFQSDRGARKRPSDLMQEAEPFMDPEAENIE-ODGETHV 535

DB 480 RDEG---SYHVESNNTYSNSAQNGAVYKEKQPSAKSANKKCKKKEYTV 529

RESULT 33

AD22_HUMAN STANDARD; PRT; 906 AA.

AC 09P0K1: 075076; 09P0K2: Q9U1A1; Q9U0K2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22)

DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein 2) (Metalloproteinase-disintegrin ADAM22-3).

GN ADAM22 OR MDC2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

RN [1] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RP MEDLINE=20504287; PubMed=11050470;

RA Harada T., Nishie A., Torigoe K., Ikezaki K., Shono T., Maehara Y., Kuwano M., Mada M.;

RT "The specific expression of three novel splice variant forms of human metalloproteinase-like disintegrin-like cysteine-rich protein 2 gene in brain tissues and gliomas."

RL Jpn. J. Cancer Res. 91:1001-1006(2000).

RN [2] SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).

RP TISSUE=Brain;

RC MEDLINE=98359734; PubMed=9693107;

RA Sagane K., Ohya Y., Hasegawa Y., Tanaka I.;

RT "Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2 and MDC3: novel human cellular disintegrins highly expressed in the brain."

RL Biochem. J. 334:93-98(1998).

RN [3] SEQUENCE FROM N.A. (ISOFORM 5).

RP TISSUE=Brain;

RA Mada M., Torigoe K., Harada T., Kuwano M.;

RT "Isolation and tissue specific expression of novel ADAM family from 7q21.1 region."

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [4] SEQUENCE OF 40-906 FROM N.A. (ISOFORM 1).

RP TISSUE=Cerebellum;

RC MEDLINE=99453762; PubMed=10524237;

RA Polinder K., Nelson N., Dubose R.F., Black R.A., Cerretti D.P.;

RT "The identification of seven metalloproteinase-disintegrin (ADAM) genes from genomic libraries."

RL Gene 237:61-70(1999).

CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON CATALYTIC METALLOPROTEINASE-LIKE PROTEIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=5;

CC Name=1; Synonym=Episilon;

CC IsoId=Q9P0K1-1; Sequence=Displayed;

CC Name=2; Synonym=Delta;

CC IsoId=Q9P0K1-2; Sequence=VSP_005482, VSP_005484;

CC Name=3; Synonym=Alpha;

CC IsoId=Q9P0K1-3; Sequence=VSP_005483;

CC Name=4; Synonym=Beta;

CC IsoId=Q9P0K1-4; Sequence=VSP_005482, VSP_005483;

CC Name=5;

CC IsoId=Q9P0K1-5; Sequence=VSP_005482;

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE BRAIN. DETECTED SLIGHTLY OR NOT AT ALL IN OTHER TISSUES.

CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY SIMILARITY).

CC -1- SIMILARITY: Belongs to peptidase family M12B.

CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -1- SIMILARITY: Contains 1 disintegrin domain.

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CC EMBL: AF153382; AAF73289.1; -

CC EMBL: AF153381; AAF73288.1; -

CC EMBL: AB009671; BAA32349.1; -

CC EMBL: AB009671; BAA32350.1; -

CC EMBL: AF073291; AAF22476.2; -

CC EMBL: AF158637; AAD55251.1; -

CC HSSP: P18619; 1FVL.

CC MEROPS: M12.978; -

CC Genew; HGNC:201; ADAM22.

CC MIM; 603709; -

CC GO; GO:0016021; C:integral to membrane; NAS.

CC GO; GO:0005178; P:integrin binding activity; NAS.

CC GO; GO:0007162; P:negative regulation of cell adhesion; NAS.

CC InterPro; IPR006586; ADAM_cysteine.

CC InterPro; IPR001762; Disintegrin.

CC InterPro; IPR006209; EGF-like.

CC InterPro; IPR002870; Pep_M12B_propep.

CC InterPro; IPR001590; Reptolysin.

CC InterPro; IPR006025; Zn_MTPepdse.

CC Pfam; PF01562; Pep_M12B_propep; 1.

CC Pfam; PF01421; Reptolysin; 1.

CC PRINTS; PR00289; DISINTEGRIN.

CC ProDom; PD000664; Disintegrin; 1.

CC SMART; SMO0608; ACR; 1.

CC SMART; SMO0050; DISIN; 1.

CC PROSITE; PS50215; ADAM_MEROP; 1.

CC PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.

CC PROSITE; PS50214; DISINTEGRIN_2; 1.

CC PROSITE; PS00022; EGF_1; 1.

CC PROSITE; PS01186; EGF_2; FALSE_NEG.

CC PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.

CC KWSignal; Glycoprotein; Transmembrane; EGF-like domain; Alternative splicing.

CC FT SIGNAL 1 25

CC FT PROPEP 26 222

CC FT CHAIN 223 906

CC FT DOMAIN 223 736

CC FT TRANSMEM 737 757

CC FT DOMAIN 758 906

CC FT DOMAIN 223 438

CC FT DOMAIN 444 531

CC FT DOMAIN 532 678

CC FT DOMAIN 532 712

CC FT DISULFID 349 433

CC FT DISULFID 503 516

CC FT DISULFID 679 694

CC FT DISULFID 688 700

CC FT DISULFID 702 711

CC FT CARBOHYD 175 175

CC FT CARBOHYD 519 519

CC FT CARBOHYD 634 634

CC FT CARBOHYD 675 675

CC FT VARSPLIC 768 803

CC FT VARSPLIC 860 906

CC FT VARSPLIC 859 859

CC FT VARSPLIC 859 859

CC /FTid=VSP_005482.

CC Missing (in isoform 3 and isoform 4).

CC /FTid=VSP_005483.

CC E -> EYLNPFKRDYVAVKVEDVKNKTEPYPR (1n

```

FT      isoform 2).
FT      /FTID=VSP_005484.
FT      P -> R (IN REF. 3 AND 4).
FT      CONFLICT      81      81
SQ      SEQUENCE      906 AA; 100432 MM; 265ECDD0FA6C088B CRC64;

Query Match      3.3%; Score 97; DB 1; Length 906;
Beet Local Similarity 19.9%; Pred. No. 14;
Matches 111; Conservative 61; Mismatches 233; Indels 154; Gaps 25;

OY      18 IFASGLSSTRSRESQTLASTSGNPFQANVEMKTF-MEREN-----LTHHQSGITY 68
DB      56 IYRSGGDESRHDLATRVRGDLGGQLTHVDAQSFQVDAFGTSFLDVLVNHDLSSRY 115
OY      69 VDL-----GQDREV-----DGLTYRPP-----AGLCPIW--GKHTELQOPDL 104
DB      116 IERNHEGKTVGVNGGHCYQGHKGNPDSFVALSTGHMGHYDGNHLYLLEPEE- 174
OY      105 PYRNNPLEDVPTEKEYKQ-----SGNPLPGFNLFVTPSGORISPPFELLEKNINIK 159
DB      175 --NDTTOEDFPHSHVYSKRLPEFSLDDLSEFOQVNTTSKFLIKRP----- 220
OY      160 STDLRCAEFARFVAMDKNNKATKYRPFVYDSKRLCHILVSMQMEGKKYCSVK- 218
DB      221 -----KRSKRQLRRYPRNVEETKYIELMIVNDHLMFKKRLSVVHT 262
OY      219 -----EPPDL-----TW-----YCKPKRSYVENHLYGSAVYGE 249
DB      263 NTYAKSVVAMADLYKQDKTRIVLVAMETWATDNKFAISENPLTLIREFMKRRDIFKE 322
OY      250 NPDA-----FISKCPQALRGVFGVWKGKRCIDYELTDVIERVESKAQCVKTF 301
DB      323 KSDAHLVBSGQPSRSSGAAYIGGICSLKGGVNEPFKTDLMNTLAOSLA----- 375
OY      302 ENDGVAADDPHTYPLTQSASMDWMLHQSDDPHSGSGRNGYFVYDVTGEGKCALSDQ 361
DB      376 HNGIISDRKL--ASGECKCEDTW-----SGCIMDGYVLPKFTQ--CNI-EE 421
OY      362 VPDCLVSDAAYSYTAAGLSLSE--ETPNPIBSNPVTPPT-----ETALQCTAK 411
DB      422 YHDFLMSGGACLFNPKSKLDPPECGNGFETEGECDCGTPBECVLEBAECCCKKTLTQ 461
OY      412 FPD-SFGACDVQACKRQKTSVCVGQIGSTSVDTADE-----ONEGCSNTALAGLAVG 465
DB      482 DSGCSGLC-----CKCKCFQPKVTQREAVNDCDIFETGSGNSQCAPNHNKMDGISC 537
OY      466 VLLALLGGCYFPAKRLDR 484.
DB      538 VQGIC-FGGRG---KTRDR 552

RESULT 34
NX1A RAT STANDARD; PRT; 1514 AA.
ID      NX1A RAT
AC      063372;
DT      28-FEB-2003 (Rel. 41, Last Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Neurexin 1-alpha precursor (Neurexin 1-alpha).
GN      NRXN1.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
ON      1)
RP      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC      TISSUE=Brain;
RX      MEDLINE=92330296; PubMed=1621094;
RA      Ushkaryov Y.A., Petrenko A.G., Geppert M., Suedhof T.C.;
RT      "Neurexins: synaptic cell surface proteins related to the alpha-
RL      latrotoxin receptor and laminin.";
RN      Science 257:50-56(1992).
RP      PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

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RX      MEDLINE=95209856; PubMed=7695896;
RA      Ullrich B., Ushkaryov Y.A., Suedhof T.C.;
RT      "Cartography of neurexins: more than 1000 isoforms generated by
RT      alternative splicing and expressed in distinct subsets of neurons.";
RN      Neuron 14:497-507(1995).
RX      [3]
RX      SEQUENCE OF N-TERMINUS, AND INTERACTION WITH NEUREXOPHILINS 1 AND 3.
RP      MEDLINE=99074239; PubMed=9856994;
RA      Miesler M., Hammer R.E., Suedhof T.C.;
RT      "Neurexophilin binding to alpha-neurexins. A single LNS domain
RT      functions as an independently folding ligand-binding unit.";
RN      J. Biol. Chem. 273:34716-34723(1998).
RX      [4]
RX      INTERACTION WITH CASK.
RP      MEDLINE=96256685; PubMed=8786425;
RA      Hata Y., Butz S., Suedhof T.C.;
RT      "CASK: a novel dig/PSD5 homolog with an N-terminal
RT      calmodulin-dependent protein kinase domain identified by interaction
RT      with neurexins.";
RN      J. Neurosci. 16:2488-2494(1996).
RX      [5]
RX      INTERACTION WITH ALPHA-LATROTOXIN.
RP      MEDLINE=99211386; PubMed=10197529;
RA      Sugita S., Khvocholev M., Suedhof T.C.;
RT      "Neurexins are functional alpha-latrotoxin receptors.";
RN      Neuron 22:489-496(1999).
RX      [6]
RX      INTERACTION WITH ALPHA-DYSTROGLYCAN.
RP      MEDLINE=21363578; PubMed=11470830;
RA      Sugita S., Saito F., Tang J., Satz J., Campbell K., Suedhof T.C.;
RT      "A stoichiometric complex of neurexins and dystroglycan in brain.";
RN      J. Cell Biol. 154:435-445(2001).
RX      [7]
RX      FUNCTION: Neuronal cell surface protein that may be involved in
RX      cell recognition and cell adhesion. May mediate intracellular
RX      signaling.
RX      [8]
RX      SUBUNIT: The cytoplasmic C-terminal region binds to CASK. Laminin
RX      alpha 4C binds to alpha-dystroglycan. Isoforms alpha 2C
RX      and alpha 4C bind to alpha-dystroglycan. Isoforms alpha 4C bind to
RX      alpha-latrotoxin.
RX      [9]
RX      SUBCELLULAR LOCATION: Type I membrane protein (Potential).
RX      [10]
RX      ALTERNATIVE PRODUCTS:
RX      Event=Alternative promoter;
RX      Comment=A number of isoforms, alpha-type (shown here) and
RX      beta-type, are produced by use of alternative promoters.
RX      Beta-type isoforms differ from alpha-type isoforms in their
RX      N-terminus;
RX      Event=Alternative splicing; Named isoforms=1;
RX      Comment=At least 96 isoforms may be produced by alternative
RX      splicing. There is a combination of five alternatively spliced
RX      domains at sites 1 to 5, each consisting of modular sequences
RX      (A-G) that seem to be used independently. For splice site 1
RX      additional splice modules might be possible thus increasing the
RX      number of possible isoforms. Beta-type isoforms (AC 063373)
RX      share the combination of two alternatively spliced domains at
RX      sites 4 and 5;
RX      Name=Alpha 1A2A3A4A5A;
RX      IsoId=063372-1; Sequence=Displayed;
RX      [11]
RX      TISSUE SPECIFICITY: Brain (neuronal synapse).
RX      [12]
RX      PTM: N- and O-glycosylated (By similarity).
RX      [13]
RX      MISCELLANEOUS: Alpha-latrotoxin competes with alpha-dystroglycan for
RX      binding.
RX      [14]
RX      SIMILARITY: Contains 6 laminin G-like domains.
RX      [15]
RX      SIMILARITY: Contains 3 EGF-like domains.
RX      [16]
RX      SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.
RX      [17]
RX      This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL, M96374; AAA41704.1; -.
DR PIR, A40228; A40228.
DR HSSP, Q63373; 1C4R.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR01791; Laminin_G.
DR InterPro: IPR03585; Neurexin-like.
DR Pfam; PF00008; EGF_3.
DR Pfam; PF00054; laminin; 6.
DR SMART; SM00284; 4.1m; I.
DR SMART; SM00181; EGF_3.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; FALSE NEG.
DR PROSITE; PS01186; EGF_2; FALSE NEG.
DR PROSITE; PS50025; LAM_G_DOMAIN; 6.
DR Signal; Transmembrane; Repeat; Cell adhesion; Glycoprotein;
KW Alternative splicing; Alternative promoter usage.
FT SIGNAL 1 30
FT CHAIN 1 1514
FT DOMAIN 31 1438
FT TRANSMEM 1439 1459
FT DOMAIN 1460 1514
FT DOMAIN 31 217
FT DOMAIN 213 255
FT DOMAIN 283 480
FT DOMAIN 487 679
FT DOMAIN 683 720
FT DOMAIN 725 898
FT DOMAIN 912 1087
FT DOMAIN 1090 1127
FT DOMAIN 1133 1331
FT DOMAIN 1361 1364
FT DOMAIN 1446 1449
FT CARBOHYD 125 125
FT CARBOHYD 190 190
FT CARBOHYD 797 797
FT CARBOHYD 1230 1230
FT VARSPIC 258 258
FT VARSPIC 258 277
FT VARSPIC 274 277
FT VARSPIC 379 393
FT VARSPIC 387 393
FT VARSPIC 790 799
FT VARSPIC 1247 1276
FT VARSPIC 1410 1411
FT SEQUENCE 1514 AA; 166167 MW; D99492302868B14 CRC64;

Query Match 3.3%; Score 97; DB 1; Length 1514;
Best Local Similarity 22.3%; Pred. No. 28;
Matches 52; Conservative 38; Mismatches 103; Indels 40; Gaps 11;

330 OSDPHSGGVGRNNGFY-----VDITGE-----GKALSDQVDDCLVSDSAVSYT 376
1295 EGQDPFGQQLS---GLYNGKLKLVMAAENDANITAVGNVRLVGVSVSMTSTSTATAMQ 1351
377 A--AGSLSEETPNFIIPNSVTPETETALQCTADKPPDSFGAC-----DVQACKRQKT 429
1352 SEMSTSMETTTTATSTARGRKPTKEPISTQTDILVNS-ACPSDDDEIDDCERS- 1409
430 SCVGGQIQSTSV-----DCTADEQNEGSGNTALIAGLAVGVLLALLGGGCFAPKRLD 483
1410 ---GGLANPTVGRGREGYPGSAEYIRSSSTTGWVGIVAAALAILILYANY--KYRN 1464

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QY 484 RNKGVQAAHHEHFEFSDRGARKRPPSDLMQAEPSFWDEAEENIE-ODGETHV 535
DB 1465 RDEG---SYHVEDSRNATISNSAOGNAGVAVKEKOPSSAKSKANKKKKNDKEYV 1514

RESULT 35
CYF ATREBE STANDARD; PRT; 320 AA.
AC Q688M4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apocycochrome f precursor.
GN PETA
OS Atropa belladonna (Belladonna) (Deadly nightshade).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Atropa.
OX NCBI_TaxId=33113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AD5p (kan);
RX MEDLINE=22189020; PubMed=12200487;
RA Schmitz-Lineweber C., Regel R., Du T.G., Hupfer H., Herrmann R.G.,
RA Maier R.M.;
RT "The plastid chromosome of Atropa belladonna and its comparison with
RT that of Nicotiana tabacum: the role of RNA editing in generating
RT divergence in the process of plant speciation."
RL Mol. Biol. Evol. 19:1602-1612(2002).
CC -1- FUNCTION: Translocates protons across the thylakoid membrane and
CC transfers electrons from photosystem II to photosystem I. It
CC receives electrons from the Rieske iron-sulfur protein and passes
CC them to plastocyanin.
CC -1- SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
CC protein (by similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-
CC anchored (by similarity).
CC -1- SIMILARITY: Belongs to the cytochrome c family.
CC
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CC
DR EMBL: AJ116582; CAC68057.1; -.
DR HAMAP: MF_00610; -1.
DR InterPro: IPR002325; Apocyt_F.
DR InterPro: IPR000345; Cyt_c_heme_bind.
DR Pfam: PF01333; Apocytocyt_F_C1.
DR PROSITE; PS00190; CYTOCHROME_C_1.
KW Electron transport; Heme; Chloroplast; Thylakoid; Photosynthesis;
KW Photosystem I; Photosystem II; Transmembrane; Signal.
FT SIGNAL 1 35
FT CHAIN 36 320
FT TRANSMEM 286 305
FT METAL 36 36
FT BINDING 56 56
FT BINDING 59 59
FT METAL 60 60
FT SEQUENCE 320 AA; 35222 MW; BD6F5BD432A3B4 CRC64;

Query Match 3.3%; Score 95.5; DB 1; Length 320;
Best Local Similarity 21.2%; Pred. No. 4.5;
Matches 67; Conservative 40; Mismatches 90; Indels 119; Gaps 19;

83 REBAGL-----CPWGHTELQOPDRLPYRNPLED-----VPTKEYKO-SGNPLP 128

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Db 48 REATGRIVCANCLANKRVEIEVPOAV-----LPDYFEAVNRIPYDMOLKQVLANCK 101
QY 129 GGFNLN--FVTPSG-----GRISPFMELLEKNKSNIKASTDLGRCAEFATKYAMDKNN 180
Db 102 GGLNVAVALILPEGEPLAPSDRISP---EMKEKIGNL-----SFOSYKPNKKN 146
QY 181 KATKRRYFVVDSSKRLCHILIVSMQMEGKKYCSVKKEPPDLTWYCKPKKSTVENHL 240
Db 147 -----LIVIGP--VPGKKY-----SEITPILISPPDKVDVHF 178
QY 241 IYGSAYVGEN-----PDATSKCPNOALRGYRFGWK-----GRCLDYELTD-- 284
Db 179 LKPYIVYAGNGRGQIYPDG--SKNNVYVATAGIYSKIRKEKGVETITDASGR 236
QY 285 TVIERVESKACQWKTFFENDGVAADPHTYPLTSQASWMDWPLHQSOPHSGVGRNYG 344
Db 237 QVVDIIPGPELVLS--EGESIKFDQ-----PLTS-----NPNVGGFGQ--- 273
QY 345 FYVYDTTGEKCALSD 360
Db 274 -----GDAETVLQD 282

RESULT 36
ID CYF_ORYSA STANDARD; PRT; 320 AA.
AC P07888;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apocytochrome f precursor.
GN
OS Oryza sativa (Rice).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriacridaceae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cev. Labelle;
RX MEDLINE=87219885; PubMed=2884170;
RA Wu N.-H., Cote J.C., Wu R.;
RT "Nucleotide sequence of the rice cytochrome f gene and the presence
RL of sequence variation near this gene.";
RN Gene 50:271-278(1986).
RP SEQUENCE FROM N.A.
RC STRAIN=cev. Nipponbare;
RX MEDLINE=89364698; PubMed=2770692;
RA Hiratsuka J., Shimada H., Whittier R., Teshigahashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugita M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct rRNA genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RN Mol. Gen. Gene. 217:185-194(1989).
CC -1- FUNCTION: Translocates protons across the thylakoid membrane and
CC transfers electrons from photosystem II to photosystem I. It
CC receives electrons from the Rieske iron-sulfur protein and passes
CC them to plastocyanin.
CC -1- SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
CC protein (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-
CC anchored (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome c family.
CC
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CC -----
CC EMBL, M15955; AAA84590.1; -.
DR EMBL, X15901; CA33961.1; -.
DR PIR, J00239; CFEZ.
DR HSSP, P36438; IHCZ.
DR Gramene; P07888; -.
DR HAMAP, MF_00610; -.
DR InterPro, IPR002325; Apocyt_F.
DR InterPro, IPR000345; Cytochrome_bind.
DR Pfam, PF01333; Apocytococh_F_C1.
DR PRINTS, PR00610; CYTOCHROME_F.
DR PROSITE, PS00190; CYTOCHROME_C_1.
KW Electron transport; Heme; Chloroplast; Thylakoid; Photosynthesis;
KW Photosystem I; Photosystem II; Transmembrane; Signal.
FT SIGNAL 1..35
FT CHAIN 36..305
FT TRANSMEM 286..305
FT METAL 36
FT BINDING 56..56
FT METAL 60..60
FT CONFLICT 14..14
FT CONFLICT 20..20
SQ SEQUENCE 320 AA; 35467 MW; 94628351A18018BF CRC64;

Query Match 3.3%; Score 95.5; DB 1; Length 320;
Best Local Similarity 21.5%; Pred. No. 4.5;
Matches 68; Conservative 39; Mismatches 90; Indels 119; Gaps 19;

QY 83 REPAGL-----CPIMGKHIEEQOPDRLPYRNPFLE-----VPEKEKYQ--SGNPLP 128
Db 48 REATGRIVCANCLANKRVEIEVPOAV-----LPDYFEAVNRIPYDMOLKQVLANCK 101
QY 129 GGFNLN--FVTPSG-----GRISPFMELLEKNKSNIKASTDLGRCAEFATKYAMDKNN 180
Db 102 GGLNVAVALILPEGEPLAPSDRISP---ELKEKIGNL-----SFOSYKPNKKN 146
QY 181 KATKRRYFVVDSSKRLCHILIVSMQMEGKKYCSVKKEPPDLTWYCKPKKSTVENHL 240
Db 147 -----LIVIGP--VPGKKY-----SEITPILISPPDKVDVHF 178
QY 241 IYGSAYVGEN-----PDATSKCPNOALRGYRFGWK-----GRCLDYELTD-- 284
Db 179 LKPYIVYAGNGRGQIYPDG--SKNNVYVATAGIYSKIRKEKGVETITDASGR 236
QY 285 TVIERVESKACQWKTFFENDGVAADPHTYPLTSQASWMDWPLHQSOPHSGVGRNYG 344
Db 237 QVVDIIPGPELVLS--EGESIKFDQ-----PLTS-----NPNVGGFGQ--- 273
QY 345 FYVYDTTGEKCALSD 360
Db 274 -----GDAETVLQD 282

RESULT 37
ID C166_MOUSE STANDARD; PRT; 583 AA.
AC C166_MOUSE
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE (ALCAM) (DM-GRASP protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NFS;

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RA MEDLINE=97353242; PubMed=9209500;
 RA Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,
 RA Kobay J., Sterling G.C., Siadak A.W., Aruffo A.,
 RT "Characterization of mouse AlCAM (CD166): the CD6 binding domain is
 RT conserved in different homologs and mediates cross-species binding.";
 RL Eur. J. Immunol. 27:11465-11478(1997).
 RN [2]
 RP SEQUENCE OF 227-583 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=94376084; PubMed=8089660;
 RA Kanki J.P., Chang S., Kuwada J.Y.,
 RT "The molecular cloning and characterization of potential chick
 RT DM-GRASP homologs in zebrafish and mouse.";
 RL J. Neurobiol. 25:831-845(1994).
 CC -1- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
 CC INTERACTIONS BETWEEN NEURONS VIA HETEROPHILIC AND HOMOPHILIC
 CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
 CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
 CC THE NERVOUS SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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 CC -----
 DR EMBL; U95030; AAC06342.1; -;
 DR EMBL; L25274; AAA37528.1; -;
 DR HSSP; Q13740; IXC
 DR MGD; MGI:1313266; Alcam.
 DR GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
 DR GO; GO:0007165; P:signal transduction; IPI.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003066; IG_MHC.
 DR Pfam; PF00047; Ig_5.
 DR SMART; SM00409; IG_3.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; FALSE NEG.
 KM Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
 KM Repeat; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 583
 FT DOMAIN 28 527
 FT TRANSMEM 528 549
 FT DOMAIN 550 583
 FT DOMAIN 28 120
 FT DOMAIN 125 234
 FT DOMAIN 245 328
 FT DOMAIN 333 409
 FT DOMAIN 416 501
 FT DISULFID 43 113
 FT DISULFID 157 220
 FT DISULFID 270 313
 FT DISULFID 354 392
 FT DISULFID 435 485
 FT CARBOHYD 167 167
 FT CARBOHYD 265 265
 FT CARBOHYD 306 306
 FT CARBOHYD 361 361
 FT CARBOHYD 457 457
 FT CARBOHYD 480 480
 FT CARBOHYD 499 499
 FT CONFLICT 227 232
 FT CONFLICT 454 454
 FT SEQUENCE 583 AA; 65161 MM; E7BAFA8FCA8F9489 CRC64;

Query Match 3.3%; Score 95.5; DB 1; Length 583;
 Best Local Similarity 19.9%; Pred. No. 10;
 Matches 118; Conservative 66; Mismatches 179; Indels 229; Gaps 28;
 QY 31 ESQTSAS-----TSGNPQANVEKRTM-----ERFVLTHHSGIYVD 70
 DB 94 ENYTLSTIANAKISDEKRFVCMVYEDNVEAPTLVVKVQPSKPEIVKAPLELDQKK 153
 QY 71 LG----ODKEVDG--TLVREBAGLCPIWGKIEIQOQRLPRVNNLEDPVTEKEY--Q 122
 DB 154 LGDCISRSYDPDGNITWRNGKVLQPVGEVAILEFKKIDP--GIQLYTVTSLSLEYKTR 211
 QY 123 SGNPLPGGFNLPVTPSGQRI-----
 DB 212 SDIQNPFCSYTYGSPGQKITYSQEIFDIYPTQVTLQVLPKNAIKEGDNITLQCL 271
 QY 144 ---SPFMELL-----EKSNIKASTLGLRCALFAFTVAMDKNKATKRYPRVY 191
 DB 272 GNGNPPPEEFMFYLPQGPBGIRSSNTYTLTVRRNATGDYCSLIDKKNMA----- 323
 QY 192 DSKKRLCHILVSMQLMGKKYCSVKGPDPULWYCFKPRKSYTENHHLIYGSAVGENP 251
 DB 324 -STITVYLDLSL-----NPKGEVTKQ-----IG-- 347
 QY 252 DAFISKCPNQLRGYRFGVWKKGR-----CLDYTE---LDTVIERVESKACQW 297
 DB 348 DTLVPSCISASRNATV--VMKNIDIRLSSPSFSLHQDAGNYVCETALQEVG----- 401
 QY 298 VKTEPNDSVADDPHTYPLTISQASWMDWPLHOSDQPHSGVGGRNYGYVDITGEGCA 357
 DB 402 LKKRESLTLVIEGKPOIKMTKK-----TDPGLSKXTI 433
 QY 358 LSDQVPCDLS--DSAAVSYTAAGSLs-----EETP-----NFIIISPSPVTPPE 402
 DB 434 I-----CHVEGFPKPAIHMTITSGSVINOTESSPYNGRYKIIISPEBNV----- 482
 QY 403 TALQCTAD-KEPDSFGACDVQACKROKTSVGGQIOSTSVDTADEQNECSNTR-LIAG 460
 DB 483 -LCTAENQGERVYNSLVNVAISIP-----EHDEADDISDENKKNVDQAKLIVG 531
 QY 461 LAVGVLLALLGGGCT--FAKR-----LDRKKVQAAAHENE 496
 DB 532 IVV-GLLIALVAGVYVWLVMKSKSTASKVHVKDGLGNMBENKKELENNHXTK 582
 RESULT 38
 MYCM_HUMAN
 ID MYCM_HUMAN STANDARD; PRT; 357 AA.
 AC P12525;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE L-myc-2 protein.
 GN MYC2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89233129; PubMed=2541066;
 RA Morton C.C., Nusseizweig M.C., Sousa R., Sorenson G.D.,
 RA Pettengill O.S., Shows T.B.,
 RT "Mapping and characterization of an X-linked processed gene related
 RT to MYC1.";
 RL Genomics 4:367-375(1989).
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. BINDS DNA AS AN HETERO-DIMER WITH MAX.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
 CC -----
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EMBL/ J03069; AAS59883.1; -
 DR PIR; A30146; TVHUL2.
 DR HSSP; P25912; IHL0.
 DR TRANSFAC; T03539; -
 DR Genem; HGNC:7556; MYCL2.
 DR MIM; 310310; -
 DR GO; GO:0003700; F:transcription factor activity; TMS.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR002418; TF_Myc.
 DR Pfam; PF00010; HLH; 1.
 DR Pfam; PF01056; MYC_N-term; 1.
 DR SMART; SM00353; HLH_1.
 DR PROSITE; PS00038; HLH_1; 1.
 DR PROSITE; PS00888; HLH_2; 1.
 DR Nuclear; protein; DNA-binding.
 DR DNA BIND 275
 FT DOMAIN 288 327
 SQ SEQUENCE 357 AA; 4113 MW; 4654F534716E0EC3 CRC64;

Query Match 3.3%; Score 95; DB 1; Length 357;
 Best Local Similarity 22.9%; Pred. No. 5.7; Indels 76; Gaps 17;
 Matches 69; Conservative 34; Mismatches 122;

238 HHLIGSAVGENPDAFISCKPNQALRGYFGWKKGRCLDYTELTD--TVIERVESKA 294
 7 HHYFD--YDG-GEDEFYRSTTSE-----DIMKK-----FELVPPPTWVRREPEP 50
 295 QCVKTFENDGVASDQPHYTP-----TSQASNDWMPHLHSDQPHSGGVGRNYGFY 347
 51 QLM-----SPGTWPVGCAGDETESQDYWKAM-----DANYASLIR----- 86
 348 VDTTEGKCALSDQVP-DCLVDSMAVSTAGSLSE-ETPFIIPSNSTVPPPETAL 405
 87 -DCWMSG--FSTQELERAVSDLLAVGAPSGVSPREFTPTD-----IPELEA 131
 406 OCTADKFPDPSFACDVQACKROKTSVCGQIOISTVCTADBEQSGNTALIGLAVGG 465
 132 GHLAIPFLPCLGEPRKIQACSRSESP---SDSEGEEDIVYKKRQSLTKPIY--IAYVA 186
 466 VLLALLGGGCVFAKRLDRNKGVQAANHEHEFQSDRGARKKR-PSDLWGEAEPSFDEAE 524
 187 DLLDPRMN---LFHISIHQQOHNVYAPRPPESCFCGAGPRMPPEKALERBAFGKDKE 243

525 E 525
 244 D 244

RESULT 39
 APC_MOUSE STANDARD; PRT; 2845 AA.
 AC Q61315; Q62044;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Adenomatous polyposis coli protein (APC protein) (mAPC).
 GN APC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS.
 RC STRAIN=C57BL/6J, and CAST/Ei; TISSUE=Brain;
 RX MEDLINE=92263101; PubMed=1350108;
 RA Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
 RA Luongo C., Gould K.A., Dove W.F.;

"Multiple intestinal neoplasia caused by a mutation in the murine homolog of the APC gene."
 RT Science 256:668-670(1992).
 RN [2]
 RP ERRATUM.
 RA Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
 RA Luongo C., Gould K.A., Dove W.F.;
 RL Science 256:1114-1114(1992).
 RN [3]
 RP SEQUENCE OF 1-45 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Dicker F., Lambertz S., Reltmair A., Ballhausen W.G.;
 RT "The murine APC gene: alternative splicing of 5' untranslated
 RT region segments."
 RL Submitted (Oct-1993) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=94061824; PubMed=8242607;
 RA Oshima M., Sugiyama H., Kitagawa K., Takeo M.;
 RT "APC gene messenger RNA: novel isoforms that lack exon 7."
 RL Cancer Res. 53:5589-5591(1993).
 CC -1- FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1
 CC and participates in Wnt signaling. APC activity is correlated with
 CC its phosphorylation state (By similarity).
 CC -1- SUBUNIT: Forms homooligomers. Associates with catenins. Binds
 CC axin (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q61315-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q61315-2; Sequence=VSP_004116;
 CC Name=3;
 CC IsoId=Q61315-3; Sequence=VSP_004117;
 CC Name=4;
 CC IsoId=Q61315-4; Sequence=VSP_004116, VSP_004117;
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, SPLEEN, KIDNEY, HEART,
 CC LUNG, BRAIN, STOMACH, INTESTINE, TESTIS AND OVARY.
 CC -1- PTM: PHOSPHORYLATED BY GSK-3B (By similarity).
 CC -1- SIMILARITY: Contains 7 ARM repeats.
 CC
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 CC or send an email to license@isb-sib.ch).

EMBL; M88127; AAB59632.1; -
 DR EMBL; U02937; AAB03443.1; -
 DR PIR; I49505; I49505.
 DR HSSP; Q02248; 3BCT..
 DR MGD; MGI:88039; APC.
 DR GO; GO:0005737; Cytoplasm; IDA.
 DR GO; GO:0005634; Cytoplasm; IDA.
 DR GO; GO:0008013; F:Wnt receptor signaling pathway; IDA.
 DR GO; GO:0016055; P:Wnt receptor signaling pathway; IDA.
 DR InterPro; IPR00225; Armadillo.
 DR Pfam; PF00514; Armadillo_seg; 4.
 DR SMART; SM00185; ARM; 5.
 DR PROSITE; PS00176; ARM_REPEAT; 1.
 KW Wnt signaling pathway; Anti-oncogene; Phosphorylation;
 KW Alternative splicing; Repeat; Coiled coil.
 FT DOMAIN 1 61
 FT DOMAIN 125 245
 FT DOMAIN 451 493
 FT REPEAT 451 493 ARM 1.
 FT REPEAT 503 545 ARM 2.
 FT REPEAT 546 589 ARM 3.
 FT REPEAT 590 636 ARM 4.
 FT REPEAT 637 681 ARM 5.
 FT REPEAT 682 723 ARM 6.

```

FT REPEAT 724 765 ARM 7.
FT DOMAIN 739 2834 SER-RICH.
FT DOMAIN 1130 1156 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1864 1891 HIGHLY CHARGED.
FT VARSPLIC 243 276 Missing (in isoform 2 and isoform 4).
FT VARSPLIC 310 410 Missing (in isoform 3 and isoform 4).
FT VARSPLIC 310 410 /FTID=VSP_004117.
FT VARIANT 120 120 T -> A (IN STRAIN CAST/ET).
FT VARIANT 493 493 V -> I (IN STRAIN CAST/ET).
FT VARIANT 797 797 Y -> F (IN STRAIN CAST/ET).
FT VARIANT 1330 1330 A -> T (IN STRAIN CAST/ET).
FT VARIANT 1618 1618 A -> S (IN STRAIN CAST/ET).
FT VARIANT 2294 2294 G -> A (IN STRAIN CAST/ET).
FT VARIANT 2496 2496 H -> Q (IN STRAIN CAST/ET).
FT VARIANT 2523 2523 T -> A (IN STRAIN CAST/ET).
FT VARIANT 2813 2813 T -> S (IN STRAIN CAST/ET).
SQ SEQUENCE 2845 AA; 311086 MW; 145CA73CF570A499 CRC64;

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Query Match 3.3%; Score 95; DB 1; Length 2845;
 Best Local Similarity 18.5%; Pred. No. 91;
 Matches 103; Conservative 65; Mismatches 185; Indels 204; Gaps 23;

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QY 19 PASGLSSSTRSRESQTLASSTGNPPOANVEMKTFMERFNL-----THHQSG-----I 67
DB FSTATSLSDLTIESPPNELAT-GDVRAIGSGEKEKRDITPTGSRSTDQAQKISIV 1707
QY 68 YVDDGGQKENVDTLYREPAGCPIWGKRIEIQDRLPYRNPFLEDPTEKEYQSGNPL 127
DB TPBDDNNKAEGDGLAEICINSAMPKSK-----SHKFR-----VKIMDQVQASST 1754
QY 128 PGCFNLNFTVPSGQR-----ISPPMEL-----LEKSNIKASTDLGRCAEPAF-----K 172
DB 1755 SSGANKQVDTKKKKKPSVPMQNTREYRVRKNTDSKNNV-----TEETPSDNDSK 1810
QY 173 TVAMDKNNAKATKYRP-----FYDSKKRLCHILYVSMQMEKKYCSVKGEPDL 223
DB 1811 KPSIQTNAAKAFNEKLPNNEDVRGTFALDSPHH-----YPIEGTP--- 1851
QY 224 TWVCFKRRKSTENHHLIYGSAYVGENPDALISCKPNOALRGYFGVKKRCCLDYELT 283
DB 1852 --YCFSRNDSL-----SLDFDDDDVLSREKEL-----RKGEKSKDEAK 1891
QY 284 DTV-----IERVESKAQCMWK-----TFENDVVASDOPHTYPLTQASWMDWFLHQSDQ 333
DB 1892 VTGCRPENSSQQAASKQASIKHPANRAQSKPVLOKQP-TPPOSK-----DG 1938
QY 334 PHSGGVGRNYGYVYDTTGECKALSDQVPCLVSDSAVSYTAAGSL----- 382
DB 1939 PDRG-----AATBEKLNLAIENTPVCFSNNSLSLSDIDQENNN 1979
QY 383 ---EETNFIIIPSPVTPPTPTALCTADKPFDSGACVQACROKTSVGGQIOST 439
DB 1980 NKSEPIKEAEPAASQSEPSKQ-----ASGYAPKSFHVEITPTVCFSSNNS-----LSSL 2029
QY 440 SVDCTADEQNECGSNTALLIAGLAVGVLLALLAGGGCVAFARLRYKNGVQAHHHEHROS 499
DB 2030 SIBEDDLQECISAM----- 2046
QY 500 DRGARKKRPDLMOEAE 516
DB 2047 ---PKKRPRLKSESE 2060

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RESULT 40
 CYF_SPTOL STANDARD; PRT; 320 AA.
 AC P16013; Q9M3L3;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apocytochrome f precursor.

```

GN PETA.
OS Spinacia oleracea (Spinach).
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RA Alt J., Herrmann R.G.;
RT "Nucleotide sequence of the gene for pre-apocytochrome f in the
RT spinach plastid chromosome.";
RL Curr. Genet. 8:551-557(1984).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Geant d'hiver, and cv. Monacol;
RX MEDLINE=21187424; PubMed=11292076;
RA Schmitz-Linneweber C., Mäler R.M., Alcaraz J.-P., Cottet A.,
RA Herrmann R.G., Maché R.;
RT "The plastid chromosome of spinach (Spinacia oleracea): complete
RT nucleotide sequence and gene organization.";
RL Plant Mol. Biol. 45:307-315(2001).
CC -I- FUNCTION: Translocates protons across the thylakoid membrane and
CC transfers electrons from photosystem II to photosystem I. It
CC receives electrons from the Rieske iron-sulfur protein and passes
CC them to plastocyanin.
CC -I- SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
CC protein (by similarity).
CC -I- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-
CC anchored (by similarity).
CC -I- SIMILARITY: Belongs to the cytochrome c family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
DR EMBL; M36602; AAA84632.1; -.
DR EMBL; AJ400848; CAB88742.1; -.
DR PIR; S00430; S00430.
DR HSSP; P36438; 1HCZ.
DR HAMAP; MF_00610; -.
DR InterPro; IPR002325; Apocyt_F.
DR InterPro; IPR000345; Cytc_heme_bind.
DR Pfam; PF01333; Apocytochr_F_C; 1.
DR PRINTS; PR00610; CYTOCHROME_F.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
KW Electron transport; Heme; Chloroplast; Thylakoid; Photosynthesis;
KW Photosystem I; Photosystem II; Transmembrane; Signal.
FT SIGNAL 1 35
FT CHAIN 36 320
FT TRANSMEM 286 305
FT METAL 36 36
FT FT
FT FT
FT BINDING 56 56 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 59 59 HEME (COVALENT) (BY SIMILARITY).
FT METAL 60 60 IRON (HEM AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 235 235 G -> R (IN REF. 1).
SQ SEQUENCE 320 AA; 35319 MW; 33B9FED0D2F19C36 CRC64;

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Query Match 3.2%; Score 94.5; DB 1; Length 320;
 Best Local Similarity 20.9%; Pred. No. 5.4;
 Matches 66; Conservative 42; Mismatches 89; Indels 119; Gaps 19;

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QY 83 REPAGL-----CPWKGHIELQOPDRLPYRNPFLEDP-----VPTKEYKQ-SGNPLP 128
DB 48 REATGRIVCANCHLANPVIDEIVPAV-----LPDVFPAVRIPIYDMQLKQVLANKGK 101
QY 129 GGFNIN--FYTPSG-----ORISPPMELLEKNXNKASTDLGRCAEPAFKTYAMDKN 180

```

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Db      102 GGLNVGAVLILPEGFELAPPRISB--EMKEKMGNL-----SFQSYRPNKON 146
OY      181 KATKYRYPFYVDSKKRLCHILYVSMQIMEGKKYCSVKGEPPDLTWYCEPKRKSVTENHHL 240
Db      147 -----ILVIGP--VPGQKY-----SEITFPILAPDPATKQDVHF 178
OY      241 IYGSAYVEEN-----PDAFISKCPNQLRGYRQVWK-----GRCLDYTELTD-- 284
Db      179 LKYPPIYVGNRGQIYPPDG--SKSNNTVYNSTATGIVKIVRKEKGGEIINIADASDGR 236
OY      285 TVIERVESKACQWKTENDGVASDQPHTYPLTSQASNNNDWWPLHQSDQPHSGGVGRNYG 344
Db      237 EVDIIPRGPELVS--EGESIKLDQ-----PLTS-----NPNVGGFRGQ--- 273
OY      345 FYVVDTTGEGKCALSD 360
Db      274 -----GDAEVVLQD 282

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Search completed: October 2, 2003, 15:49:45
 Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 2, 2003, 15:52:30 ; Search time 83 Seconds
(without alignments)
1034.591 Million cell updates/sec

Title: UB-10-039-770A-1
Perfect score: 541
Sequence: 1 MGLVGVQVLVLVADCTIFA.....EAENIEDQGETHWVGGDY 541

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

AGeneSeq_19Jun03:*

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24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	86	15.9	86	ABP56991	Toxoplasma gondii
2	8	1.5	39	AA607963	Arabidopsis thaliana
3	8	1.5	39	AA649409	Arabidopsis thaliana
4	8	1.5	60	AA64731	Human 5' EST relat
5	8	1.5	75	ABP56974	E. tenella microne
6	8	1.5	106	AAO21315	Soybean KCP-like p
7	8	1.5	133	AB683392	Drosophila melanog
8	8	1.5	200	ABU05787	M. tuberculosis an
9	8	1.5	238	AB58791	Breast and ovarian

10	8	1.5	255	AA674269	Human colon cancer
11	8	1.5	256	AA60923	Alternatively spliced
12	8	1.5	266	AA68706	Human transcriptio
13	8	1.5	276	AA60922	Human CLAR1 protei
14	8	1.5	287	AA60577	Escherichia coli
15	8	1.5	287	AA605216	Antigen G5401 an
16	8	1.5	437	AA667722	Human tumour anti
17	8	1.5	437	AA667722	PRO1663, a novel t
18	8	1.5	437	AA687750	Human PRV-1 protei
19	8	1.5	437	AA67261	Human signal pepti
20	8	1.5	437	AA66737	Membrane-bound pro
21	8	1.5	437	AA612404	Human PRO161 poly
22	8	1.5	437	AA670851	Human PRV-1 protei
23	8	1.5	437	AA65260	Human PRO1181 (UNQ
24	8	1.5	437	ABG31399	Human PRO1863 poly
25	8	1.5	437	ABG91359	Novel human secret
26	8	1.5	437	ABG32707	Human secreted pro
27	8	1.5	437	AA683672	Human PRO protein,
28	8	1.5	437	AA680767	Human granulocyte
29	8	1.5	437	AB66802	Human PRO polypept
30	8	1.5	437	AB667078	Human secreted/tra
31	8	1.5	437	ABU59883	Novel secreted and
32	8	1.5	437	ABU50811	Human secreted/tra
33	8	1.5	437	ABG73312	Human secreted/tra
34	8	1.5	437	ABU59153	Human PRO1863 poly
35	8	1.5	437	ABU59300	Novel human secret
36	8	1.5	437	ABU59449	Human secreted/tra
37	8	1.5	437	ABU50584	Novel human secret
38	8	1.5	437	ABU58075	Human secreted/tra
39	8	1.5	437	ABU59006	Human PRO polypept
40	8	1.5	437	ABU33966	Human secreted/tra
41	8	1.5	437	AA610921	Human PRO1181 poly
42	8	1.5	437	ABU5921	Human PRO polypept
43	8	1.5	535	AA61249	Rat liver anion tr
44	8	1.5	585	AA63788	Human polypeptide,
45	8	1.5	616	AA619347	Human PRO113 (UNQ
46	8	1.5	616	AA629102	Human PRO polypept
47	8	1.5	616	AA66096	Protein of the inv
48	8	1.5	616	ABU71190	Human PRO13 prote
49	8	1.5	616	ABU56647	Human secreted/tra
50	8	1.5	616	ABU55980	Novel human secret
51	8	1.5	616	ABU67484	Human secreted/tra
52	8	1.5	616	ABU55342	Human PRO polypept
53	8	1.5	616	ABU58478	Human PRO polypept
54	8	1.5	616	ABU56014	Human secreted/tra
55	8	1.5	616	ABU57009	Human PRO polypept
56	8	1.5	616	ABU0588	Human secreted/tra
57	8	1.5	692	ABP57859	Human secreted/tra
58	8	1.5	1129	ABG20477	Novel human diapo
59	8	1.5	2189	ABG05222	Antigen G5401FL e
60	8	1.5	3433	ABP06647	E. maximo 250 kDa
61	8	1.5	3433	ABP06647	Amino acid sequenc
62	8	1.5	10	AA632582	West Nile virus BC
63	8	1.5	13	AA674276	West Nile virus (W
64	8	1.5	15	AA65179	Immunoglobulin E F
65	8	1.5	32	AA650409	Human cytochrome c
66	8	1.5	41	AA670553	Human microtubule
67	8	1.5	50	ABP03189	Heterologous signa
68	8	1.5	52	AAU44403	Human ORF protein
69	8	1.5	53	ABP26162	Protonionbacterium
70	8	1.5	56	AAU60385	Streptococcus poly
71	8	1.5	59	ABG57756	Protonionbacterium
72	8	1.5	59	ABG42331	Human liver peptid
73	8	1.5	59	ABG25822	Peptide #9837 enco
74	8	1.5	59	AA663217	Protein #7821 enco
75	8	1.5	59	AA663030	Human brain expres
76	8	1.5	59	AA620777	Human bone marrow
77	8	1.5	59	AA620777	Peptide #7211 enco
78	8	1.5	59	AA636137	Peptide #10174 enco
79	8	1.5	59	ABG5438	Human peptide enco
80	8	1.5	70	ABG58999	Human liver peptid
81	8	1.5	70	ABG43622	Peptide #1118 enco
82	8	1.5	70	AA64563	Human brain expres
	7	1.3	70	AA677366	Human bone marrow

83	7	1.3	70	22	AAW21289	Peptide #7723 enco	156	7	1.3	182	21	AAV96234
84	7	1.3	70	22	AAW37516	Peptide #11553 enc	157	7	1.3	183	21	AAV96232
85	7	1.3	70	23	ABG46380	Human peptide enco	158	7	1.3	193	17	AAV96281
86	7	1.3	70	24	ABP56985	Sarcocystis muris	159	7	1.3	193	22	AAU3487
87	7	1.3	77	22	AAU48074	Propionibacterium	160	7	1.3	197	15	AAK45778
88	7	1.3	80	22	ABG51385	Human liver peptid	161	7	1.3	197	22	AAK31586
89	7	1.3	80	22	ABK31332	Peptide #3983 enco	162	7	1.3	198	22	ABK66929
90	7	1.3	80	22	ABK36538	Peptide #4044 enco	163	7	1.3	198	22	ABK66930
91	7	1.3	80	22	ABK21879	Protein #3878 enco	164	7	1.3	202	21	AAV96806
92	7	1.3	80	22	AAW57300	Human brain expres	165	7	1.3	202	24	ABP76743
93	7	1.3	80	22	AAW69705	Human bone marrow	166	7	1.3	202	24	ABP79559
94	7	1.3	80	22	AAW17517	Peptide #3951 enco	167	7	1.3	215	14	AAK38690
95	7	1.3	80	22	AAW30039	Peptide #4076 enco	168	7	1.3	215	14	AAK41759
96	7	1.3	80	22	AAW05189	Peptide #3871 enco	169	7	1.3	215	14	AAK43315
97	7	1.3	80	23	ABG39320	Human peptide enco	170	7	1.3	216	20	AAW69013
98	7	1.3	86	22	AAO09816	Human polypeptide	171	7	1.3	216	22	ABK51091
99	7	1.3	88	22	AAU57891	Propionibacterium	172	7	1.3	217	22	AAW64401
100	7	1.3	89	22	AAU45812	Propionibacterium	173	7	1.3	220	22	AAW64675
101	7	1.3	92	22	AAU55470	Propionibacterium	174	7	1.3	221	23	AAO17599
102	7	1.3	95	21	AAW40526	Human ORF ORF290	175	7	1.3	222	21	AAW56236
103	7	1.3	95	22	AAO07633	Human polypeptide	176	7	1.3	232	22	AAK31585
104	7	1.3	100	20	AAW89015	Polypeptide triage	177	7	1.3	234	22	ABG10662
105	7	1.3	100	22	ABK51093	Human secreted pro	178	7	1.3	234	22	AAW73028
106	7	1.3	107	22	ABK17371	Human nervous syst	179	7	1.3	234	23	AAK19930
107	7	1.3	112	21	AAK21372	Zea mays protein f	180	7	1.3	235	13	AAK26064
108	7	1.3	112	22	AAW64006	Propionibacterium	181	7	1.3	238	22	AAU39177
109	7	1.3	112	23	AAW83335	Novel secreted pro	182	7	1.3	246	21	AAW59547
110	7	1.3	113	22	AAW63171	Propionibacterium	183	7	1.3	247	23	ABK49250
111	7	1.3	113	22	AAW04068	Rat zeytor 10 cyto	184	7	1.3	247	24	ABJ25658
112	7	1.3	115	22	ABG25336	Novel human diago	185	7	1.3	250	21	AAW17920
113	7	1.3	123	22	AAW66407	Propionibacterium	186	7	1.3	250	21	AAW59272
114	7	1.3	127	21	AAW64657	Human 5' EST relat	187	7	1.3	250	21	AAW59465
115	7	1.3	129	23	ABP32868	Human complement p	188	7	1.3	252	22	AAW9289
116	7	1.3	130	22	AAU47977	Propionibacterium	189	7	1.3	253	23	ABP69108
117	7	1.3	131	22	AAW65178	Human cytochrome c	190	7	1.3	253	23	ABK49402
118	7	1.3	133	22	AAU57948	Propionibacterium	191	7	1.3	256	22	AAW92545
119	7	1.3	136	13	AAK22387	Antigen tc-33c. E	192	7	1.3	257	10	AAW90385
120	7	1.3	137	20	AAW87495	Murine GLR protei	193	7	1.3	257	11	AAW05025
121	7	1.3	137	21	AAW91442	Human secreted pro	194	7	1.3	257	12	AAK14772
122	7	1.3	137	22	ABK64531	Gene 35 human secr	195	7	1.3	257	14	AAK42336
123	7	1.3	139	22	ABG28850	Novel human diago	196	7	1.3	257	18	AAW24066
124	7	1.3	148	22	ABG52204	Human liver peptid	197	7	1.3	257	19	AAW61190
125	7	1.3	148	22	ABG58832	Human liver peptid	198	7	1.3	257	19	AAW48094
126	7	1.3	148	22	ABK312148	Peptide #4799 enco	199	7	1.3	257	22	AAW74667
127	7	1.3	148	22	ABK37398	Peptide #4904 enco	200	7	1.3	257	22	AAK31584
128	7	1.3	148	22	ABK43456	Peptide #10962 enc	201	7	1.3	257	23	ABG32801
129	7	1.3	148	22	ABK14896	Human nervous syst	202	7	1.3	257	23	ABP45241
130	7	1.3	148	22	ABK26425	Protein #8424 enco	203	7	1.3	258	24	ABJ26258
131	7	1.3	148	22	AAW64387	Human brain expres	204	7	1.3	260	21	AAW96230
132	7	1.3	148	22	AAW70527	Human bone marrow	205	7	1.3	271	21	AAV95751
133	7	1.3	148	22	AAW77209	Peptide #4799 enco	206	7	1.3	277	23	ABP65842
134	7	1.3	148	22	AAW18365	Peptide #7574 enco	207	7	1.3	277	23	ABP29865
135	7	1.3	148	22	AAW21140	Peptide #11382 enc	208	7	1.3	281	12	AAK13867
136	7	1.3	148	22	AAW37345	Peptide #4647 enco	209	7	1.3	281	12	AAK13868
137	7	1.3	148	22	AAW05965	Human peptide enco	210	7	1.3	281	12	AAK13869
138	7	1.3	148	23	ABG46420	Novel human diago	211	7	1.3	281	12	AAK13870
139	7	1.3	149	22	ABG10601	Streptococcus poly	212	7	1.3	291	23	ABK47465
140	7	1.3	156	23	ABP30498	Novel human secret	213	7	1.3	301	22	ABG05867
141	7	1.3	157	23	AAU84379	Zea mays protein f	214	7	1.3	312	21	AAW17919
142	7	1.3	160	21	AAW21371	Streptococcus poly	215	7	1.3	312	21	AAW59271
143	7	1.3	162	23	ABP26616	Streptococcus poly	216	7	1.3	312	21	AAW59545
144	7	1.3	166	23	ABP28242	Human sfc-epilomr	217	7	1.3	314	23	ABK54787
145	7	1.3	172	20	AAV3185	Human phfepilomr	218	7	1.3	325	23	ABG76899
146	7	1.3	172	21	AAV94211	Human phfepilomr	219	7	1.3	344	13	AAK10899
147	7	1.3	172	22	AAW31587	A Fc epsilon recep	220	7	1.3	344	13	AAK21775
148	7	1.3	176	21	AAV94210	Human phfepilomr	221	7	1.3	344	15	AAK51948
149	7	1.3	176	22	AAW65597	Amino acid sequenc	222	7	1.3	345	24	ABP80534
150	7	1.3	176	22	AAW65598	Hepatitis GB virus	223	7	1.3	348	12	AAW92524
151	7	1.3	177	16	AAW81432	Hepatitis GB virus	224	7	1.3	349	12	AAK10900
152	7	1.3	177	21	AAW09009	Hepatitis GB virus	225	7	1.3	349	13	AAK21776
153	7	1.3	178	22	ABK17489	Human nervous syst	226	7	1.3	349	15	AAK51949
154	7	1.3	178	22	AAU27668	Human protein AFP6	227	7	1.3	361	21	AAW59270
155	7	1.3	178	22	AAW03375	Human gene 2 encod	228	7	1.3	367	21	AAW17918

Recombinant human
 Recombinant human
 IGE high affinity
 Enterococcus faeca
 Human dihydrofolat
 A Fc epsilon recep
 Drosophila melanog
 Streptococcus agal
 N. gonorrhoeae ami
 N. gonorrhoeae ami
 Pcp. Bacillus amy
 Bacillus subtilis
 Polypeptide subclis
 Polypeptide fragme
 Human secreted pro
 Amino acid sequenc
 Novel human diago
 E. goesslyi protein
 Human secreted pro
 Amino acid sequenc
 Novel human diago
 Olfactory receptor
 Soybean 3-hydroxy
 Human FcBRI alpha-
 Propionibacterium
 Arabidopsis thalia
 Listeria monocytog
 Aspergillus fumiga
 Arabidopsis thalia
 Arabidopsis thalia
 Arabidopsis thalia
 Human protein SEQ
 Human polypeptide
 Listeria monocytog
 C. glutamicum prote
 Alpha subunit of h
 Alpha subunit of h
 Human Fc(epsilon)R
 Human FcERI alpha.
 Human polypeptide
 The alpha subunit of h
 Human IgE receptor
 Human immunoglobul
 Amino acid sequenc
 Human IGE receptor
 Human Blys binding
 Aspergillus fumiga
 Human Fc receptor,
 Bifidobacterium lo
 Streptococcus poly
 Hybrid Fc(epsilon)
 Hybrid Fc(epsilon)
 Hybrid Fc(epsilon)
 Hybrid Fc(epsilon)
 Novel human diago
 Arabidopsis thalia
 Arabidopsis thalia
 Arabidopsis thalia
 Lactococcus lactis
 Human ileal sodiun
 Rat phospholipase
 Phospholipase A2 i
 Phospholipase A2 i
 N. gonorrhoeae ami
 Human protein sequ
 Human phospholipase
 Phospholipase A2 i
 Phospholipase A2 i
 Arabidopsis thalia

229	7	1.3	377	23	AAE28936	Human sodium/bile-	302	7	1.3	1009	23	AAU84380	Novel human secret
230	7	1.3	377	24	AAE29906	Human transporter	303	7	1.3	1013	21	AAV4687	Amino acid sequenc
231	7	1.3	390	22	ABBS9303	Drosophila melanog	304	7	1.3	1013	22	AAE11053	Ashbya gossypii GT
232	7	1.3	399	22	ABBS5336	Lactococcus lactis	305	7	1.3	1078	22	ABBS3389	Drosophila melanog
233	7	1.3	399	24	ABBS1967	Bacillus subtilis	306	7	1.3	1085	22	ABG27847	Novel human diagno
234	7	1.3	406	21	ABBS3205	Human ORFX ORF2969	307	7	1.3	1091	23	ABBS4828	Listeria monocytog
235	7	1.3	424	24	ABJ18745	Pseudomonas aerugi	308	7	1.3	1097	22	ABG25216	Novel human diagno
236	7	1.3	456	24	AAO16594	Human GLYT1 proteol	309	7	1.3	1151	22	AAAB83939	Amino acid sequenc
237	7	1.3	458	24	ABPS7706	Saccharopolyspora	310	7	1.3	1192	22	ABG02038	Novel human diagno
238	7	1.3	459	21	AAV57687	Streptococcus pneu	311	7	1.3	1202	22	AAW78807	Human protein SEQ
239	7	1.3	459	23	AAU83249	S. pneumoniae ABC	312	7	1.3	1225	22	ABG03949	Novel human diagno
240	7	1.3	459	24	ABU00977	S. pneumoniae type	313	7	1.3	1234	24	ABG72921	Human prostate can
241	7	1.3	460	21	AAV81545	Streptococcus pneu	314	7	1.3	1239	21	AAAB42729	Human ORFX ORF2493
242	7	1.3	469	23	AAU72939	Neisseria meningit	315	7	1.3	1240	22	AAU30861	Novel human secret
243	7	1.3	470	19	AAU47172	Glucosyl transfera	316	7	1.3	1251	16	AAAB79475	Mouse lTRP-3. Mus
244	7	1.3	470	20	AAV06274	Tomato dehydrodico	317	7	1.3	1251	22	AAAB14481	Mouse lTRP-3. prot
245	7	1.3	471	20	AAW98009	Medium-chain UDP-g	318	7	1.3	1251	22	AAAB14483	Human TANGO 300 ex
246	7	1.3	474	22	ABG19636	Novel human diagno	319	7	1.3	1253	21	AAAB12271	Mouse Latent TGF-b
247	7	1.3	492	22	AAAG2209	C glutamincum prote	320	7	1.3	1253	22	AAAB11420	Murine TANGO 275 p
248	7	1.3	495	23	ABBS1922	Human fibroblast g	321	7	1.3	1270	24	ABU11749	Human MDR1 polypep
249	7	1.3	517	23	ABBS07872	Human ankyrin homo	322	7	1.3	1398	22	ABBS4969	Drosophila melanog
250	7	1.3	518	22	ABBS6436	Drosophila melanog	323	7	1.3	1540	22	ABG25976	Novel human diagno
251	7	1.3	526	14	ABBS3375	Brevibacterium fla	324	7	1.3	1592	18	AAW34623	Human C3 protein m
252	7	1.3	526	22	AAAG1406	C glutamincum prote	325	7	1.3	1611	18	AAW22604	Tylosine synthase
253	7	1.3	526	22	AAAB79695	Corynebacterium gl	326	7	1.3	1635	18	AAW34624	Human C3 protein m
254	7	1.3	548	23	ABG70356	Novel human thromb	327	7	1.3	1657	18	AAW34629	Human C3 protein m
255	7	1.3	550	22	ABBS00211	Human transcritp	328	7	1.3	1659	24	ABBS1332	Streptococcus pneu
256	7	1.3	554	22	ABBS1243	Drosophila melanog	329	7	1.3	1659	24	ABU00861	S. pneumoniae type
257	7	1.3	554	22	ABBS1246	Drosophila melanog	330	7	1.3	1661	18	AAW34625	Human C3 protein m
258	7	1.3	557	22	ABBS66431	Drosophila melanog	331	7	1.3	1663	17	AAAB94028	Human C3 precursor
259	7	1.3	563	23	ABBS1144	Herbicidially activ	332	7	1.3	1663	17	AAAB94029	Human modified C3
260	7	1.3	570	21	AAV91944	Human chaperrone pr	333	7	1.3	1663	17	AAAB94030	Human modified C3
261	7	1.3	570	21	AAV94912	Human secreted pro	334	7	1.3	1663	18	AAW34619	Human C3 protein m
262	7	1.3	572	23	ABPA1775	Human ovarian anti	335	7	1.3	1663	18	AAW34620	Human C3 protein m
263	7	1.3	578	20	AAV09065	Human complement E	336	7	1.3	1663	18	AAW34621	Human C3 protein m
264	7	1.3	582	21	AAAB19338	Amino acid sequenc	337	7	1.3	1663	18	AAW34627	Human C3 protein m
265	7	1.3	600	23	ABBS1520	Herbicidially activ	338	7	1.3	1663	18	AAW34628	Human C3 protein m
266	7	1.3	635	22	AAAB31594	Fc epsilon recepto	339	7	1.3	1663	18	AAW34630	Human C3 protein m
267	7	1.3	638	23	AAU93126	Arabidopsis transc	340	7	1.3	1663	18	AAW40988	Human C3 protein m
268	7	1.3	657	22	ABBS14461	Novel human diagno	341	7	1.3	1663	18	AAW40989	Human C3 protein m
269	7	1.3	660	22	AAAB31593	Fc epsilon recepto	342	7	1.3	1663	18	AAW40990	Human C3 protein m
270	7	1.3	669	23	ABBS09771	Amino acid sequenc	343	7	1.3	1663	18	AAW34606	Human C3 protein m
271	7	1.3	669	22	ABBS09781	Amino acid sequenc	344	7	1.3	1663	18	AAW34607	Human C3 protein m
272	7	1.3	679	22	ABBS2564	Novel human diagno	345	7	1.3	1663	18	AAW34608	Human C3 protein m
273	7	1.3	690	22	ABBS1234	Drosophila melanog	346	7	1.3	1663	18	AAW34609	Human C3 protein m
274	7	1.3	712	22	ABBS18031	Novel human diagno	347	7	1.3	1663	18	AAW34610	Human C3 protein m
275	7	1.3	727	23	AAU74448	Human protein sequ	348	7	1.3	1663	18	AAW34611	Human C3 protein m
276	7	1.3	731	22	AAAB31591	Amino acid sequenc	349	7	1.3	1663	18	AAW34612	Human C3 protein m
277	7	1.3	746	17	AAAB31270	GST-INL fusion int	350	7	1.3	1663	18	AAW34613	Human C3 protein m
278	7	1.3	756	22	AAAB31590	Amino acid sequenc	351	7	1.3	1663	18	AAW34614	Human C3 protein m
279	7	1.3	775	22	AAU67605	Propionibacterium	352	7	1.3	1663	18	AAW34615	Human C3 protein m
280	7	1.3	782	23	ABBS9330	Herbicidially activ	353	7	1.3	1663	18	AAW34616	Human C3 protein m
281	7	1.3	795	22	ABBS1567	Drosophila melanog	354	7	1.3	1663	18	AAW34617	Human C3 protein m
282	7	1.3	802	23	AAAB16588	Human fibroblast g	355	7	1.3	1663	18	AAW34618	Human C3 protein m
283	7	1.3	804	23	ABBS64757	Human protein SEQ	356	7	1.3	1667	18	AAW34626	Human C3 protein m
284	7	1.3	831	22	AAW78806	Human protein SEQ	357	7	1.3	1667	18	AAW34631	Human C3 protein m
285	7	1.3	839	23	AAU86145	Human PRO7168 poly	358	7	1.3	1782	22	ABBS5685	Drosophila melanog
286	7	1.3	839	23	ABBS4056	Human PRO7168 poly	359	7	1.3	1795	22	ABBS5806	Drosophila melanog
287	7	1.3	840	22	ABBS3702	Novel human diagno	360	7	1.3	1836	24	ABBS25404	Aspergillus fumiga
288	7	1.3	840	22	ABBS3955	Novel human diagno	361	7	1.3	1857	24	ABBS26003	Aspergillus fumiga
289	7	1.3	867	22	AAW79790	Human protein SEQ	362	7	1.3	1916	22	ABBS62043	Drosophila melanog
290	7	1.3	885	17	AAAB85754	Human axl recepto	363	7	1.3	1916	22	ABBS66089	Drosophila melanog
291	7	1.3	885	23	AAU84262	Human endometrial	364	7	1.3	1964	20	AAW95557	Mus musculus notch
292	7	1.3	891	22	AAW78870	Human protein SEQ	365	7	1.3	1980	22	ABBS7589	Drosophila melanog
293	7	1.3	894	17	AAAB85753	Human axl recepto	366	7	1.3	2047	22	AAAB9541	Human CLASP-7 prot
294	7	1.3	894	22	AAAB90763	Human shear stress	367	7	1.3	2047	23	ABBS1707	Human cadherin-1lik
295	7	1.3	947	22	ABG22182	Novel human diagno	368	7	1.3	2062	23	AAU99400	Human tumour suppr
296	7	1.3	971	22	ABG05866	Novel human diagno	369	7	1.3	2067	24	ABU11831	Human MDR1 polypep
297	7	1.3	976	22	ABG07373	Novel human diagno	370	7	1.3	3080	10	AAAB93285	Sequence of clone
298	7	1.3	978	19	AAAB8096	Human serum albumi	371	7	1.3	3210	9	AAAB1771	Deduced sequence e
299	7	1.3	978	23	ABBS2803	Human IGF recepto	372	7	1.3	3257	22	ABBS67502	Drosophila melanog
300	7	1.3	995	22	ABG22184	Novel human diagno	373	7	1.3	3931	24	ABU07377	Human protein NOV9
301	7	1.3	1009	23	AAE25387	Human NZMS-11 prot	374	7	1.3	7	20	AAV30095	Cyclin binding dom

375	6	1.1	7	23	ABG77648	Targeting peptide	448	6	1.1	22	22	ABG79009	Consensus signal s
376	6	1.1	8	16	AAR73413	Human TSH receptor	449	6	1.1	22	22	AAB13402	Consensus signal p
377	6	1.1	9	20	AAV5442	HLA binding p1u-1	450	6	1.1	22	22	AAW52570	Consensus signal p
378	6	1.1	9	20	AAV46021	Immunogenic peptid	451	6	1.1	22	22	AAE13132	Consensus signal p
379	6	1.1	9	20	AAV46424	Immunogenic peptid	452	6	1.1	22	22	AAE12406	Consensus signal p
380	6	1.1	9	20	AAV46487	Immunogenic peptid	453	6	1.1	22	22	ABG71500	Consensus signal p
381	6	1.1	9	20	AAV00811	HLA-A24 antigenic	454	6	1.1	22	22	ABG36476	Human myeloid prog
382	6	1.1	9	20	AAW97259	Cytotoxic T-cell e	455	6	1.1	22	22	AAU99514	Consensus signal s
383	6	1.1	9	22	AAW88457	HER2/NEU DR superm	456	6	1.1	22	22	ABG63324	Synthetic signal p
384	6	1.1	9	22	AAW88591	HER2/NEU DR superm	457	6	1.1	22	22	AAE20851	Consensus signal p
385	6	1.1	9	22	AAW88599	HER2/neu epitope H	458	6	1.1	22	22	AAU79154	Synthetic consensu
386	6	1.1	9	22	AAU02236	HLA binding TADG-1	459	6	1.1	22	22	AAU75223	Consensus signal p
387	6	1.1	9	22	AAU02263	HLA binding TADG-1	460	6	1.1	22	22	AAU75412	Tumour necrosis fa
388	6	1.1	9	22	AAU02274	HLA binding TADG-1	461	6	1.1	22	22	AAU75409	Calcineurin bindin
389	6	1.1	9	22	AAU02293	HLA binding TADG-1	462	6	1.1	22	22	AAU75408	EBV VCA-p18 fragme
390	6	1.1	9	22	AAU02297	HLA binding TADG-1	463	6	1.1	22	22	AAU74987	Epstein-Barr virus
391	6	1.1	9	22	AAU02315	HLA binding TADG-1	464	6	1.1	22	22	AAU75012	EBV virus peptide
392	6	1.1	9	22	AAU02334	Human complementar	465	6	1.1	22	22	AAU75012	Human ErbB2 CD4+ T
393	6	1.1	10	22	AAW97586	Saccharomyces cere	466	6	1.1	22	22	AAW97586	Human ErbB2 CD4+ T
394	6	1.1	10	22	AAW97586	Saccharomyces cere	467	6	1.1	22	22	AAW97586	Bacterial DnaB1
395	6	1.1	10	22	AAW97586	Saccharomyces cere	468	6	1.1	22	22	AAW97586	Cloned bovine inte
396	6	1.1	10	22	AAW97586	Saccharomyces cere	469	6	1.1	22	22	AAW97586	Pro-opiomelanocort
397	6	1.1	10	22	AAW97586	Saccharomyces cere	470	6	1.1	22	22	AAW97586	Human PREGF N-term
398	6	1.1	10	22	AAW97586	Saccharomyces cere	471	6	1.1	22	22	AAW97586	Human secreted pro
399	6	1.1	10	22	AAW97586	Saccharomyces cere	472	6	1.1	22	22	AAW97586	Human secreted pro
400	6	1.1	10	22	AAW97586	Saccharomyces cere	473	6	1.1	22	22	AAW97586	Human novel secret
401	6	1.1	10	22	AAW97586	Saccharomyces cere	474	6	1.1	22	22	AAW97586	Human novel secret
402	6	1.1	10	22	AAW97586	Saccharomyces cere	475	6	1.1	22	22	AAW97586	Human novel secret
403	6	1.1	10	22	AAW97586	Saccharomyces cere	476	6	1.1	22	22	AAW97586	Human novel secret
404	6	1.1	10	22	AAW97586	Saccharomyces cere	477	6	1.1	22	22	AAW97586	Human novel secret
405	6	1.1	10	22	AAW97586	Saccharomyces cere	478	6	1.1	22	22	AAW97586	Human novel secret
406	6	1.1	10	22	AAW97586	Saccharomyces cere	479	6	1.1	22	22	AAW97586	Human novel secret
407	6	1.1	10	22	AAW97586	Saccharomyces cere	480	6	1.1	22	22	AAW97586	Human novel secret
408	6	1.1	10	22	AAW97586	Saccharomyces cere	481	6	1.1	22	22	AAW97586	Human novel secret
409	6	1.1	10	22	AAW97586	Saccharomyces cere	482	6	1.1	22	22	AAW97586	Human novel secret
410	6	1.1	10	22	AAW97586	Saccharomyces cere	483	6	1.1	22	22	AAW97586	Human novel secret
411	6	1.1	10	22	AAW97586	Saccharomyces cere	484	6	1.1	22	22	AAW97586	Human novel secret
412	6	1.1	10	22	AAW97586	Saccharomyces cere	485	6	1.1	22	22	AAW97586	Human novel secret
413	6	1.1	10	22	AAW97586	Saccharomyces cere	486	6	1.1	22	22	AAW97586	Human novel secret
414	6	1.1	10	22	AAW97586	Saccharomyces cere	487	6	1.1	22	22	AAW97586	Human novel secret
415	6	1.1	10	22	AAW97586	Saccharomyces cere	488	6	1.1	22	22	AAW97586	Human novel secret
416	6	1.1	10	22	AAW97586	Saccharomyces cere	489	6	1.1	22	22	AAW97586	Human novel secret
417	6	1.1	10	22	AAW97586	Saccharomyces cere	490	6	1.1	22	22	AAW97586	Human novel secret
418	6	1.1	10	22	AAW97586	Saccharomyces cere	491	6	1.1	22	22	AAW97586	Human novel secret
419	6	1.1	10	22	AAW97586	Saccharomyces cere	492	6	1.1	22	22	AAW97586	Human novel secret
420	6	1.1	10	22	AAW97586	Saccharomyces cere	493	6	1.1	22	22	AAW97586	Human novel secret
421	6	1.1	10	22	AAW97586	Saccharomyces cere	494	6	1.1	22	22	AAW97586	Human novel secret
422	6	1.1	10	22	AAW97586	Saccharomyces cere	495	6	1.1	22	22	AAW97586	Human novel secret
423	6	1.1	10	22	AAW97586	Saccharomyces cere	496	6	1.1	22	22	AAW97586	Human novel secret
424	6	1.1	10	22	AAW97586	Saccharomyces cere	497	6	1.1	22	22	AAW97586	Human novel secret
425	6	1.1	10	22	AAW97586	Saccharomyces cere	498	6	1.1	22	22	AAW97586	Human novel secret
426	6	1.1	10	22	AAW97586	Saccharomyces cere	499	6	1.1	22	22	AAW97586	Human novel secret
427	6	1.1	10	22	AAW97586	Saccharomyces cere	500	6	1.1	22	22	AAW97586	Human novel secret
428	6	1.1	10	22	AAW97586	Saccharomyces cere	501	6	1.1	22	22	AAW97586	Human novel secret
429	6	1.1	10	22	AAW97586	Saccharomyces cere	502	6	1.1	22	22	AAW97586	Human novel secret
430	6	1.1	10	22	AAW97586	Saccharomyces cere	503	6	1.1	22	22	AAW97586	Human novel secret
431	6	1.1	10	22	AAW97586	Saccharomyces cere	504	6	1.1	22	22	AAW97586	Human novel secret
432	6	1.1	10	22	AAW97586	Saccharomyces cere	505	6	1.1	22	22	AAW97586	Human novel secret
433	6	1.1	10	22	AAW97586	Saccharomyces cere	506	6	1.1	22	22	AAW97586	Human novel secret
434	6	1.1	10	22	AAW97586	Saccharomyces cere	507	6	1.1	22	22	AAW97586	Human novel secret
435	6	1.1	10	22	AAW97586	Saccharomyces cere	508	6	1.1	22	22	AAW97586	Human novel secret
436	6	1.1	10	22	AAW97586	Saccharomyces cere	509	6	1.1	22	22	AAW97586	Human novel secret
437	6	1.1	10	22	AAW97586	Saccharomyces cere	510	6	1.1	22	22	AAW97586	Human novel secret
438	6	1.1	10	22	AAW97586	Saccharomyces cere	511	6	1.1	22	22	AAW97586	Human novel secret
439	6	1.1	10	22	AAW97586	Saccharomyces cere	512	6	1.1	22	22	AAW97586	Human novel secret
440	6	1.1	10	22	AAW97586	Saccharomyces cere	513	6	1.1	22	22	AAW97586	Human novel secret
441	6	1.1	10	22	AAW97586	Saccharomyces cere	514	6	1.1	22	22	AAW97586	Human novel secret
442	6	1.1	10	22	AAW97586	Saccharomyces cere	515	6	1.1	22	22	AAW97586	Human novel secret
443	6	1.1	10	22	AAW97586	Saccharomyces cere	516	6	1.1	22	22	AAW97586	Human novel secret
444	6	1.1	10	22	AAW97586	Saccharomyces cere	517	6	1.1	22	22	AAW97586	Human novel secret
445	6	1.1	10	22	AAW97586	Saccharomyces cere	518	6	1.1	22	22	AAW97586	Human novel secret
446	6	1.1	10	22	AAW97586	Saccharomyces cere	519	6	1.1	22	22	AAW97586	Human novel secret
447	6	1.1	10	22	AAW97586	Saccharomyces cere	520	6	1.1	22	22	AAW97586	Human novel secret

521	6	1.1	50	24	ABU13234	Novel human muscul	594	6	1.1	66	21	AA602678	Human secreted pro
522	6	1.1	51	22	AAU0783	Proionbacterium	595	6	1.1	66	21	AA933417	Amino acid sequenc
523	6	1.1	51	22	AAU5983	Proionbacterium	596	6	1.1	66	22	AAW87394	Human immune/haema
524	6	1.1	51	23	ABP32097	Human ORP1070 prot	597	6	1.1	66	23	AB877029	Human protein sequ
525	6	1.1	52	22	AAU39818	Proionbacterium	598	6	1.1	66	23	ABG64907	Human albumin fusi
526	6	1.1	52	23	AAO17043	Human pro-optimela	599	6	1.1	66	23	ABP33374	Human nuclease-1lx
527	6	1.1	53	22	AAU48443	Proionbacterium	600	6	1.1	67	16	AAW95507	Branched-chain alp
528	6	1.1	54	21	AAAS2020	Human secreted pro	601	6	1.1	67	20	AAV16956	Human PRO617 prote
529	6	1.1	54	22	AAU5867	Proionbacterium	602	6	1.1	67	21	AAAB4252	Human PRO617 (UNQ3
530	6	1.1	54	22	AAU56762	Proionbacterium	603	6	1.1	67	21	AAAB19581	Human PRO617 used
531	6	1.1	54	22	AAU61571	Proionbacterium	604	6	1.1	67	21	AAAG00473	Human secreted pro
532	6	1.1	54	22	AAU628926	Novel human diagno	605	6	1.1	67	22	AAU47924	Proionbacterium
533	6	1.1	55	19	AAW50261	Mouse BID truncate	606	6	1.1	67	22	AAU28155	Novel human secret
534	6	1.1	55	20	AAU29334	Human secreted pro	607	6	1.1	67	23	AAU74938	Human clone DNA483
535	6	1.1	55	20	AAU04939	Mycobacterium spec	608	6	1.1	67	24	AAU61082	Human PRO617 polyp
536	6	1.1	55	20	AAU07809	Human secreted pro	609	6	1.1	68	22	AAU52189	Proionbacterium
537	6	1.1	55	20	AAU11793	Human 5' EST seque	610	6	1.1	68	22	AAU54459	Proionbacterium
538	6	1.1	55	22	AAU39060	Human secreted pro	611	6	1.1	68	22	AAU21358	Human novel foetal
539	6	1.1	55	22	AAU92035	Human digestive sy	612	6	1.1	68	24	ABP77907	N. gonorrhoeae ami
540	6	1.1	55	23	ABBS5769	Human polypeptide	613	6	1.1	69	21	AAAB39425	Human secreted pro
541	6	1.1	56	16	AAW74989	Epsstein-Barr virus	614	6	1.1	69	22	AAU48474	Proionbacterium
542	6	1.1	56	22	AAW91222	Human immune/haema	615	6	1.1	69	23	ABP11893	Human ORF866 prote
543	6	1.1	56	23	ABBS4793	Lactococcus lactis	616	6	1.1	70	22	ABG09739	Novel human diagno
544	6	1.1	57	22	ABG54874	Human liver peptid	617	6	1.1	70	22	ABBI7856	Human nervous syst
545	6	1.1	57	22	AAU56904	Proionbacterium	618	6	1.1	70	22	AAW79621	Human protein SEQ
546	6	1.1	57	22	AAU64825	Proionbacterium	619	6	1.1	70	22	AAW82784	Peptide #2821 enco
547	6	1.1	57	22	ABBS39784	Peptide #7290 enco	620	6	1.1	70	22	AAW63695	Human gastric canc
548	6	1.1	57	22	ABBS24405	Protein #6404 enco	621	6	1.1	70	23	ABG38058	Human peptide enco
549	6	1.1	57	22	AAW60505	Human brain expres	622	6	1.1	70	23	ABP03136	Human ORFX protein
550	6	1.1	57	22	AAW73158	Human bone marrow	623	6	1.1	70	23	AAO16979	Pro-optimelanocort
551	6	1.1	57	22	AAU19863	Peptide #6297 enco	624	6	1.1	71	19	AAW58982	Homo sapiens adult
552	6	1.1	57	22	AAU33371	Peptide #7408 enco	625	6	1.1	71	23	AAO16980	Adrenocorticotroph
553	6	1.1	57	22	AAW06402	Human foetal prote	626	6	1.1	72	20	AAV07892	Human secreted pro
554	6	1.1	57	23	ABG43004	Human peptide enco	627	6	1.1	72	21	AAW08954	Human secreted pro
555	6	1.1	58	20	AAW99320	Epsstein-Barr virus	628	6	1.1	73	21	AAW01106	Human secreted pro
556	6	1.1	58	22	AAU48641	Proionbacterium	629	6	1.1	73	21	AAW01228	Human secreted pro
557	6	1.1	58	22	AAW91931	Human digestive sy	630	6	1.1	73	22	AAW82180	Human immune/haema
558	6	1.1	58	22	AAU19776	Human liver associ	631	6	1.1	73	23	ABP05456	Human ORFX protein
559	6	1.1	58	23	ABP40837	Human liver antiqf	632	6	1.1	73	23	AAO16981	Adrenocorticotroph
560	6	1.1	59	20	AAW89036	Sequence ID #736 f	633	6	1.1	74	22	AAU47759	Proionbacterium
561	6	1.1	59	22	ABG54184	Human liver peptid	634	6	1.1	74	22	AAU66372	Proionbacterium
562	6	1.1	59	22	AAU57143	Proionbacterium	635	6	1.1	74	23	AAO16982	Adrenocorticotroph
563	6	1.1	59	22	ABBS39240	Peptide #6746 enco	636	6	1.1	75	23	AAO16983	Alpha-MSH-f constr
564	6	1.1	59	22	ABBS1161	Human secreted pro	637	6	1.1	75	21	AAAB32763	Eucalyptus grandis
565	6	1.1	59	22	AAW72493	Human bone marrow	638	6	1.1	75	24	ABPS6973	E. maxima immunod
566	6	1.1	59	23	ABG42313	Human peptide enco	639	6	1.1	76	21	AAW35660	Arabidopsis thalia
567	6	1.1	60	22	AAU54186	Proionbacterium	640	6	1.1	76	21	AAW25755	Arabidopsis thalia
568	6	1.1	60	23	ABP34807	Human ORF3780 prot	641	6	1.1	76	22	AAW47587	Mouse heat shock a
569	6	1.1	61	21	AAW08913	Human secreted pro	642	6	1.1	76	22	AAW47589	Rat CD24 peptide.
570	6	1.1	61	22	AAW80465	Human haematologic	643	6	1.1	77	22	AAU42054	Proionbacterium
571	6	1.1	61	22	AAW82055	Human secreted pro	644	6	1.1	77	22	AAW83526	Human immune/haema
572	6	1.1	61	22	AAW75279	Human secreted pro	645	6	1.1	77	22	AAU02981	Angiotensin conver
573	6	1.1	62	20	AAW67929	Fragment of human	646	6	1.1	77	23	ABP43357	Human secreted pro
574	6	1.1	62	21	AAW33049	Zea mays protein f	647	6	1.1	77	23	ABP08119	Human ORFX protein
575	6	1.1	62	21	AAW03233	Human secreted pro	648	6	1.1	77	24	ABP56108	Human IGFBP6 amino
576	6	1.1	62	22	AAU56522	Proionbacterium	649	6	1.1	78	21	AAV54008	Calcineurin bindin
577	6	1.1	62	22	ABG22753	Novel human diagno	650	6	1.1	79	21	AAAB33962	Human cancer assoc
578	6	1.1	63	22	AAU52943	Proionbacterium	651	6	1.1	79	23	ABP07114	Human ORFX protei
579	6	1.1	63	23	ABP35402	Human ORF4375 prot	652	6	1.1	80	22	AAU44362	Proionbacterium
580	6	1.1	64	13	AAW42332	Tracheal antiinflam	653	6	1.1	80	22	AAU46205	Proionbacterium
581	6	1.1	64	16	AAW66205	Bovine tracheal an	654	6	1.1	80	22	AAU61639	Proionbacterium
582	6	1.1	64	16	AAW66204	Bovine tracheal an	655	6	1.1	80	22	AAW47588	Human CD24 peptid
583	6	1.1	64	17	AAW66894	Prepro-LAP. Bos t	656	6	1.1	80	22	AAW65481	Human immune/haema
584	6	1.1	64	19	AAW69696	Human tracheal ant	657	6	1.1	80	22	AAW87022	Human immune/haema
585	6	1.1	64	21	AAW00593	Human secreted pro	658	6	1.1	80	23	ABP68613	Human pancreatic c
586	6	1.1	64	22	AAW63939	Proionbacterium	659	6	1.1	80	23	ABP64138	Human ORF508. Hom
587	6	1.1	64	22	ABW03561	Human musculoskele	660	6	1.1	80	24	ABW47740	Breast cancer asso
588	6	1.1	64	23	AAU90965	Transplant media a	661	6	1.1	80	24	ABP75965	Human GENSER prote
589	6	1.1	64	24	ABU12855	Novel human muscul	662	6	1.1	80	24	ABP76132	Human GENSER prote
590	6	1.1	65	17	AAW68896	Prepro-LAP #2. Sy	663	6	1.1	81	13	AAW26875	Rat intestinal tre
591	6	1.1	65	22	AAU58392	Proionbacterium	664	6	1.1	81	18	AAW27630	Rat trefoll factor
592	6	1.1	65	22	AAW81287	Human AFP protein	665	6	1.1	81	21	AAV99887	Rat intestinal tre
593	6	1.1	66	21	AAW00326	Human secreted pro	666	6	1.1	81	21	AAW59318	Arabidopsis thalia

667	6	1.1	81	21	AAV54567	Amino acid sequenc
668	6	1.1	81	22	ABG18234	Novel human diagno
669	6	1.1	81	22	ABG20201	Novel human diagno
670	6	1.1	81	23	AAE16433	Rat intestinal tre
671	6	1.1	82	19	AAW56582	Petlecan splice va
672	6	1.1	82	21	AAW53397	Human secreted pro
673	6	1.1	82	21	AAW56557	Arabidopsis thalia
674	6	1.1	82	22	AAW66045	Propionibacterium
675	6	1.1	82	22	AAW24316	Human EST encoded
676	6	1.1	82	23	ABJ10914	Human secreted pro
677	6	1.1	82	23	ABP07904	Human ORFX protei
678	6	1.1	82	24	AAE23929	Human Lp321 protei
679	6	1.1	83	20	AAV21863	Mouse agouti-relat
680	6	1.1	83	22	ABW96420	Human testicular a
681	6	1.1	83	22	AAU50182	Propionibacterium
682	6	1.1	83	22	AAU51473	Novel bacterium
683	6	1.1	83	22	ABG26049	Novel human diagno
684	6	1.1	83	22	AAW95889	Human reproductive
685	6	1.1	83	21	ABP10957	Human ORFX protei
686	6	1.1	84	21	AAW32887	Zea mays protein f
687	6	1.1	84	21	AAW59026	Arabidopsis thalia
688	6	1.1	84	21	AAW59317	Arabidopsis thalia
689	6	1.1	84	22	ABG50231	Human liver peptid
690	6	1.1	84	22	ABG11106	Novel human diagno
691	6	1.1	84	22	ABW30201	Peptide #2852 enco
692	6	1.1	84	22	ABW35364	Peptide #2870 enco
693	6	1.1	84	22	ABW15019	Human nervous syst
694	6	1.1	84	22	ABW20806	Human protein #2805 enco
695	6	1.1	84	22	AAW56195	Human brain expres
696	6	1.1	84	22	AAW68568	Human bone marrow
697	6	1.1	84	22	AAW16376	Peptide #2810 enco
698	6	1.1	84	22	AAW28873	Peptide #2910 enco
699	6	1.1	84	22	AAW04112	Peptide #2794 enco
700	6	1.1	84	23	ABP43617	PR02160 protein.
701	6	1.1	84	23	ABP64393	Human ORF63. Hom
702	6	1.1	84	23	ABG38146	Human peptide enco
703	6	1.1	85	20	AAV37018	Protein which is s
704	6	1.1	85	21	AAW42841	Human ORFX ORF2605
705	6	1.1	85	21	AAW44148	Human cancer assoc
706	6	1.1	85	22	AAW05338	Human polypeptide
707	6	1.1	85	22	ABP01434	Human ORFX protei
708	6	1.1	86	23	ABP04214	Human ORFX protei
709	6	1.1	86	23	ABP08692	Human ORFX protei
710	6	1.1	87	22	AAU42531	Propionibacterium
711	6	1.1	87	22	AAU61289	Propionibacterium
712	6	1.1	87	22	AAW04065	Human polypeptide
713	6	1.1	87	23	ABR40468	Human secreted pro
714	6	1.1	87	23	ABP30595	Streptococcus poly
715	6	1.1	88	22	ABW16278	Human nervous syst
716	6	1.1	88	23	ABR40547	Human secreted pro
717	6	1.1	88	23	ABP63192	Human connector en
718	6	1.1	88	23	ABP04325	Human ORFX protei
719	6	1.1	89	22	AAU20811	Human novel foetal
720	6	1.1	90	21	AAW59071	Breast and ovarian
721	6	1.1	90	22	AAU53037	Propionibacterium
722	6	1.1	90	22	ABP59035	Human Fe-S protein
723	6	1.1	91	21	AAW59316	Arabidopsis thalia
724	6	1.1	91	22	ABW96261	Human testicular a
725	6	1.1	91	22	AAU47709	Propionibacterium
726	6	1.1	91	22	AAW95586	Human reproductive
727	6	1.1	91	22	AAW64684	Human secreted pro
728	6	1.1	91	22	ABW53926	Lactococcus lactis
729	6	1.1	92	21	AAW25754	Arabidopsis thalia
730	6	1.1	92	23	ABW62966	Human polypeptide
731	6	1.1	92	23	AAU83176	Novel secreted pro
732	6	1.1	92	24	ABU52387	Human GPCR related
733	6	1.1	92	24	ABU52388	Human GPCR related
734	6	1.1	93	22	ABG56066	Human liver peptid
735	6	1.1	93	22	ABW40617	Peptide #8123 enco
736	6	1.1	93	22	AAW61474	Human brain expres
737	6	1.1	93	22	AAW74266	Human bone marrow
738	6	1.1	93	23	AAW34378	Peptide #8415 enco
739	6	1.1	93	23	ABG44204	Human peptide enco
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813	6	1.1	109	21	AAB40429	Human ORFX ORF193
814	6	1.1	109	23	ABP01336	Human ORFX protein
815	6	1.1	110	21	AAB40867	Human ORFX-ORF631
816	6	1.1	110	21	AAG32886	zea mays protein f
817	6	1.1	110	22	AAU52797	Proiontobacterium
818	6	1.1	110	23	ABP07862	Human ORFX protein
819	6	1.1	111	13	AAK26955	Human T lymphocyte
820	6	1.1	111	22	ABK71018	Drosophila melanog
821	6	1.1	111	22	AAK64616	Human brain expres
822	6	1.1	111	22	AAK65087	Human brain expres
823	6	1.1	111	23	ABK92268	Herbicidally activ
824	6	1.1	112	14	AAK33433	LT-8-2. Ganoderma
825	6	1.1	112	21	AAK33149	Pinus radiata tran
826	6	1.1	112	22	AAU47112	Proiontobacterium
827	6	1.1	112	22	AAU49273	Proiontobacterium
828	6	1.1	112	22	AAU57895	Proiontobacterium
829	6	1.1	112	22	ABK15275	Proiontobacterium
830	6	1.1	112	22	AAK23810	Human nervous syst
831	6	1.1	112	23	ABP38038	Human EST encoded
832	6	1.1	112	23	AAK49275	Staphylococcus epi
833	6	1.1	112	20	AAK21866	Human cell signal/
834	6	1.1	113	21	AAK44227	Amino acid sequenc
835	6	1.1	113	21	ABK70281	Human cancer assoc
836	6	1.1	113	22	ABK46609	Drosophila melanog
837	6	1.1	113	22	ABK19319	Proiontobacterium
838	6	1.1	113	22	AAK90165	Novel human diagno
839	6	1.1	113	23	ABP08125	C glutamicum prote
840	6	1.1	114	22	AAU42767	Human ORFX protein
841	6	1.1	114	22	AAU48548	Proiontobacterium
842	6	1.1	114	22	AAK78304	Proiontobacterium
843	6	1.1	114	22	AAK91711	Human bone marrow
844	6	1.1	114	22	AAK92226	Human immune/haema
845	6	1.1	114	23	ABP34022	C glutamicum prote
846	6	1.1	114	24	ABJ37122	Human transport pr
847	6	1.1	115	18	AAK89769	NOVX protein seque
848	6	1.1	116	22	ABK18098	Staphylococcus aur
849	6	1.1	116	22	AAK79486	Novel human diagno
850	6	1.1	117	20	AAK21867	Human protein SBO
851	6	1.1	117	21	AAK15659	Amino acid sequenc
852	6	1.1	117	22	ABU52900	Arabidopsis thalia
853	6	1.1	117	22	ABK12950	Human uterus-deriv
854	6	1.1	117	22	ABK72462	Novel human diagno
855	6	1.1	118	6	AAK50294	Partial WSIP. Ory
856	6	1.1	118	11	AAK07611	Sequence of mamma
857	6	1.1	118	22	AAK39722	Murine granulocyte
858	6	1.1	118	22	AAK68611	Human VAPB-1. Ho
859	6	1.1	118	23	ABK32647	Human vacuolar pro
860	6	1.1	118	24	ABJ18744	Pseudomonas aerugi
861	6	1.1	119	22	AAK64551	Proiontobacterium
862	6	1.1	119	22	ABK1820	Novel human diagno
863	6	1.1	119	22	ABK17376	Human nervous syst
864	6	1.1	120	21	AAK00195	Human secreted pro
865	6	1.1	120	22	AAU51164	Proiontobacterium
866	6	1.1	120	23	AAK04170	Human polypeptide
867	6	1.1	120	23	AAK02052	Hepatitis C virus
868	6	1.1	121	17	AAK07541	Clone 99, human pr
869	6	1.1	121	22	ABK52650	Human liver peptid
870	6	1.1	121	22	AAK58441	Human brain expres
871	6	1.1	121	22	AAK25299	Human brain expres
872	6	1.1	122	19	AAK50260	Mouse BID truncate
873	6	1.1	122	20	AAK16801	Protein which is s
874	6	1.1	122	20	AAK00094	Enterococcus faeca
875	6	1.1	122	22	ABK16676	Novel human diagno
876	6	1.1	122	23	ABK97768	Human secretory po
877	6	1.1	122	23	ABK43313	E faecalis EF046 p
878	6	1.1	122	23	ABK1499	Human cytochrome x
879	6	1.1	122	23	AAU5737	AAV293 anti- (MCP) -
880	6	1.1	122	23	AAU57545	AAV293 anti- (MCP) -
881	6	1.1	122	24	ABU13592	Enterococcus faeca
882	6	1.1	122	24	ABK79046	N. gonorrhoeae ami
883	6	1.1	123	23	ABK1574	Human ORF547 prote
884	6	1.1	124	17	AAK90940	DDD4 polypeptide #
885	6	1.1	124	21	AAK42908	Human ORFX ORF2672
886	6	1.1	124	21	AAK08733	Amino acid sequenc
887	6	1.1	124	21	AAK3165	MAGE5 polypeptide.
888	6	1.1	124	22	AAU48123	Proiontobacterium
889	6	1.1	124	22	AAU55784	Proiontobacterium
890	6	1.1	124	22	AAK01820	Human gene 12 enco
891	6	1.1	124	23	ABK64131	Human albumin fusi
892	6	1.1	124	23	ABK31689	Human ORF662 prote
893	6	1.1	125	21	AAK33726	Arabidopsis thalia
894	6	1.1	125	22	AAK62578	Proiontobacterium
895	6	1.1	125	22	ABK00193	Novel human diagno
896	6	1.1	126	13	AAK22188	Sequence of rat C-
897	6	1.1	126	21	AAK03056	Human secreted pro
898	6	1.1	126	22	AAK013263	Human polypeptide
899	6	1.1	126	22	AAK48092	Protein encoded by
900	6	1.1	126	24	AAK33512	Streptococcus pneu
901	6	1.1	126	24	AAK33518	Streptococcus pneu
902	6	1.1	126	24	ABU00447	S. pneumoniae type
903	6	1.1	127	10	AAK1061	Human granulocyte-
904	6	1.1	127	10	AAK1890	Amino acid sequenc
905	6	1.1	127	11	AAK08268	Cysteine recombi
906	6	1.1	127	12	AAK13215	Oxidised GM-CSF.
907	6	1.1	127	14	AAK11540	r-h-GM-CSF. Homo
908	6	1.1	127	14	AAK33774	Recombinant human
909	6	1.1	127	14	AAK33775	Human Leu23-GM-CSF
910	6	1.1	127	16	AAK72357	Human granulocyte
911	6	1.1	127	16	AAK13057	HIV-2 provirus--enc
912	6	1.1	127	20	AAK49918	Human GM-CSF prote
913	6	1.1	127	20	AAK35046	Chlamydia pneumonia
914	6	1.1	127	21	AAK59024	Arabidopsis thalia
915	6	1.1	127	21	AAK69025	Amino acid sequenc
916	6	1.1	127	22	ABK49250	Human liver peptid
917	6	1.1	127	22	ABK29256	Peptide #1907 enco
918	6	1.1	127	22	ABK34421	Peptide #1927 enco
919	6	1.1	127	22	AAK31317	Mature human GM-CS
920	6	1.1	127	22	AAK31318	Mature rat GM-CSF
921	6	1.1	127	22	ABK19833	Protein #1832 enco
922	6	1.1	127	22	AAK55211	Human brain expres
923	6	1.1	127	22	AAK67606	Human bone marrow
924	6	1.1	127	22	AAK15413	Peptide #1847 enco
925	6	1.1	127	22	AAK27902	Peptide #1939 enco
926	6	1.1	127	22	AAK03175	Peptide #1857 enco
927	6	1.1	127	23	ABK78399	Amino acid sequenc
928	6	1.1	127	23	ABK37196	Human peptide enco
929	6	1.1	127	24	ABK99813	Human granulocyte
930	6	1.1	128	9	AAK81001	Sequence (I) of hu
931	6	1.1	128	10	AAK90115	Synthetic human gr
932	6	1.1	128	10	AAK90118	Synthetic human gr
933	6	1.1	128	11	AAK03199	New human granular
934	6	1.1	128	16	AAK79338	PMON13012 peptide.
935	6	1.1	128	16	AAK00328	Modified human col
936	6	1.1	128	16	AAK00329	Modified human col
937	6	1.1	128	17	AAK00102	Granulocyte macroph
938	6	1.1	128	17	AAK00103	Granulocyte macroph
939	6	1.1	128	17	AAK90941	D3d4 polypeptide #
940	6	1.1	128	19	AAK54144	GM-KSF activity ex
941	6	1.1	128	21	AAK53217	Human G-CSF mutant
942	6	1.1	128	22	AAK14011	Chemically modifie
943	6	1.1	128	22	AAK04223	Human gene 6 encod
944	6	1.1	128	23	ABK97784	Human interleukin-
945	6	1.1	128	23	ABK64481	Human albumin fusi
946	6	1.1	128	24	ABK64185	Human interleukin
947	6	1.1	129	8	AAK70612	Mammal interleukin-
948	6	1.1	129	8	AAK70616	Human interleukin-
949	6	1.1	129	12	AAK12788	Human IL-4 and pep
950	6	1.1	129	14	AAK47182	Human IL-4 mutein. Homo
951	6	1.1	129	14	AAK47183	IL-4 mutein Y124X.
952	6	1.1	129	14	AAK47184	IL-4 mutein Y124G.
953	6	1.1	129	15	AAK58630	Human interleukin-
954	6	1.1	129	20	AAK37560	Protein involved i
955	6	1.1	129	21	AAK41881	Human ORFX ORF1645
956	6	1.1	129	21	AAK12569	zea mays protein f
957	6	1.1	129	21	AAK57324	Human interleukin-
958	6	1.1	129	21	AAK69035	Amino acid sequenc

959	6	1.1	129	21	AAV53593	Rat agouti-related
960	6	1.1	129	22	ABG60262	Human ovarian anti-
961	6	1.1	129	22	AAV4546	Human reproductive
962	6	1.1	129	22	AAV41508	Human polypeptide
963	6	1.1	129	23	ABG92913	Human interleukin-
964	6	1.1	129	23	ABG61733	Novel ovarian rela
965	6	1.1	129	23	ABG60658	Human interleukin-
966	6	1.1	129	23	ABP31472	Human ORF445 prote
967	6	1.1	129	23	AAO14758	Mature human Inter
968	6	1.1	129	23	AAU83552	Mature wild type h
969	6	1.1	130	21	AAU07664	Arabidopsis thalia
970	6	1.1	130	21	AAV53925	Arabidopsis thalia
971	6	1.1	130	21	AAV53960	Arabidopsis thalia
972	6	1.1	130	22	AAV90325	Human immune/haema
973	6	1.1	130	22	AAO01995	Human polypeptide
974	6	1.1	130	23	ABP43871	Clone RPS-85SD21.
975	6	1.1	130	23	ABP26330	Streptococcus poly
976	6	1.1	131	8	AAV60350	Human granulocyte
977	6	1.1	131	8	AAV70364	Sequence of human
978	6	1.1	131	8	AAV70351	Sequence of granul
979	6	1.1	131	19	AAV26779	Mouse agouti-regul
980	6	1.1	131	20	AAV49104	Mouse agouti-relat
981	6	1.1	131	22	AAO09636	Human polypeptide
982	6	1.1	131	22	AAV38858	Human polypeptide
983	6	1.1	131	23	AAO19090	Human granulocyte-
984	6	1.1	131	23	ABG31632	Human granulocyte-
985	6	1.1	131	23	ABV08135	Human GM-CSF polype
986	6	1.1	132	8	AAV70363	Sequence of human
987	6	1.1	132	21	AAV44085	Human cancer assoc
988	6	1.1	132	22	ABV96173	Human testicular a
989	6	1.1	132	22	AAV95489	Human reproductive
990	6	1.1	132	22	AAV59518	Human secreted pro
991	6	1.1	132	23	ABV51422	Helicobacter pylori
992	6	1.1	133	12	AAV13164	HGM-CSF [leu2]Aep27
993	6	1.1	133	15	AAV66997	Human interleukin-
994	6	1.1	133	16	AAV72358	Human granulocyte
995	6	1.1	133	19	AAV61232	Streptococcus pneu
996	6	1.1	133	22	ABV62907	Drosophila melanog
997	6	1.1	133	23	ABV54650	S. pneumoniae SPI0
998	6	1.1	133	23	ABG59943	Human DITRP polype
999	6	1.1	133	24	ABV98963	Phosphatase 2A cat
1000	6	1.1	134	16	AAV91236	Interleukin-4 circ

ALIGNMENTS

RESULT 1

ID ABP56991 standard; Peptide; 86 AA.

AC ABP56991;

DT 10-APR-2003 (first entry)

XX Toxoplasma gondii AMA1 amino acid sequence fragment.

XX Eimeria maxima; 250 kDa antigen; sporozoite; merozoite; infection;

KW vaccine; antiparasitic; gene therapy.

XX Toxoplasma gondii.

OS Synthetic.

XX WO2003004684-A2.

XX 16-JAN-2003.

PF 03-JUL-2002; 2002WO-US21237.

PR 06-JUL-2001; 2001US-303670P.

XX (WITC/) WITCOMBE D.

PA (SMIT/) SMITH N C.

ID AAG07963 standard; Protein; 39 AA.

AC AAG07963;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 5315.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

QY 456 AIIAGLAVGCVLLALLGGCGCFARLRNKGVOAAHHEHFOSSRGARKRPSDLMGEA 515
 DB 1 AIIAGLAVGCVLLALLGGCGCFARLRNKGVOAAHHEHFOSSRGARKRPSDLMGEA 60
 QY 516 EPSFWDEABENIEQDETHWVEGDPY 541
 DB 61 EPSFWDEABENIEQDETHWVEGDPY 86

RESULT 2

ID AAG07963 standard; Protein; 39 AA.

AC AAG07963;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 5315.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PA (WALL/) WALLACH M.
 XX Witcombe D, Smith NC, Wallach M;
 PI WPI; 2003-201556/19.
 DR New nucleic acid comprising a sequence encoding a 250 kDa polypeptide
 XX from sporozoites/merozoites of Eimeria maxima, useful for preparing a
 PT vaccine against Eimeria infection -
 PT Example 5; Fig 33; 198pp; English.

PS The present invention describes a nucleic acid (1) comprising a
 XX sequence encoding a 250 kDa polypeptide from Sporozoites/Merozoites of
 CC Eimeria maxima or its homologue or complement. Also described: (1) a
 CC vector comprising the nucleic acid; (2) a host cell comprising the
 CC vector; (3) a plasmid comprising the nucleic acid; (4) a transformed
 CC cell comprising the nucleic acid; (5) producing a recombinant 250 kDa
 CC polypeptide; (6) a recombinant polypeptide; (7) a vaccine against
 CC E. tenella, E. acervulina, E. necatrix, E. praecox, E. maxima, E. mitis
 CC or E. brunetti or a microorganism expressing an immunologically
 CC cross-reactive antigen; (8) immunising a subject against infection by
 CC Eimeria, or a microorganism expressing an immunologically cross-reactive
 CC antigen; (9) conferring upon a newborn subject of an avian species
 CC maternal immunity against infection by Eimeria; (10) a fertilised egg
 CC from an avian species having an air sac, where the air sac is inoculated
 CC with the vaccine; and (11) reducing the output of Eimeria oocytes in
 CC faeces from a newborn subject of an avian species. (1) has antiparasitic
 CC activity and can be used in a vaccine and in gene therapy. The nucleic
 CC acid is useful for preparing a vaccine against E. tenella, E. acervulina,
 CC E. necatrix, E. praecox, E. maxima, E. mitis or E. brunetti infection.
 CC The present sequence represents an amino acid sequence used in an example
 CC from the present invention.

SQ Sequence 86 AA;

Query Match 15.9%; Score 86; DB 24; Length 86;
 Best Local Similarity 100.0%; Pred. No. 3.7e-76;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0133048.
PR 30-APR-1999; 99US-0133407.
PR 04-MAY-1999; 99US-0132484.
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PR 11-MAY-1999; 99US-0134256.
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PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134761.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135153.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137502.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
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PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
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PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139765.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141847.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.
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PR 21-JUL-1999; 99US-0144814.
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PR 21-JUL-1999; 99US-0145086.
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PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155119.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 26-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.

PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 16-OCT-1999; 99US-0159584.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 1.5%; Score 8; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 GVLIIALL 472
Db 17 GVLIIALL 24

RESULT 3

AA049409
ID AA049409 standard; Protein; 39 AA.

XX AC AA049409;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 62504.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX XX 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132047.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144686.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149724.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149902.
PR 25-AUG-1999; 99US-0149930.
PR 26-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157117.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0158294.
PR 13-OCT-1999; 99US-0159295.

PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 1.5%; Score 8; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 GVLLALL 472
|||
DB 17 GVLLALL 24

RESULT 4
AAV64731
ID AAV64731 standard; Protein; 60 AA.
XX AAV64731;
AC
XX
DT 01-FEB-2000 (first entry)
XX
DE Human 5' EST related polypeptide SEQ ID NO:892.
XX
XX Human, 5' EST; expressed sequence tag; secreted protein; diagnosis;
KW gene therapy; chromosome mapping; upstream regulatory sequence;
KW forensic; location; development; protein synthesis; stability;
KW regulation; identification.
XX
OS Homo sapiens.
XX
XX
XX W09953051-A2.
XX
XX PD 21-OCT-1999.
XX
XX PF 09-APR-1999; 99WO-IB00712.
XX
XX PR 09-APR-1998; 98US-0057719.
XX PR 28-APR-1998; 98US-0069047.
XX
XX PA (GEST) GENSET.
XX
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WP1; 2000-038446/03.
XX DR N-PSDB; AAZ42345.
XX
XX PT Novel secreted protein 5' expressed sequence tag sequences used in
XX diagnostic, forensic, gene therapy, and chromosome mapping procedures
XX
XX PS Claim 3; Page 625; 837bp; English.
XX

CC AA242265 to AA243075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AAY64651 to CC AAY65438 represent the EST-related proteins corresponding to AA242265 to CC AA243052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated CC regions (UTRs) and upstream regulatory regions which control the CC location, development stage, rate, and quantity of protein synthesis, as CC well as stability of mRNA. The ESTs are also useful as probes for CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can CC also be used in forensic procedures to identify individuals, or in CC diagnostic procedures to identify individuals having genetic diseases CC resulting from abnormal gene expression. The products may also be used in CC gene therapy protocols. The nucleic acids encoding signal peptides can be CC used for directing extracellular secretion of a polypeptide or the CC insertion of a polypeptide into a membrane, or importing a polypeptide CC into a cell. The proteins encoded by the EST sequences may be useful in CC treating a variety of human conditions. Secreted proteins have CC therapeutic value, and the identification of new secreted proteins is CC valuable. AA242249 to AA242264 and AAY64644 to AAY64650 represent CC sequences used in the exemplification of the present invention.

XX Sequence 60 AA;

Query Match 1.5%; Score 8; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLLG 473
Db 4 VLLALLLG 11

RESULT 5
ID ABP56974 standard; Peptide; 75 AA.
XX ABP56974;
XX 10-APR-2003 (first entry)
XX
XX E. tenella microneme 4 protein amino acid sequence fragment.
DE
XX Eimeria maxima; 250 kDa antigen; sporozoite; merozoite; infection;
KW vaccine; antiparasitic; gene therapy.
XX
XX Eimeria tenella.
OS Synthetic.
XX
XX WO2003004684-A2.
XX
XX 16-JUN-2003.
XX
XX 03-JUL-2002; 2002WO-US21237.
XX
XX 06-JUL-2001; 2001US-303670P.
XX
XX (WITC/) WITCOMBE D.
XX (SMIT/) SMITH N C.
XX (WALL/) WALLACH M.
XX
XX WITCOMBE D, Smith NC, Wallach M;
XX WPI; 2003-201556/19.
XX
XX New nucleic acid comprising a sequence encoding a 250 kDa polypeptide
PT from sporozoites/merozoites of Eimeria maxima, useful for preparing a
PT vaccine against Eimeria infection
XX
XX Example 5; Fig 33; 198bp; English.
XX
XX The present invention describes a nucleic acid (1) comprising a
CC sequence encoding a 250 kDa polypeptide from Sporozoites/Merozoites of
CC Eimeria maxima or its homologue or complement. Also described: (1) a

CC vector comprising the nucleic acid; (2) a host cell comprising the
CC vector; (3) a plasmid comprising the nucleic acid; (4) a transformed
CC cell comprising the nucleic acid; (5) producing a recombinant 250 kDa
CC polypeptide; (6) a recombinant polypeptide; (7) a vaccine against
CC E. tenella, E. acerulina, E. necatrix, E. praecox, E. maxima, E. mltis
CC or E. brunetti or a microorganism expressing an immunologically
CC cross-reactive antigen; (8) immunising a subject against infection by
CC Eimeria, or a microorganism expressing an immunologically cross-reactive
CC antigen; (9) conferring upon a newborn subject of an avian species
CC maternal immunity against infection by Eimeria; (10) a fertilised egg
CC from an avian species having an air sac, where the air sac is inoculated
CC with the vaccine; and (11) reducing the output of Eimeria oocytes in
CC faeces from a newborn subject of an avian species. (1) has antiparasitic
CC activity and can be used in a vaccine and in gene therapy. The nucleic
CC acid is useful for preparing a vaccine against E. tenella, E. acerulina,
CC E. necatrix, E. praecox, E. maxima, E. mltis or E. brunetti infection.
CC The present sequence represents an amino acid sequence used in an example
CC from the present invention.

XX Sequence 75 AA;

Query Match 1.5%; Score 8; DB 24; Length 75;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 463 VGVVLLLA 470
Db 7 VGVVLLLA 14

RESULT 6
AA021315
ID AA021315 standard; Protein; 106 AA.
XX AA021315;
XX
XX 05-AUG-2002 (first entry)
XX
XX Soybean KCP-like protein, SEQ ID NO 70.
DE
XX Antimicrobial, transgenic; plant; potato snakin antimicrobial protein;
KW GAS44; GAS45; GAS1 homologue; lysine- and cysteine- rich peptide;
KW KCP-like polypeptide; modulating; disease resistance.
XX
XX Glycine max.
OS
XX WO200222821-A2.
XX
XX 21-MAR-2002.
XX
XX 13-SEP-2001; 2001WO-US28429.
XX
XX 13-SEP-2000; 2000US-232569P.
XX
XX 11-SEP-2001; 2001US-0950933.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Simmons CR, Navarro Acevedo PA;
XX WPI; 2002-425842/45.
XX
XX N-PSDB; AAL37842.
XX
XX New polynucleotide encoding lysine- and cysteine-rich peptides-like
PT polypeptide useful for modulating the polypeptide level in a plant
PT cell, enhancing disease resistance
XX
XX Claim 1; Page 152; 163bp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide which is related to potato snakin antimicrobial protein and
CC GAS44 or GAS45 or GAS1 homologue, which is referred to as lysine- and
CC cysteine- rich peptides (KCP)-like polypeptide, having a nucleotide
CC sequence from 36 sequences of defined base pairs, given in the

CC specification. A recombinant expression cassette comprising the isolated
 CC polynucleotide of the invention is useful for modulating the level of
 CC (KCP)-like polypeptides in a plant cell, where the level of (KCP)-like
 CC polypeptides is increased, and disease resistance is enhanced. This
 CC sequence represents a KCP-like protein encoded by an isolated
 CC polynucleotide of the invention.

XX Sequence 106 AA;

Query Match 1.5%; Score 8; DB 23; Length 106;

Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLG 473

Db 9 VLLALLG 16

RESULT 7

ABB69392 standard; Protein; 133 AA.

XX ABB69392;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 34968.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-655860/75.

XX N-P5DB; ABL13495.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure; SEQ ID NO 34968; 21pp + Sequence listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB85737-AB872072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 133 AA;

Query Match 1.5%; Score 8; DB 22; Length 133;

Best Local Similarity 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLG 473

Db 6 VLLALLG 13

RESULT 8

ABU05787 standard; Protein; 200 AA.

XX ABU05787;

XX 08-APR-2003 (first entry)

XX M. tuberculosis and M. leprae marker protein #438.

XX Mycobacteriosis; survival; virulence; protective antigen; vaccine;
 KM mycobacterial disease; tuberculosis; leprosy.

XX Mycobacterium tuberculosis.

XX Mycobacterium leprae.

XX WO200274903-A2.

XX 26-SEP-2002.

XX 22-FEB-2002; 2002WO-IB01973.

XX 22-FEB-2001; 2001US-270123P.

XX (INSP) INST PASTEUR.

XX Cole S;

XX WPI; 2002-759865/82.

XX Identifying and selecting genes for survival or virulence of
 PT mycobacteria by a comparative genomic analysis of the sequences of
 PT Mycobacterium tuberculosis and M. leprae -

XX Claim 17; Page 640-642; 874pp; English.

XX This invention relates to a novel method for identifying essential genes
 CC for survival or virulence of mycobacteria species. The method comprises
 CC aligning the genomic sequence of a first mycobacterium species on a
 CC genomic sequence of a second mycobacterium species and selecting a
 CC polynucleotide sequence that is highly conserved in both genomes with no
 CC counterparts in other bacterial genomic sequences and that corresponds
 CC to an essential gene for the survival or virulence of mycobacterium
 CC species. The method of the invention is useful for detecting M.
 CC tuberculosis or M. leprae infection. The method reduces the number of
 CC potential new targets and protective antigens for new drugs and vaccine
 CC compositions to treat and prevent mycobacterial diseases, particularly
 CC tuberculosis and leprosy. The present sequence represents a marker
 CC protein from Mycobacterium tuberculosis and Mycobacterium leprae
 CC identified using the method of the invention.

XX Sequence 200 AA;

Query Match 1.5%; Score 8; DB 23; Length 200;

Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 467 VLLALLG 474

Db 88 VLLALLG 95

RESULT 9

AAB58791 standard; Protein; 238 AA.

XX AAB58791;

DT 27-MAR-2001 (first entry)
 XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 499.
 DE
 XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KW nocotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antiinflammatory; anticancer; vulnery; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200055173-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05881.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI: 2000-611515/58.
 XX
 DR N-PSDB; AAF21694.
 XX
 PT New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention,
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular
 PT disorders and neurological diseases -
 XX
 PS Claim 11; Page 931; 1299pp; English.
 XX
 CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB59711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;
 CC nocotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 CC antidiabetic; antiinflammatory; anticancer; vulnery; anticonvulsant;
 CC antibacterial; antifungal; antiparasitic and cardiac activity. The
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,
 CC particularly breast and ovarian cancer. The nucleic acid sequences,
 CC proteins, agonists and antagonists may also be used in the diagnosis,
 CC prevention and treatment of immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; cardiovascular disorders such as
 CC myocardial ischaemia; wound healing; neurological diseases such as
 CC cerebral anoxia and epilepsy; and infectious diseases.
 XX
 SQ Sequence 238 AA;
 XX
 Query Match 1.5%; Score 8; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 379 GSLSEPT 386
 XX |||||
 XX |||||
 DB 136 GSLSEPT 143
 XX
 RESULT 10
 AAG74269
 ID AAG74269 standard; Protein; 255 AA.
 XX
 AC, AAG74269;

XX 03-SEP-2001 (first entry)
 DT
 XX Human colon cancer antigen protein SEQ ID NO:5033.
 DE
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma.
 KW
 OS Homo sapiens.
 XX
 PN WO200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137.
 XX
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX
 DR WPI: 2001-235357/24.
 XX
 DR N-PSDB; AAH33700.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 11; Page 6764-6765; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated P,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAG77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 255 AA;
 XX
 Query Match 1.5%; Score 8; DB 22; Length 255;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 466 VLLALLG 473
 XX |||||
 XX |||||
 DB 6 VLLALLG 13
 XX
 RESULT 11
 AAU00923
 ID AAU00923 standard; Protein; 256 AA.
 XX
 AC AAU00923;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE Alternatively spliced Human CLAR1 protein sequence.
 XX
 KW CLAR1, human; late stage-specific marker; prostate cancer progression;

PT cancer progression
 XX
 PS Claim 13, Page 44; 70pp; English.
 CC This sequence is the human CLAR1 of the invention. CLAR1 was
 CC isolated from a human adult heart cDNA library and is a late
 CC stage-specific marker for prostate cancer progression. The CLAR1 nucleic
 CC acid molecules (including oligonucleotides as probes/primers) and
 CC antibodies against CLAR1 form kits for detecting expression of the CLAR1
 CC gene associated with a susceptibility to cancer. The nucleic acids are
 CC also useful for identifying and characterizing related genes from other
 CC species. They are useful for identifying genes encoding proteins that
 CC interact with CLAR1, which facilitates further study of the role of these
 CC cellular signalling mechanisms in cancer progression. The nucleic acids
 CC are also useful for controlling CLAR1 protein production. The CLAR1
 CC polypeptides are useful in screening for molecules (especially
 CC antibodies) that affect or modulate its activity or function. Such
 CC molecules may be therapeutically useful. The isolated CLAR1 nucleic acid
 CC molecule enables the generation of a transgenic animal, which can be
 CC used as a model for prostate cancer to allow screening and identification
 CC of compounds for the treatment of prostate cancer. Such an animal
 CC expresses the CAR1 protein at a higher level than that of a normal
 CC animal.
 XX
 SQ Sequence 276 AA;
 Query Match 1.5%; Score 8; DB 20; Length 276;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 379 GSLSEETP 386
 Db 174 GSLSEETP 181
 RESULT 14
 AAP60577
 ID AAP60577 standard; Protein; 287 AA.
 XX
 AC AAP60577;
 XX
 DT 25-MAR-2003 (updated)
 DT 31-JUL-1991 (first entry)
 XX
 DE Eimeria tenella S401 sporozoite antigen.
 XX
 KW Antigen; vaccine; poultry; fowl; avian coccidiosis; immunization.
 XX
 OS Eimeria tenella.
 XX
 PN WO6600528-A.
 PN
 PD 30-JAN-1986.
 PD
 PF 05-JUL-1985; 85WO-US01274.
 PF
 PR 19-JUN-1985; 85US-0746520.
 PR 05-JUL-1984; 84US-0627811.
 XX
 PA (GENEX) GENEX CORP.
 PA
 PI Anderson DM, McCandliss RJ;
 PI WPI; 1986-042037/06.
 DR N-PSDB; AAN60488.
 DR
 XX
 PT New cloned gene expressing Eimeria antigen - useful in vaccines
 PT for protecting poultry against coccidiosis
 XX
 PS Claim 42; Fig 1; 82pp; English.
 XX
 CC The antigenic protein binds with an antibody directed against an
 CC antigenic protein of avian coccidia, (esp. a protein of E. tenella

CC sporozoite). It may be used for immunising birds against avian
 CC coccidiosis.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 287 AA;
 Query Match 1.5%; Score 8; DB 7; Length 287;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 463 VGVVLLLA 470
 Db 219 VGVVLLLA 226
 RESULT 15
 AAR05216
 ID AAR05216 standard; protein; 287 AA.
 XX
 AC AAR05216;
 XX
 DT 25-MAR-2003 (updated)
 DT 02-AUG-1990 (first entry)
 XX
 DE Antigens GX5401 and GX3264 encoded by cDNA of Eimeria tenella oocyte.
 XX
 KW Eimeria tenella; antigen GX5401; antigen GX3264; avian coccidiosis.
 XX
 OS Eimeria tenella.
 XX
 PN WO9000403-A.
 PN
 PD 25-JAN-1990.
 PD
 PF 05-JUL-1989; 89WO-US02918.
 PF
 PR 05-JUL-1988; 88US-0215162.
 XX
 PA (GENEX) GENEX CORP.
 PA
 PI Anderson DM, McCandliss RJ, Strausberg SL, Strausberg RL;
 PI WPI; 1990-051586/07.
 DR N-PSDB; AAG03317.
 DR
 PT Cloned gene or fragment encoding antigenic protein -
 PT which binds with antibodies against avian coccidia, and
 PT transformed cells used in vaccine
 XX
 PS Claim 1; Page 93; Fig 1; 134pp; English.
 XX
 CC They are antigenic proteins (AP) which bind with a monoclonal antibody
 CC (Mab) or polyvalent Ab directed against an AP of avian coccidia. GX5401
 CC is claimed in claim 1, and GX3264 is claimed in claim 2. Also new
 CC are an expression vector contg. their cloned gene, and host cells
 CC transformed with the vector. The transformed cells are used in a
 CC vaccine to immunise birds against avian coccidiosis. By labelling the
 CC peptides, they can be used as a type-specific probe. They may also be
 CC used in an assay to detect Ab against the coccidia. The Abs are used to
 CC identify transformed cells contg. the DNA.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 287 AA;
 Query Match 1.5%; Score 8; DB 11; Length 287;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 VGGVLLLA 470
XX |||||
Db 219 VGGVLLLA 226

RESULT 16

AAW67722 standard; Protein; 437 AA.

AAW67722;
AC

16-MAR-1999 (first entry)

Human tumour antigen zsig15 protein sequence.

Secretion; differentiation marker; tumour; epithelial cell; colon; blood;
breast; prostate; growth; development; antagonist; receptor; bone marrow;
cancer; metastasis.

Homo sapiens.

WO9850552-A1.

12-NOV-1998.

06-MAY-1998; 98WO-US09584.

06-MAY-1997; 97US-0045703.

(ZYMO) ZYMOGENETICS INC.

Grossmann A, Shepard PO;

WPI; 1999-034723/03.

N-PSDB; AAV81394.

New nucleic acid encoding secreted polypeptide zsig15 - used as a
marker for tumour cells, useful for diagnosis and treatment of
cancers, inflammation and hyperplasia

Claim 16; Page 81-84; 100pp; English.

This sequence is of a secreted polypeptide, designated zsig15, which
is a marker for differentiation in normal and tumour cells (particularly
epithelial cells and derived tumours of colon, breast and prostate).
The zsig15 protein is useful for the promotion of growth and development
of epithelial cells; to identify specific (ant)agonists, also where
conjugated to a toxin, to deliver these to cells expressing the cognate
receptor (e.g. to kill cells of blood, colon, breast and bone marrow
cancers), and to identify/isolate receptors involved in cancer
metastases. The sequence was isolated from a colon cancer library
after screening an EST (expressed sequence tag) database for sequences
containing putative secretion signal sequences.

Sequence 437 AA;

Query March 1.5%; Score 8; DB 20; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLLG 473
XX |||||
Db 4 VLLALLLG 11

RESULT 17

AA96733 standard; Protein; 437 AA.

AA96733;
AC

26-SEP-2000 (first entry)

PRO1863, a novel transmembrane protein.
PRO1863; secreted protein; transmembrane protein; recombinant production;
gene therapy.

Homo sapiens.

Key
Peptide
Location/Qualifiers
1..15
/label= Signal_peptide

Modified-site
46..49
/note= "N-glycosylation site"

Modified-site
51..54
/note= "Glycosaminoglycan attachment site"

Modified-site
54..59
/note= "N-myristoylation site"

Modified-site
75..80
/note= "N-myristoylation site"

Modified-site
141..146
/note= "N-myristoylation site"

Modified-site
154..159
/note= "N-myristoylation site"

Modified-site
168..173
/note= "N-myristoylation site"

Modified-site
169..174
/note= "N-myristoylation site"

Modified-site
189..192
/note= "N-glycosylation site"

Modified-site
198..203
/note= "N-myristoylation site"

Modified-site
243..260
/label= Transmembrane_domain

Modified-site
254..259
/note= "N-myristoylation site"

Modified-site
261..266
/note= "N-myristoylation site"

Modified-site
269..274
/note= "N-myristoylation site"

Modified-site
284..289
/note= "N-myristoylation site"

Modified-site
333..338
/note= "N-myristoylation site"

Modified-site
347..352
/note= "N-myristoylation site"

Modified-site
359..362
/note= "Glycosaminoglycan attachment site"

Modified-site
360..365
/note= "N-myristoylation site"

Modified-site
361..366
/note= "N-myristoylation site"

Modified-site
382..385
/note= "N-myristoylation site"

Modified-site
388..393
/note= "N-glycosylation site"

Modified-site
408..413
/note= "N-myristoylation site"

Modified-site
419..424
/note= "N-myristoylation site"

WO200036102-A2.

22-JUN-2000.

01-DEC-1999; 99WO-US28634.

16-DEC-1998; 98US-0112851.

16-DEC-1998; 98US-0113145.

22-DEC-1998; 98US-0113511.

12-JAN-1999; 99US-0115558.

12-JAN-1999; 99US-0115565.

09-FEB-1999; 99US-0115733.

PR 10-FEB-1999; 99US-0119537.
 PR 12-FEB-1999; 99US-0119965.
 PR 02-JUN-1999; 99WO-US12252.
 XX
 XX (GETH) GENENTECH INC.
 PA Boretstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WI;
 DR WPI; 2000-431586/37.
 DR N-PSDB; AAA51263.
 XX
 PT Isolated nucleic acid molecule encodes a PRO polypeptide which is a
 PT transmembrane polypeptide
 XX
 PS Claim 12; Fig 10; 154BP; English.
 XX
 CC This is PRO1863, a novel transmembrane protein. The invention
 CC concerns novel secreted and transmembrane proteins, designated PRO
 CC polypeptides. The cDNA and gene sequences are useful in the recombinant
 CC production of PRO polypeptides, as a hybridization probe to screen
 CC libraries to isolate cDNAs with sequence identity to PRO polypeptides or
 CC to map the gene encoding the PRO polypeptides and analyzing genetic
 CC disorders. The cDNA/gene can also be used to produce transgenic animals
 CC useful for the development and screening of therapeutically useful
 CC reagents. They can also be used in gene therapy, e.g. to replace a
 CC defective gene.
 CC
 SQ Sequence 437 AA;
 Query Match 1.5%; Score 8; DB 21; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 466 VLLALLLG 473
 Db 4 VLLALLLG 11
 RESULT 18
 AA87750
 ID AAY87750 standard; Protein; 437 AA.
 AC AAY87750;
 DT 17-AUG-2000 (first entry)
 XX
 DE Human PRV-1 protein.
 XX
 KW PRV-1; human; polycythaemia rubra vera; PRV; antiproliferative;
 KW treatment; detection; diagnosis.
 OS Homo sapiens.
 XX
 PN DE19849044-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 23-OCT-1998; 98DE-1049044.
 XX
 PR 23-OCT-1998; 98DE-1049044.
 XX
 PA (UYFR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.
 XX
 PI Pahl H, Temerinac S;
 XX
 DR WPI; 2000-319347/28.
 DR N-PSDB; AAA12386.
 XX
 PT New polycythemia rubra vera-related polypeptide useful for diagnosis
 PT and for developing therapeutic antibodies
 XX

PS Claim 6; Fig 2; 6pp; German.
 XX
 CC This invention describes a novel PRV-1 protein (I) detected in humans
 CC suffering from the condition polycythaemia rubra vera (PRV). The product
 CC of the invention has antiproliferative activity. The encoding nucleic
 CC acid sequence is used to express recombinant PRV-1 polypeptides and as a
 CC source of antisense sequences that can be expressed in vivo for treatment
 CC of PRV. (I) is used to raise specific mono or polyclonal antibodies and
 CC these are used to diagnose PRV (by detecting (I), or its epitopes, in
 CC immunoassays) or for treatment of PRV (optionally when coupled to a
 CC cytotoxin). This sequence represents the human PRV-1 protein described in
 CC the method of the invention.
 CC
 SQ Sequence 437 AA;
 Query Match 1.5%; Score 8; DB 21; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 466 VLLALLLG 473
 Db 4 VLLALLLG 11
 RESULT 19
 AA87261
 ID AAY87261 standard; Protein; 437 AA.
 AC AAY87261;
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSPB-38 SEQ ID NO:38.
 XX
 KW Human; signal peptide-containing protein; HSPB; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14484.
 XX
 PR 26-JUN-1998; 98US-0090762.
 XX
 PR 31-JUL-1998; 98US-0094983.
 XX
 PR 01-OCT-1998; 98US-0102686.
 XX
 PR 11-DEC-1998; 98US-0112129.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guejler KJ, Baughn MR;
 PI Akerblom IE, Au-Yang J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 DR WPI; 2000-160673/14.
 DR N-PSDB; AA298146.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 XX
 PS Claim 1; Page 185-186; 327pp; English.
 XX
 CC AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the

PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,
PI Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
DR N-PSDB; AA265083.
XX
XX Membrane-bound proteins and related nucleotide sequences -
XX
XX claim 12; Fig 250; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences
XX will also be useful for the preparation of PRO polypeptides, especially
XX by recombinant techniques.

XX
SQ Sequence 437 AA;
Query Match 1.5%; Score 8; DB 21; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 466 VLLALALG 473
Db 4 VLLALALG 11
RESULT 21
AAU12404
ID AAU12404 standard; Protein; 437 AA.
XX
XX AAU12404;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human PRO1181 polypeptide sequence.
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
XX breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
XX cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
XX adipocyte; A-peptide; factor VIIA; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200140466-A2.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US32678.
XX
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 09-DEC-1999; 99US-0170262.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 20-DEC-1999; 99WO-US30999.
XX 30-DEC-1999; 99WO-US31243.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 22-FEB-2000; 2000WO-US04342.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05064.
XX 01-MAR-2000; 2000WO-US05601.
XX 20-MAR-2000; 2000WO-US07377.
XX 21-MAR-2000; 2000WO-US07532.
XX 30-MAR-2000; 2000WO-US08439.
XX 17-MAY-2000; 2000WO-US13705.
XX 22-MAY-2000; 2000WO-US14042.
XX 30-MAY-2000; 2000WO-US14941.
XX 02-JUN-2000; 2000WO-US15264.
XX 10-NOV-2000; 2000WO-US30873.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerlitsen ME, Goddard A, Goddard PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-408281/43.
DR N-PSDB; AA521476.
XX
XX Isolated, secretory, and transmembrane PRO polypeptide used to detect

other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -

Claim 12; Fig 466; 813pp; English.

AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

Sequence 437 AA;

Query Match 1.5%; Score 8; DB 22; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLG 473
| | | | |
Db 4 VLLALLG 11

RESULT 22
AAB70851

ID AAB70851 standard; Protein; 437 AA.

XX AAB70851;

DT 29-JUN-2001 (first entry)

XX Human PRV-1 protein.

KW PRV-1; human; hemostatic; polycythemia rubra vera; antisense therapy; treatment; diagnosis; pancytopenia; bone-marrow; blood; growth factor; pancytopenia; hematopoietic system disorder.

XX Homo sapiens.

OS DE19947010-A1.

XX 05-APR-2001.

PD 30-SEP-1999; 99DE-1047010.

XX 30-SEP-1999; 99DE-1047010.

XX (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.

XX Pahl H;

XX WPI; 2001-246167/26.

DR N-PSDB; AAF61560.

XX New cloned PRV-1 gene associated with polycythemia rubra vera, e.g.
PT useful for preparing antisense molecules or polypeptides for treatment
or diagnosis of disorders of the hematopoietic system -
XX

PS Claim 3; Fig 2; 10pp; German.

XX This invention describes a novel cloned PRV-1 gene (1) which has
CC hemostatic activity and is associated with polycythemia rubra vera
CC (PRV). (1) is useful for: (1) producing a recombinant PRV-1 polypeptide;
CC (2) producing antisense molecules useful for diagnosis and treatment of
CC PRV; (3) preparing medicaments for treating pancytopenias and
CC pancytopenias of the bone-marrow and blood. The polypeptide is useful:
CC (1) as a growth factor for inducing hematopoietic stem cells to form
CC erythroid colonies; (2) for preparing medicaments for treating
CC pancytopenias and pancytopenias of the bone-marrow and blood; (3) for
CC treating and/or multiplying autologous cells and/or established cell
CC lines ex vivo or in vitro; and (4) for producing antibodies useful for
CC diagnosis of PRV or other disorders of the hematopoietic system. This
CC sequence represents the human PRV-1 protein described in the invention.

Sequence 437 AA;

Query Match 1.5%; Score 8; DB 22; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLG 473
| | | | |
Db 4 VLLALLG 11

RESULT 23
AAB65260

ID AAB65260 standard; Protein; 437 AA.

XX AAB65260;

DT 02-APR-2001 (first entry)

XX Human PRO1181 (UNQ595) protein sequence SEQ ID NO:355.

KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing; diagnostic assay.

XX Homo sapiens.

OS WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 07-JUL-1999; 99US-0143048.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 17-AUG-1999; 99US-0149396.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 08-OCT-1999; 99US-0158663.

XX 30-NOV-1999; 99WO-US28301.

XX 01-DEC-1999; 99WO-US28301.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US04914.

XX 24-FEB-2000; 2000WO-US05004.

XX 02-MAR-2000; 2000WO-US05841.

XX 15-MAR-2000; 2000WO-US06884.

XX 20-MAR-2000; 2000WO-US07377.

XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnayers L, Eaton DL;
 XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Gocowski PJ;
 PI Grimaldi CJ, Gunney AL, Kijaviri IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
 PI Zhang Z;
 XX WPI, 2001-032160/04.
 DR N-PSDB; AAF44229.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 250; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB5515 to AAB55300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 437 AA:
 Query Match 1.5%; Score 8; DB 22; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 466 VLLALLLG 473
 Db 4 VLLALLLG 11
 RESULT 24
 ABG31399 standard; Protein; 437 AA.
 XX
 AC ABG31399;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Human PRO1863 polypeptide.
 XX
 KW Human; secreted and transmembrane polypeptide; PRO polypeptide;
 KW T-lymphocyte proliferation; inflammatory disease; rheumatoid arthritis;
 KW inflammatory bowel disease; Sjogren's syndrome; thyrotoxicosis;
 KW autoimmune haemolytic anaemia; diabetes mellitus; multiple sclerosis;
 KW hepatitis; contact dermatitis; allergic disease; psoriasis; vitiligo;
 KW immune related disease; kidney disease; anti-inflammatory; antithyroid;
 KW antirheumatic; antiarthritic; immunosuppressive; antianaemic;
 KW antidiabetic; neuroprotective; hepatocytic; antiinflammatory;
 KW dermatological; anti-allergic; antipsoriatic; PRO1863.
 KW
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..15
 FT /label= signal_peptide
 FT Protein 16..437
 FT /label= Mature_PRO1863
 FT Modified-site 46..49
 FT /note= "N-glycosylation site"

FT Region
 FT 51..54
 FT /note= "Glycosaminoglycan attachment site"
 FT 54..59
 FT /note= "N-myristoylation site"
 FT 75..80
 FT /note= "N-myristoylation site"
 FT 141..146
 FT /note= "N-myristoylation site"
 FT 154..159
 FT /note= "N-myristoylation site"
 FT 168..173
 FT /note= "N-myristoylation site"
 FT 169..174
 FT /note= "N-myristoylation site"
 FT 189..192
 FT /note= "N-glycosylation site"
 FT 198..203
 FT /note= "N-myristoylation site"
 FT 243..260
 FT /label= Transmembrane_domain
 FT 254..259
 FT /note= "N-myristoylation site"
 FT 261..266
 FT /note= "N-myristoylation site"
 FT 269..274
 FT /note= "N-myristoylation site"
 FT 284..289
 FT /note= "N-myristoylation site"
 FT 333..338
 FT /note= "N-myristoylation site"
 FT 347..352
 FT /note= "N-myristoylation site"
 FT 359..362
 FT /note= "Glycosaminoglycan attachment site"
 FT 360..365
 FT /note= "N-myristoylation site"
 FT 361..366
 FT /note= "N-myristoylation site"
 FT 382..385
 FT /note= "N-glycosylation site"
 FT 388..393
 FT /note= "N-myristoylation site"
 FT 408..413
 FT /note= "N-myristoylation site"
 FT 419..424
 FT /note= "N-myristoylation site"
 XX
 XX US2002098507-A1.
 PN
 XX
 PD 25-JUL-2002.
 XX
 PP 27-DEC-2001; 2001US-0033326.
 XX
 XX 02-JUN-1999; 99WO-US12252.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US14941.
 PR 30-MAY-2000; 2000WO-US15264.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 01-DEC-2000; 2000WO-US13678.
 PR 16-DEC-1998; 98US-113145P.
 PR 22-DEC-1998; 98US-113111P.
 PR 12-JAN-1999; 99US-115558P.
 PR 12-JAN-1999; 99US-115565P.
 PR 12-JAN-1999; 99US-115733P.
 PR 09-FEB-1999; 99US-119341P.
 PR 10-FEB-1999; 99US-119537P.
 PR 12-FEB-1999; 99US-119965P.
 PR 29-OCT-1999; 99US-162506P.
 XX

PA (GETH) GENENTECH INC.
 XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 XX Wood WI;
 DR WPI; 2002-673823/72.
 DR N-PSDB; ABS53475.
 XX
 PT Novel PRO polypeptides and nucleic acids encoding the polypeptides,
 PT useful for preparing a medicament for the treatment of inflammatory and
 PT immune related disorders -
 XX
 XX Claim 12; Fig 10; 125pp; English.
 PS
 XX The present invention relates to the isolation of novel human
 CC secreted and transmembrane polypeptides, designated PRO polypeptides,
 CC and the polynucleotide sequences encoding them. The PRO polypeptides
 CC of the invention include PRO1800, PRO539, PRO982, PRO1434, PRO1863,
 CC PRO1917, PRO1868, PRO3434 and PRO1927. The PRO polypeptides can
 CC inhibit the stimulation of T-lymphocyte proliferation. The PRO
 CC polypeptides are useful for the diagnosis and treatment of inflammatory
 CC diseases (e.g. inflammatory bowel disease, rheumatoid arthritis, diabetes
 CC Sjgren's syndrome, autoimmune haemolytic anaemia, thyroiditis, allergic
 CC mellitus, multiple sclerosis, hepatitis, contact dermatitis, allergic
 CC diseases and psoriasis), immune related diseases, and kidney diseases
 CC in humans. The present sequence represents human PRO1863 polypeptide.
 CC
 XX Sequence 437 AA;
 SQ
 Query Match 1.5%; Score 8; DB 23; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 466 VLLALLLG 473
 Db 4 VLLALLLG 11

RESULT 25
 ABG91359
 ID ABG91359 standard; Protein; 437 AA.
 XX
 AC ABG91359;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Novel human secreted protein #5.
 XX
 KW Human; secreted protein; transmembrane protein; gene mapping;
 KW transgenic; immunogenic.
 XX
 OS Homo sapiens.
 XX
 PN US2002098505-A1.
 PD
 DT 25-JUL-2002.
 XX
 PF 28-DEC-2001; 2001US-0033246.
 XX
 XX 02-JUN-1999; 99WO-US12252.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 02-JUN-2000; 2000WO-US14941.
 PR 01-DEC-2000; 2000WO-US15264.
 PR 16-DEC-1998; 98US-113145P.
 PR 22-DEC-1998; 98US-113511P.
 PR 12-JAN-1999; 99US-115558P.

PR 12-JAN-1999; 99US-115565P.
 PR 12-JAN-1999; 99US-115733P.
 PR 09-FEB-1999; 99US-119341P.
 PR 10-FEB-1999; 99US-119537P.
 PR 12-FEB-1999; 99US-119965P.
 PR 29-OCT-1999; 99US-162506P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WI;
 DR WPI; 2002-665999/71.
 DR N-PSDB; ABS67458.
 XX
 PT New human secreted and transmembrane (PRO) polypeptides, useful for
 PT treating conditions requiring PRO polypeptides, for screening PRO
 PT antagonists and agonists useful as drug candidates -
 XX
 XX Claim 12; Figure 10; 125pp; English.
 PS
 CC The invention relates to new human secreted and transmembrane proteins
 CC (PRO) and nucleic acids of the invention. The polypeptides can be
 CC administered therapeutically, especially by expressing encoding
 CC polynucleotides, e.g. in therapeutic compositions. They can be used to
 CC screen for PRO polypeptide antagonists and agonists useful to identify
 CC drug candidates. They can also be used to produce antibodies, useful to
 CC detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
 CC therapeutically (e.g. as antagonists or to target and/or deliver
 CC cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
 CC produce antisense sequences to inhibit polypeptide production. They can
 CC be used to produce probes and primers useful to detect or isolate
 CC sequences encoding PRO polypeptides or similar sequences e.g. variants or
 CC sequences from other species. They are also useful for gene mapping and
 CC to generate transgenic animals. ABG91355-ABG91363 represent human PRO
 CC amino acid sequences of the invention.
 CC
 XX Sequence 437 AA;
 SQ
 Query Match 1.5%; Score 8; DB 23; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 466 VLLALLLG 473
 Db 4 VLLALLLG 11

RESULT 26
 ABG92707
 ID ABG92707 standard; Protein; 437 AA.
 XX
 AC ABG92707;
 XX
 DT 18-NOV-2002 (first entry)
 XX
 DE Human secreted protein PRO1863.
 XX
 KW Human; secreted and transmembrane protein; PRO1800; PRO539;
 KW PRO982; PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
 KW inflammatory disorder; immune related disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
 KW autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
 KW psoriasis; allergic disease of the lung; graft-versus host disease;
 KW tumour; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2002098506-A1.
 PD
 DT 25-JUL-2002.

PF 27-DEC-2001; 2001US-0033301.
 XX 04-AUG-1998; 98US-095325P.
 PR 16-DEC-1998; 98US-112851P.
 PR 16-DEC-1998; 98US-113145P.
 PR 22-DEC-1998; 98US-113511P.
 PR 12-JAN-1999; 98US-115585P.
 PR 12-JAN-1999; 98US-115565P.
 PR 12-JAN-1999; 98US-115733P.
 PR 09-FEB-1999; 98US-119341P.
 PR 10-FEB-1999; 98US-119537P.
 PR 12-FEB-1999; 98US-119665P.
 PR 29-OCT-1999; 98US-162806P.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-DEC-1999; 98WO-US28634.
 PR 02-DEC-1999; 98WO-US28551.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 30-MAY-2000; 2000WO-US19441.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 01-DEC-2000; 2000WO-US32678.
 XX (GETH) GENENTECH INC.
 XX Bocstein D, Desnoyers L, Ferrara N, Feng S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood W;
 XX MPI; 2002-690475/74.
 DR N-PSDB; ABS68390.
 XX Novel secreted and transmembrane polypeptides and polynucleotides
 PT useful for diagnosis and treatment of inflammatory disorders and
 PT immune-related diseases, and identifying modulators -
 XX
 PS Claim 12; Fig 10; 125pp; English.
 CC The invention relates to an isolated polypeptide having at least 80%
 CC amino acid sequence identity to secreted and transmembrane polypeptides
 CC PRO1800, PRO539, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
 CC PRO1927 and their encoding nucleic acids. Also included are vectors, host
 CC cells and antibodies against PRO polypeptides. PRO proteins are useful
 CC for identifying modulators of the polypeptide. PRO1868 useful for the
 CC diagnosis and treatment of inflammatory and immune related diseases
 CC including systemic lupus erythematosus, rheumatoid arthritis, systemic
 CC sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
 CC infectious hepatitis, psoriasis, allergic diseases of the lung and
 CC graft-versus host disease and tumours. PRO nucleic acids are useful for
 CC constructing hybridisation probes for mapping the gene that encodes that
 CC PRO and for the genetic analysis of individuals with genetic disorders,
 CC and for generating transgenic animals which are useful in the development
 CC and screening of therapeutically useful reagents. PRO nucleic acids are
 CC also useful for gene therapy, chromosome identification, and tissue
 CC typing. PRO proteins are useful as molecular weight markers for protein
 CC electrophoresis purposes. The anti-PRO antibodies are useful in
 CC diagnostic assays for PRO, e.g. detecting its expression in specific
 CC cells, tissues or serum and for affinity purification of PRO.
 CC The present sequence represents a PRO protein.
 XX
 SQ Sequence 437 AA;
 QY Query Match 1.5%; Score 8; DB 23; Length 437;
 DB Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 466 VILLALLG 473
 4 VILLALLG 11
 RESULT 27

AAU83672
 ID AAU83672 standard; Protein; 437 AA.
 AC AAU83672;
 XX 08-MAY-2002 (first entry)
 DT
 XX Human PRO protein, Seq ID No 162.
 DE
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 CS Homo sapiens.
 XX
 EN WO200208288-A2.
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US21066.
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US33522.
 PR 24-AUG-2000; 2000WO-US33328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001WO-US054280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood W;
 XX MPI; 2002-172001/22.
 DR N-PSDB; ABK33616.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 PS Claim 11; Figure 162; 359pp; English.
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,

CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.

XX
SQ Sequence 437 AA;

Query Match 1.5%; Score 8; DB 23; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLLG 473
|||||
4 VLLALLLG 11

DB

RESULT 28
AAG80767
ID AAG80767 standard; Protein; 437 AA.

XX AAG80767;

DT 17-APR-2002 (first entry)

XX Human granulocyte HNA-2a antigen.

XX Human, neutrophilic granulocyte; chromosome 19; HNA-2a; antigen;
KW human neutrophil antigen-2a; NB-1 antigenic determination; diagnosis;
KW alloantibody detection; neonatal; immunoneutropenia; iatrogenic;
KW transplant-associated acute pulmonary insufficiency;
KW bone marrow transplant; autoimmunoneutropenia.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21
FT Protein /label= signal_peptide
FT /label= mature_peptide
FT /note= "HNA-2a (previously called NB-1)"

DE10028725-A1.

13-DEC-2001.

09-JUN-2000; 2000DE-1028725.

09-JUN-2000; 2000DE-1028725.

XX (BUXJ/) BUX J.

XX Bux J, Kissel K;

XX WPI; 2002-148930/20.

DR N-PSDB; ABA97156.

XX Primary structure and nucleic acid of the human neutrophil antigen-2a,
PT useful for antigen detection, e.g. diagnosis of various forms of
PT neutropenia

XX Disclosure: Page 4-6; 8pp; German.

XX This invention describes the human neutrophil antigen-2a (HNA-2a,
CC previously described as NB-1), expressed on neutrophilic granulocytes.
CC The nucleic acid and amino acid sequences of HNA-2a are used in RNA- or
CC DNA-based methods of antigen determination, e.g. polymerase chain
CC reaction with sequence-specific primers, hybridisation with
CC sequence-specific oligonucleotides or DNA sequencing. They are also used
CC for recombinant production of the antigen for detection of specific
CC alloantibodies. Allo- and auto-antibodies against HNA-2a are implicated
CC in neonatal immunoneutropenia, transplant-associated acute pulmonary
CC insufficiency, immunoneutropenia after bone marrow transplant, iatrogenic
CC iatrogenic immunoneutropenia and autoimmunoneutropenia. Using HNA-2a,
CC or its nucleic acid, for diagnosis, overcomes the stability problems
CC associated with use and transport of very unstable granulocytes. The

CC nucleic acid also allows large-scale production of the antigen. This
CC sequence represents the human granulocyte HNA-2a (NB-1) antigen found on
CC chromosome 19 described in the invention.

XX
SQ Sequence 437 AA;

Query Match 1.5%; Score 8; DB 23; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLLG 473
|||||
4 VLLALLLG 11

DB

RESULT 29
ABU66802
ID ABU66802 standard; Protein; 437 AA.

XX ABU66802;

DT 23-MAY-2003 (first entry)

XX Human PRO polypeptide #233.

XX Human; PRO polypeptide; secreted and transmembrane protein;
KW tumor necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytosolic.

XX Homo sapiens.

XX US2003036180-A1.

20-FEB-2003.

09-MAY-2002; 2002US-0143114.

31-MAR-1997; 97WO-US05230.

12-JUN-1998; 98WO-US12456.

14-JUL-1998; 98WO-US14552.

28-AUG-1998; 98WO-US17888.

10-SEP-1998; 98WO-US18824.

14-SEP-1998; 98WO-US19093.

14-SEP-1998; 98WO-US19094.

14-SEP-1998; 98WO-US19177.

16-SEP-1998; 98WO-US19330.

17-SEP-1998; 98WO-US19437.

29-OCT-1998; 98WO-US22991.

29-OCT-1998; 98WO-US22992.

20-NOV-1998; 98WO-US24855.

01-DEC-1998; 98WO-US25108.

05-JAN-1999; 99WO-US00106.

08-MAR-1999; 99WO-US05028.

10-MAR-1999; 99WO-US05190.

20-APR-1999; 99WO-US08615.

14-MAY-1999; 99WO-US10733.

02-JUN-1999; 99WO-US12252.

01-SEP-1999; 99WO-US20111.

08-SEP-1999; 99WO-US20594.

13-SEP-1999; 99WO-US20944.

15-SEP-1999; 99WO-US21090.

15-SEP-1999; 99WO-US21547.

05-OCT-1999; 99WO-US23089.

29-NOV-1999; 99WO-US28214.

30-NOV-1999; 99WO-US28313.

01-DEC-1999; 99WO-US28409.

01-DEC-1999; 99WO-US28301.

01-DEC-1999; 99WO-US28634.

02-DEC-1999; 99WO-US28551.

02-DEC-1999; 99WO-US28564.

02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 05-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000WO-US21735.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806889.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882536.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETN) GENENTECH INC.
 XX
 PI Baker KP, Bershtei M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR MPI; 2003-332040/31.
 DR N-PSDB; ACA03835.

XX New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification
 PS Claim 12; Fig 466; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. AB06570-AB06684 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC segdata.uspto.gov/patidentry.html.
 CC
 SQ Sequence 437 AA;
 Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 466 VLLALLG 473
 Db 4 VLLALLG 11
 RESULT 30
 AB067078
 ID AB067078 standard; Protein; 437 AA.
 XX
 AC AB067078;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane, PRO, protein SEQ ID 466.
 XX
 KW Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; blosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
 XX
 OS Homo sapiens.
 XX
 PN US200302155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.

PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 98WO-US00106.
 PR 08-MAR-1999; 98WO-US05028.
 PR 10-MAR-1999; 98WO-US05190.
 PR 20-APR-1999; 98WO-US08615.
 PR 14-MAY-1999; 98WO-US10733.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 08-SEP-1999; 98WO-US20594.
 PR 13-SEP-1999; 98WO-US20944.
 PR 15-SEP-1999; 98WO-US21090.
 PR 05-OCT-1999; 98WO-US21547.
 PR 29-NOV-1999; 98WO-US23089.
 PR 30-NOV-1999; 98WO-US28214.
 PR 30-NOV-1999; 98WO-US28313.
 PR 01-DEC-1999; 98WO-US28409.
 PR 01-DEC-1999; 98WO-US28301.
 PR 02-DEC-1999; 98WO-US28634.
 PR 02-DEC-1999; 98WO-US28551.
 PR 02-DEC-1999; 98WO-US28564.
 PR 16-DEC-1999; 98WO-US28565.
 PR 20-DEC-1999; 98WO-US30095.
 PR 20-DEC-1999; 98WO-US30911.
 PR 22-DEC-1999; 98WO-US30999.
 PR 30-DEC-1999; 98WO-US30720.
 PR 30-DEC-1999; 98WO-US31243.
 PR 30-DEC-1999; 98WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08433.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14044.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30953.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-074259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-331925/31.
 DR N-PSDB; ACA04256.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer
 XX
 PS Claim 12; Fig 466; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peritoneal blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIa,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleic acid sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.
 XX
 SQ Sequence 437 AA;
 Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 466 VLLIALLG 473
 Db 4 VLLIALLG 11

RESULT 31
ABUS9883
ID ABUS9883 standard; Protein; 437 AA.
XX
AC ABUS9883;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO181.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disease;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
OS Homo sapiens.
PN US2003017563-A1.
XX
XX 23-JAN-2003.
PD
XX
PF 07-MAY-2002; 2002US-0140808.
XX
XX 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 02-DEC-1999; 99WO-US28654.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31374.
PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000WO-US21735.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0806705.
PR 14-MAR-2001; 2001US-0806889.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0826366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GENTH) GENENTECH INC.
PA
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gertsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-148238/14.
DR N-PSDB; ABX89373.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -
XX
PS Claim 12; Fig 466; 659pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1366 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentum, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other's
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.

XX Sequence 437 AA;

Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLLG 473
 |||||
 Db 4 VLLALLLG 11

RESULT 32
 ABU60811 standard; Protein; 437 AA.

XX ABU60811;

DT 06-MAY-2003 (first entry)

XX Human secreted/transmembrane protein, #5.

XX Human, PRO; secreted; transmembrane; pharmaceutical;
 KW diagnostic; biosensor; bioreactor; therapeutic; gene therapy; tumour;
 KW inflammatory disease; immune-related disease; inflammatory bowel disease;
 KW IBD; systemic lupus erythematosus; rheumatoid arthritis; thyroiditis;
 KW diabetes mellitus; glomerulonephritis; multiple sclerosis; cirrhosis;
 KW psoriasis; graft rejection; antiinflammatory; immunosuppressive;
 KW neuroprotective; hepatotropic.

XX Homo sapiens.

XX US2002160392-A1.

XX 31-OCT-2002.

XX 27-DEC-2001; 2001US-0033245.

XX 02-JUN-1999; 99WO-US12252.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

XX 11-FEB-2000; 2000WO-US03565.

XX 22-FEB-2000; 2000WO-US04414.

PR 02-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 04-AUG-1998; 98US-095325P.
 PR 16-DEC-1998; 98US-112851P.
 PR 16-DEC-1998; 98US-113145P.
 PR 22-DEC-1998; 98US-113511P.
 PR 12-JAN-1999; 99US-115558P.
 PR 12-JAN-1999; 99US-115565P.
 PR 12-JAN-1999; 99US-115733P.
 PR 09-FEB-1999; 99US-119341P.
 PR 10-FEB-1999; 99US-119537P.
 PR 12-FEB-1999; 99US-119656P.
 PR 29-OCT-1999; 99US-162506P.
 PR 09-DEC-1999; 99US-170262P.
 PR 03-MAR-2000; 2000US-187202P.
 PR 25-MAY-2001; 2001US-0866034.

XX (GENTH) GENENTECH INC.

PI Borstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Guhney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WI;

XX WPI; 2003-275292/27.
 DR N-PSDB; ABX96007.

XX New isolated PRO polypeptide, e.g. PRO1800 or PRO539, useful for
 PT diagnosing, preventing and treating tumors and inflammatory or
 PT immune-related diseases, e.g. systemic lupus erythematosus,
 PT thyroiditis, diabetes or psoriasis

XX Claim 12; Fig 10; 119pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
 CC comprising a sequence without signal peptide and the nucleic acid
 CC encoding them. The polypeptides can be used to raise antibodies that
 CC specifically bind to the PRO polypeptide, for linking a bioactive
 CC molecule to a cell expressing a PRO protein and for modulating at least
 CC one biological activity of a cell. The PRO polypeptides and the antibody
 CC are useful for diagnosing, preventing and treating tumours and
 CC inflammatory or immune-related diseases, such as inflammatory bowel
 CC disease (IBD), systemic lupus erythematosus, rheumatoid arthritis,
 CC thyroiditis, diabetes mellitus, glomerulonephritis, multiple sclerosis,
 CC cirrhosis, psoriasis or graft rejection. The proteins and the antibody
 CC may also be used in preparing medicines and medicaments for treating the
 CC above-mentioned diseases. The polynucleotide is useful in molecular
 CC biology, including uses as hybridisation probes, in chromosome and gene
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
 CC polynucleotide may also be used in preparing PRO polypeptides by
 CC recombinant techniques, and in generating either transgenic animals or
 CC knock-out animals which, in turn, are useful in the development and
 CC screening of therapeutically useful reagents. The sequences presented in
 CC ABU60807-ABU60815 are the human PRO polynucleotides of the invention.

XX Sequence 437 AA;

Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLLG 473
 |||||
 Db 4 VLLALLLG 11

RESULT 33

ABG73312 standard; Protein; 437 AA.

XX ABG73312;

XX 30-APR-2003 (first entry)
 DE Human PRO1863 polypeptide.
 XX Human: secreted and transmembrane polypeptide; PRO polypeptide;
 KW inflammatory diseases; immune-related diseases; diabetes mellitus;
 KW rheumatoid arthritis; glomerulonephritis; multiple sclerosis;
 KW immun-mediated skin disease; contact dermatitis; graft rejection;
 KW transplantation associated disease; graft-versus-host disease;
 KW tumour diagnosis; tumour cell; antiinflammatory; immunosuppressive;
 KW cytotoxic; antineoplastic; antineumatic; antiarthritis; antithyroid;
 KW antidiabetic; nephrotoxic; antiproliferative; dermatological; haemostatic;
 KW hepatotropic; virucide; neuroprotective; PRO1863.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..15
 FT /label= Signal_peptide
 FT Protein 16..437
 FT /label= Mature_PRO1863_polypeptide
 XX US2002164646-A1.
 XX 07-NOV-2002.
 XX 27-DEC-2001; 2001US-0033223.
 XX 02-JUN-1999; 99WO-US12252.
 XX 01-DEC-1999; 99WO-US28634.
 XX 02-DEC-1999; 99WO-US28551.
 XX 11-FEB-2000; 2000WO-US03565.
 XX 22-FEB-2000; 2000WO-US04414.
 XX 02-MAR-2000; 2000WO-US05841.
 XX 30-MAR-2000; 2000WO-US08439.
 XX 30-MAY-2000; 2000WO-US14941.
 XX 02-JUN-2000; 2000WO-US15264.
 XX 01-DEC-2000; 2000WO-US32678.
 XX 16-DEC-1998; 98US-113145P.
 XX 22-DEC-1998; 98US-113511P.
 XX 12-JAN-1999; 99US-115558P.
 XX 12-JAN-1999; 99US-115733P.
 XX 12-JAN-1999; 99US-115733P.
 XX 09-FEB-1999; 99US-119341P.
 XX 10-FEB-1999; 99US-119537P.
 XX 12-FEB-1999; 99US-119565P.
 XX 29-OCT-1999; 99US-162506P.
 XX (GENTH) GENENTECH INC.
 XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WJ;
 XX MPI: 2003-238305/23.
 XX N-PSDB; ABX11171.
 XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing
 PT or treating inflammatory diseases or immune-related diseases, e.g.
 PT inflammatory bowel disease, systemic lupus erythematosus or rheumatoid
 PT arthritis
 XX Claim 12; Fig 10; 119pp; English.
 XX The present invention relates to the isolation of novel human
 CC secreted and transmembrane polypeptides designated PRO polypeptides
 CC (PRO1800, PRO339, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434
 CC and PRO1927), and the polynucleotide sequences encoding them. The PRO
 CC polypeptides and polynucleotide sequences of the invention are useful
 CC in diagnosing or treating inflammatory diseases or immune-related
 CC diseases (e.g. inflammatory bowel disease, systemic lupus
 CC erythematosus, rheumatoid arthritis, Sjogren's syndrome, autoimmune

CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, glomerulonephritis, multiple sclerosis, infectious hepatitis,
 CC immune-mediated skin diseases including psoriasis or contact dermatitis,
 CC and transplantation associated diseases including graft rejection or
 CC graft-versus-host disease). The PRO polypeptides are also useful for
 CC diagnosing tumours, and for inhibiting the growth of tumour cells. The
 CC PRO polynucleotide sequences may be used as hybridisation probes in
 CC chromosome and gene mapping, and in generating antisense RNA and DNA.
 CC They are also useful in preparing PRO polypeptides, in assays to
 CC identify other proteins or molecules involved in a binding reaction,
 CC to generate transgenic animals or knockout animals, which in turn are
 CC useful in the development and screening of therapeutically useful
 CC reagents, for chromosome identification, and tissue typing. The PRO
 CC polynucleotide sequences are also useful in gene therapy. Anti-PRO
 CC antibodies may be used in diagnostic assays for PRO polypeptides.
 CC The present sequence represents human PRO1863 polypeptide.
 XX
 XX Sequence 437 AA;
 SQ
 QY 466 VLLDALIG 473
 DB 4 VLLDALIG 11
 Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 34
 ABUS9153
 ID ABUS9153 standard; Protein; 437 AA.
 XX
 AC ABUS9153;
 XX
 DT 28-APR-2003 (first entry)
 XX
 DE Novel human secreted or transmembrane protein PRO181.
 XX
 KW Human: PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 XX US2002132252-A1.
 XX 19-SEP-2002.
 XX 14-NOV-2001; 2001US-0990442.
 XX 05-NOV-1997; 97WO-US20069.
 XX 16-SEP-1998; 98WO-US19330.
 XX 17-SEP-1998; 98WO-US19437.
 XX 07-OCT-1998; 98WO-US21141.
 XX 01-DEC-1998; 98WO-US25108.
 XX 05-JAN-1999; 99WO-US00106.
 XX 08-MAR-1999; 99WO-US05028.
 XX 02-JUN-1999; 99WO-US12252.
 XX 15-SEP-1999; 99WO-US21090.
 XX 15-SEP-1999; 99WO-US21547.
 XX 30-NOV-1999; 99WO-US28313.
 XX 01-DEC-1999; 99WO-US28301.
 XX 01-DEC-1999; 99WO-US28634.
 XX 16-DEC-1999; 99WO-US30095.
 XX 20-DEC-1999; 99WO-US30911.
 XX 06-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 02-MAR-2000; 2000WO-US05004.
 PR 10-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06319.
 PR 20-MAR-2000; 2000WO-US06884.
 PR 30-MAR-2000; 2000WO-US07377.
 PR 15-MAY-2000; 2000WO-US13358.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUN-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23528.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 16-JUN-1997; 97US-049787P.
 PR 17-OCT-1997; 97US-062250P.
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 PR 28-AUG-2001; 2001US-0941992.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Garber H, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AU, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WL;
 PI Zhang Z;
 XX
 XX MPI; 2003-247083/24.
 DR N-PSDB; ABX80352.
 XX
 XX
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments
 XX
 XX Claim 12; Fig 250; 648pp; English.
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiforms or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.
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 DB 4 VLLALLLG 11
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 ID ABUS9300 standard; Protein; 437 AA.
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 XX AC ABUS9300;
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 DT 22-APR-2003 (first entry)
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 XX Human secreted/transmembrane protein, #143.

XX Human; PRO; secreted; transmembrane; pharmaceutical;
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.
XX Homo sapiens.
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Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 36
ABUS9449

ID ABUS9449 standard; Protein; 437 AA.

AC ABUS9449;

DT 22-APR-2003 (first entry)

XX Novel human secreted or transmembrane protein PRO1182.

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;

KW cardiac insufficiency disorder; cancer; tumour; immune response;

KW adrenal cortical capillary endothelial growth; c-fos induction;

KW vascular endothelial growth factor inhibition; VEGF inhibition;

KW endothelial cell growth inhibitor; T-lymphocytes stimulation;

KW retinal neurons cell survival; rod photoreceptor cell survival;

KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
OS Homo sapiens.
XX US2003027985-A1.
XX 06-FEB-2003.
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PR 26-AUG-1998; 98US-097978P.
PR 26-AUG-1998; 98US-097979P.
PR 26-AUG-1998; 98US-097986P.
PR 26-AUG-1998; 98US-098014P.

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Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches: 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VILLALIG 473
 DB 4 VILLALIG 11

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RESULT 37
ABU60584
ID ABU60584 standard; Protein; 437 AA.
XX
AC ABU60584;
XX
XX
DT 01-MAY-2003 (first entry)
DE Human secreted/transmembrane protein, #143.
XX
XX Human; PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
XX US2002160384-A1.
XX
PD 31-OCT-2002.
XX
XX 14-NOV-2001; 2001US-0992598.
XX
XX 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.

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PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
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PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049787P.
PR 17-OCT-1997; 97US-062250P.
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PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.
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PR 05-JUN-1998; 98US-088167P.
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PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088734P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088742P.
PR 10-JUN-1998; 98US-088810P.
PR 10-JUN-1998; 98US-088824P.

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PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088858P.
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PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089440P.
PR 16-JUN-1998; 98US-089514P.
PR 16-JUN-1998; 98US-089512P.
PR 17-JUN-1998; 98US-089532P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089599P.
PR 17-JUN-1998; 98US-089600P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089801P.
PR 18-JUN-1998; 98US-089807P.
PR 18-JUN-1998; 98US-089908P.
PR 28-AUG-2001; 2001US-094192.

XX
XX
XX (GETH ) GENENTECH INC.;
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers I, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
XX Zhang Z;
XX
XX MPI. 2003-288106/28.
XX N-PSDB; ABX90330.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, or in generating probes -
XX
XX Claim 12; Fig 250; 650bp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX comprising a sequence without signal peptide and the nucleic acid
XX encoding them. The polypeptides can be used to raise antibodies that
XX specifically bind to the PRO polypeptide, for linking a bioactive
XX molecule to a cell expressing a PRO protein and for modulating at least
XX one biological activity of a cell. The PRO polypeptides or
XX polynucleotides are also useful in gene therapy, in chromosome
XX identification, as chromosome markers, or in generating probes. The PRO
XX polypeptides are useful as molecular markers for protein
XX electrophoresis, and the isolated nucleic acids may be used for
XX recombinantly expressing those markers. The PRO polypeptides and nucleic
XX acids may also be used in tissue typing. Anti-PRO antibodies are useful
XX in diagnostic assays for PRO, and in affinity purification of PRO from
XX recombinant cell culture or natural sources. The sequences presented in
XX ABU60478-ABU60624 are the PRO polynucleotides of the invention.
XX Note: The sequence data for this patent is also available in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX
XX SQ Sequence 437 AA;
XX
XX Query Match 1.5%; Score 8; DB 24; Length 437;
XX Best Local Similarity. 100.0%; Pred. No. 71;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 466 VLLALLLG 473
XX |||||
XX Db 4 VLLALLLG 11
XX
XX RESULT 38
XX ABUS8075
XX ID ABUS8075 standard; Protein; 437 AA.
XX
XX AC ABUS8075;
XX
XX DT 14-APR-2003 (first entry)
XX

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DE Human PRO polypeptide #107.
XX
XX Human; PRO; cytostratic; tumour; cancer; breast; lung; stomach; liver;
KW horse; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrgug therapy.
XX
OS Homo sapiens.
XX
XX US2003027163-A1.
XX
XX
XX 06-FEB-2003.
XX
XX
XX 15-NOV-2001; 2001US-0997666.
XX
XX
XX 05-NOV-1997; 97WO-US20069.
XX 16-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 07-OCT-1998; 98WO-US21141.
XX 01-DEC-1998; 98WO-US25108.
XX 05-JAN-1999; 99WO-US00106.
XX 08-MAR-1999; 99WO-US05028.
XX 02-JUN-1999; 99WO-US12252.
XX 15-SEP-1999; 99WO-US21090.
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XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
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XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04411.
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XX 02-MAR-2000; 2000WO-US05004.
XX 10-MAR-2000; 2000WO-US05841.
XX 15-MAR-2000; 2000WO-US06319.
XX 20-MAR-2000; 2000WO-US06884.
XX 30-MAR-2000; 2000WO-US07377.
XX 15-MAY-2000; 2000WO-US08439.
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XX 22-MAY-2000; 2000WO-US14042.
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XX 24-AUG-2000; 2000WO-US23328.
XX 08-NOV-2000; 2000WO-US30952.
XX 01-DEC-2000; 2000WO-US32678.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-JUN-2001; 2001WO-US17800.
XX 20-JUN-2001; 2001WO-US19692.
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XX 13-NOV-1997; 97US-065311P.
XX 24-NOV-1997; 97US-066770P.
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XX 10-JUL-1998; 98US-092472P.
XX 20-JUL-1998; 98US-093339P.
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Query Match 1.5%; Score 8; DB 24; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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4 VLLALLLG 11

RESULT 39
ABUS9006
ID ABUS9006 standard; Protein; 437 AA.

XX ABUS9006;

DT 16-APR-2003 (first entry)

DE Human secreted/transmembrane protein, #143.

KX Human; PRO; secreted; transmembrane; signal peptide;

KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
colon cancer; lung cancer; breast cancer; cancer; gene therapy.

XX Homo sapiens.

XX US2002142961-A1.
XX 03-OCT-2002.
XX 19-NOV-2001; 2001US-0969721.
XX 05-NOV-1997; 97WO-US20069.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US28634.
PR 20-DEC-1999; 99WO-US30095.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 02-MAR-2000; 2000WO-US05004.
PR 10-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06319.
PR 20-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUN-2000; 2000WO-US07010.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US230952.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-062877P.
PR 17-OCT-1997; 97US-062250P.
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PR 13-NOV-1997; 97US-065311P.
PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083222P.
PR 07-MAY-1998; 98US-083222P.
PR 28-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.
PR 02-JUN-1998; 98US-087607P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088021P.
PR 04-JUN-1998; 98US-088025P.
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PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088030P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.

PR 05-JUN-1998; 98US-088212P.
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 PR 10-JUN-1998; 98US-088858P.
 PR 11-JUN-1998; 98US-088861P.
 PR 11-JUN-1998; 98US-088876P.
 PR 12-JUN-1998; 98US-089105P.
 PR 16-JUN-1998; 98US-089440P.
 PR 16-JUN-1998; 98US-089512P.
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 PR 18-JUN-1998; 98US-089801P.
 PR 18-JUN-1998; 98US-089907P.
 PR 18-JUN-1998; 98US-089908P.
 PR 28-AUG-2001; 2001US-094199Z.
 (GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerlitsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoletti NF;
 PI Roy MA, Stewart RA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX WPI; 2003-155950/15.

XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers
 PT -

XX Claim 12; Fig 250; 647pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
 CC comprising a sequence without signal peptide and the nucleic acid
 CC encoding them. The polypeptides can be used to raise antibodies that
 CC specifically bind to the PRO polypeptide, for linking a bioactive
 CC molecule to a cell expressing a PRO protein and for modulating at least
 CC one biological activity of a cell. The PRO polypeptides or
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors, for detecting or treating e.g. tumors in
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.
 CC colon, lung or breast cancers) and diagnostic determination of the
 CC presence of these cancers. The PRO polypeptides are also useful as
 CC molecular weight markers or for chromosome identification. The PRO genes
 CC are useful as hybridization probes or for screening libraries of human
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
 CC therapy, particularly for replacing a defective gene. The sequences
 CC presented in ABUS8900-ABUS9046 are the PRO polypeptides of the invention.

XX Sequence 437 AA;

Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLIG 473
 DB 4 VLLALLIG 11

RESULT 40
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 XX AC ABU13966;
 XX 26-FEB-2003 (first entry)
 DT XX
 DE Human PRO1181 polypeptide.
 XX Human; PRO polypeptide; secreted protein; transmembrane protein;
 KW genetic disorder; antibacterial; immunosuppressive.
 XX Homo sapiens.
 OS US2002103125-A1.
 PN 01-AUG-2002.
 PD 20-NOV-2001; 2001US-0989731.
 XX 05-NOV-1997; 97WO-US20069.
 PR 16-SEP-1998; 96WO-US19330.
 PR 17-SEP-1998; 96WO-US19437.
 PR 07-OCT-1998; 96WO-US21141.
 PR 01-DEC-1998; 96WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US42252.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 06-JAN-2000; 2000WO-US00219.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 15-MAY-2000; 2000WO-US13358.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
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 PR 16-JUN-1997; 97US-049787P.
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 PR 13-NOV-1997; 97US-065311P.
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 PR 07-MAY-1998; 98US-084600P.

PR 28-MAY-1998; 98US-087106P.
 PR 02-JUN-1998; 98US-087607P.
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 PR 03-JUN-1998; 98US-087827P.
 PR 04-JUN-1998; 98US-088021P.
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 PR 16-JUN-1998; 98US-089440P.
 PR 16-JUN-1998; 98US-089512P.
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 PR 18-JUN-1998; 98US-089907P.
 PR 18-JUN-1998; 98US-089908P.
 PR 28-AUG-2001; 2001US-0941992.

(GETH) GENENTECH LTD.

PR Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PR Ferrara N, Fong S, Gerber H, Gerltzen ME, Goddard A, Godowski RJ;
 PR Grimaldi JC, Gurney AL, Kijavini IU, Napier MA, Pan J, Peoni NF;
 PR Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PR Zhang Z;

PR MPI; 2003-102117/09.
 PR N-PSDB; ABX64176.

PR Novel secreted and transmembrane polypeptide for modulating biological
 PR activity of cell expressing the polypeptide, identifying agonists or
 PR antagonists of polypeptide, and as molecular weight markers

PR Claim 12; Fig 250; 649pp; English.

CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The polynucleotide sequences encoding PRO polypeptides are useful as
 CC hybridization probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
 CC generating transgenic animals or knockout animals, to construct
 CC hybridization probes for mapping the gene which encodes the PRO
 CC polypeptide, and for the genetic analysis of individuals with genetic
 CC disorders, in gene therapy, for chromosome identification, as

CC chromosome markers, and for generating probes for PCR, Northern
 CC analysis, Southern analysis and Western analysis. ABU13860-ABU14006
 CC represent the human PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/patident/identity.html.

XX SQ Sequence 437 AA;

Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 4 VLLALALG 11

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 Job time: 110 secs

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OM protein - protein search, using SW model

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Title: US-10-039-770A-1

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Searched: 328717 seqs, 42310858 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	8	1.5	437	4 US-09-996-243-355	Sequence 355, App
5	8	1.5	497	6 5486473-4	Patent No. 5486473
6	8	1.5	689	4 US-09-252-991A-18990	Sequence 18990, A
7	7	1.3	87	2 US-08-332-562A-88	Sequence 88, Appli
8	7	1.3	100	4 US-09-205-258-1046	Sequence 1046, Ap
9	7	1.3	137	4 US-09-904-615-163	Sequence 163, Ap
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17	7	1.3	177	4 US-08-467-344A-52	Sequence 52, Appli
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144	6	1.1	65	1	US-08-248-016-12	Sequence 12, Appl1	217	6	1.1	128	4	US-08-446-872A-160	Sequence 160, App
145	6	1.1	65	1	US-08-451-501-12	Sequence 12, Appl	218	6	1.1	128	4	US-08-762-227A-160	Sequence 160, App
146	6	1.1	65	2	US-08-117-952-770	Sequence 770, App	219	6	1.1	128	5	PCT-US95-01185-160	Sequence 160, App
147	6	1.1	65	5	PCT-US95-06761-12	Sequence 12, Appl	220	6	1.1	129	1	US-08-049-503-1	Sequence 1, Appl1
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150	6	1.1	67	1	US-08-485-069-6	Sequence 6, Appl1	223	6	1.1	129	2	US-08-874-697-1	Sequence 1, Appl1
151	6	1.1	72	3	US-08-946-329A-108	Sequence 108, App	224	6	1.1	129	3	US-08-722-258-2	Sequence 2, Appl1
152	6	1.1	76	1	US-08-868-252-4	Sequence 4, Appl1	225	6	1.1	129	3	US-08-897-020-1	Sequence 1, Appl1
153	6	1.1	76	3	US-09-083-521-5	Sequence 5, Appl1	226	6	1.1	129	3	US-08-765-012A-16	Sequence 16, Appl1
154	6	1.1	77	4	US-08-311-731A-239	Sequence 239, App	227	6	1.1	129	3	US-08-765-012A-17	Sequence 17, Appl
155	6	1.1	78	4	US-09-252-991A-17531	Sequence 17531, A	228	6	1.1	129	3	US-08-765-012A-18	Sequence 18, Appl
156	6	1.1	80	1	US-08-848-252-2	Sequence 2, Appl1	229	6	1.1	129	3	US-08-765-012A-19	Sequence 19, Appl
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163	6	1.1	90	3	US-08-912-314A-24	Sequence 24, Appl	236	6	1.1	129	5	US-09-033-275-10	Sequence 10, Appl
164	6	1.1	93	4	US-09-134-001C-5186	Sequence 5186, Ap	237	6	1.1	129	5	US-08-765-012A-6	Sequence 6, Appl1
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166	6	1.1	95	1	US-07-928-611-2	Sequence 2, Appl1	239	6	1.1	130	3	US-08-765-012A-11	Sequence 11, Appl
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169	6	1.1	95	4	US-09-060-694-2	Sequence 2, Appl1	242	6	1.1	130	3	US-08-765-012A-14	Sequence 14, Appl
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172	6	1.1	96	1	US-08-518-878B-35	Sequence 35, Appl	245	6	1.1	131	3	US-08-765-012A-6	Sequence 6, Appl1
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309	6	1.1	166	2	US-08-487-231-3	Sequence 3, Appli	382	6	1.1	219	4	US-09-847-185-2	Sequence 2, Appli
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313	6	1.1	167	3	US-08-513-974B-363	Sequence 363, App	386	6	1.1	222	4	US-08-740-036-3	Sequence 3, Appli
314	6	1.1	167	3	US-08-513-974B-367	Sequence 367, App	387	6	1.1	222	4	US-08-740-036-3	Sequence 3, Appli
315	6	1.1	167	3	US-08-776-971-101	Sequence 101, App	388	6	1.1	222	6	5185431-4	Patent No. 5185431
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422	6	1.1	247	2	US-09-372-422A-48	Sequence 48, Appl	495	6	1.1	300	4	US-09-596-747-7	Sequence 7, Appli
423	6	1.1	249	4	US-09-372-422A-22	Sequence 22, Appl	496	6	1.1	300	4	US-09-252-991A-28367	Sequence 28367, A
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425	6	1.1	250	1	US-08-234-939-2	Sequence 2, Appli	498	6	1.1	301	3	US-08-468-609A-142	Sequence 142, App
426	6	1.1	250	1	US-08-558-865-2	Sequence 2, Appli	499	6	1.1	301	4	US-08-762-227A-142	Sequence 142, App
427	6	1.1	250	3	US-08-654-025-2	Sequence 2, Appli	500	6	1.1	301	4	US-08-762-227A-142	Sequence 142, App
428	6	1.1	250	3	US-08-654-025-7	Sequence 7, Appli	501	6	1.1	301	5	PCT-US95-01185-142	Sequence 142, App
429	6	1.1	250	4	US-09-372-422A-24	Sequence 24, Appl	502	6	1.1	305	4	US-09-252-991A-17408	Sequence 17408, A
430	6	1.1	250	4	US-09-252-991A-33114	Sequence 33114, A	503	6	1.1	309	1	US-08-729-202-1	Sequence 1, Appli
431	6	1.1	251	4	US-09-461-325-377A	Sequence 374, App	504	6	1.1	309	1	US-08-896-371-1	Sequence 1, Appli
432	6	1.1	251	4	US-09-252-991A-22677	Sequence 22677, A	505	6	1.1	309	4	US-09-522-714-10	Sequence 10, Appl
433	6	1.1	254	4	US-09-252-991A-23519	Sequence 23519, A	506	6	1.1	311	4	US-09-252-991A-18916	Sequence 18916, A
434	6	1.1	255	4	US-09-107-532A-3831	Sequence 3831, Ap	507	6	1.1	311	4	US-09-252-991A-25748	Sequence 25748, A
435	6	1.1	256	4	US-09-252-991A-17168	Sequence 17168, A	508	6	1.1	312	1	US-08-414-625-2	Sequence 2, Appli
436	6	1.1	258	4	US-09-252-991A-29089	Sequence 29089, A	509	6	1.1	312	4	US-09-023-942A-4	Sequence 4, Appli
437	6	1.1	259	3	US-08-469-318-141	Sequence 141, App	510	6	1.1	314	3	US-09-008-271A-3	Sequence 3, Appli
438	6	1.1	259	3	US-08-468-609A-141	Sequence 141, App	511	6	1.1	314	4	US-09-023-942A-6	Sequence 6, Appli
439	6	1.1	259	4	US-08-446-872A-141	Sequence 141, App	512	6	1.1	315	4	US-08-118-270-28	Sequence 28, Appl
440	6	1.1	259	4	US-08-762-227A-141	Sequence 141, App	513	6	1.1	315	5	PCT-US93-08528-28	Sequence 28, Appl
441	6	1.1	259	4	US-09-252-991A-32989	Sequence 32989, A	514	6	1.1	316	4	US-09-134-001C-5547	Sequence 5547, Ap
442	6	1.1	259	5	PCT-US95-01185-141	Sequence 141, App	515	6	1.1	318	3	US-08-537-942A-1	Sequence 1, Appli
443	6	1.1	266	4	US-09-589-287B-19	Sequence 19, Appl	516	6	1.1	318	3	US-08-997-252A-1	Sequence 1, Appli
444	6	1.1	266	4	US-09-879-919-24	Sequence 24, Appl	517	6	1.1	318	4	US-09-517-739-1	Sequence 31823, Ap
445	6	1.1	266	4	US-09-252-991A-31767	Sequence 31767, A	518	6	1.1	320	4	US-09-134-001C-3823	Sequence 30676, A
446	6	1.1	266	4	US-09-588-947A-19	Sequence 19, Appl	519	6	1.1	320	4	US-09-252-991A-30676	Sequence 18807, A
447	6	1.1	267	3	US-08-718-905-3	Sequence 3, Appli	520	6	1.1	321	4	US-09-252-991A-18807	Sequence 18807, A
448	6	1.1	267	3	US-09-550-497-3	Sequence 3, Appli	521	6	1.1	322	6	5212074-1	Patent No. 5212074
449	6	1.1	267	4	US-09-147-982-3	Sequence 3, Appli	522	6	1.1	325	2	US-09-018-576-3	Sequence 12, Appl
450	6	1.1	267	4	US-09-549-839A-3	Sequence 3, Appli	523	6	1.1	325	2	US-09-018-576-12	Sequence 12, Appl
451	6	1.1	267	4	US-09-581-130-4	Sequence 4, Appli	524	6	1.1	325	3	US-09-248-137-3	Sequence 3, Appli
452	6	1.1	268	4	US-09-107-532A-5683	Sequence 5683, Ap	525	6	1.1	325	3	US-09-248-137-12	Sequence 12, Appl
453	6	1.1	268	4	US-08-871-483-11	Sequence 11, Appl	526	6	1.1	327	4	US-09-252-991A-35058	Sequence 25058, A
454	6	1.1	268	4	US-09-216-393B-90	Sequence 90, Appl	527	6	1.1	327	4	US-09-328-352-6432	Sequence 6432, Ap
455	6	1.1	268	4	US-09-252-991A-30350	Sequence 30350, A	528	6	1.1	328	3	US-09-073-359-6	Sequence 6, Appli
456	6	1.1	272	4	US-09-252-991A-29301	Sequence 29301, A	529	6	1.1	328	4	US-09-187-999-31	Sequence 31, Appl
457	6	1.1	273	4	US-09-134-001C-3917	Sequence 3917, Ap	530	6	1.1	328	4	US-09-252-991A-20830	Sequence 20830, A
458	6	1.1	274	3	US-08-469-318-144	Sequence 144, App	531	6	1.1	329	1	US-07-991-587A-7	Sequence 7, Appli
459	6	1.1	274	3	US-08-468-609A-144	Sequence 144, App	532	6	1.1	330	1	US-08-309-985-7	Sequence 2, Appli
460	6	1.1	274	4	US-08-446-872A-144	Sequence 144, App	533	6	1.1	330	1	US-08-238-163-2	Sequence 2, Appli
461	6	1.1	274	4	US-08-762-227A-144	Sequence 144, App	534	6	1.1	331	3	US-08-961-083-212	Sequence 212, App
462	6	1.1	274	5	PCT-US95-01185-144	Sequence 144, App	535	6	1.1	331	3	US-09-536-78A-212	Sequence 212, App
463	6	1.1	277	4	US-09-252-991A-21417	Sequence 21417, A	536	6	1.1	332	2	US-08-446-875-12	Sequence 12, Appl
464	6	1.1	278	3	US-08-663-082-4	Sequence 4, Appli	537	6	1.1	332	2	US-08-102-385G-12	Sequence 12, Appl
465	6	1.1	280	4	US-09-247-155-178	Sequence 178, App	538	6	1.1	332	4	US-09-252-991A-29873	Sequence 29873, A

539	6	1.1	333	1	US-07-991-587A-2	Sequence 2, Appl1	612	6	1.1	379	4	US-09-107-532A-5334	Sequence 5334, Ap
540	6	1.1	333	1	US-08-309-985-2	Sequence 2, Appl1	613	6	1.1	381	3	US-09-216-295-17	Sequence 22, Appl
541	6	1.1	336	5	US-08-118-270-54	Sequence 54, Appl	614	6	1.1	381	4	US-09-569-804-17	Sequence 17, Appl
542	6	1.1	336	5	PCT-US93-08528-54	Sequence 54, Appl	615	6	1.1	381	4	US-09-252-991A-29970	Sequence 29970, A
543	6	1.1	339	4	US-09-690-454-66	Sequence 66, Appl	616	6	1.1	382	1	US-08-470-299-10	Sequence 7, Appl1
544	6	1.1	340	4	US-09-690-454-174	Sequence 174, App	617	6	1.1	382	1	US-08-470-299-10	Sequence 10, Appl
545	6	1.1	340	4	US-09-107-533A-5663	Sequence 4563, Ap	618	6	1.1	384	4	US-09-252-991A-26780	Sequence 26780, A
546	6	1.1	341	4	US-08-894-454-161	Sequence 30760, A	619	6	1.1	384	1	US-08-220-958-2	Sequence 2, Appl1
547	6	1.1	343	4	US-08-961-083-192	Sequence 192, App	620	6	1.1	385	3	US-08-475-742-2	Sequence 2, Appl1
548	6	1.1	344	4	US-09-134-001C-5004	Sequence 5004, Ap	621	6	1.1	385	4	US-08-261-293-2	Sequence 2, Appl1
549	6	1.1	344	4	US-09-536-784-182	Sequence 192, App	622	6	1.1	385	4	US-08-261-293-2	Sequence 2, Appl1
550	6	1.1	344	4	US-09-536-784-182	Sequence 192, App	623	6	1.1	386	4	US-09-252-991A-24274	Sequence 24274, A
551	6	1.1	346	4	US-09-328-352-5835	Sequence 5835, Ap	624	6	1.1	387	1	US-07-626-618A-17	Sequence 17, Appl
552	6	1.1	349	3	US-09-032-523-3	Sequence 1, Appl1	625	6	1.1	387	1	US-08-123-161A-10	Sequence 10, Appl
553	6	1.1	350	3	US-08-204-196A-1	Sequence 1, Appl1	626	6	1.1	387	1	US-08-086-439C-3	Sequence 3, Appl1
554	6	1.1	350	4	US-09-252-991A-27973	Sequence 27973, A	627	6	1.1	387	1	US-08-056-051-2	Sequence 2, Appl1
555	6	1.1	350	4	US-09-252-991A-32358	Sequence 32358, A	628	6	1.1	387	1	US-07-928-611-18	Sequence 18, Appl
556	6	1.1	352	1	US-08-482-577B-4	Sequence 4, Appl1	629	6	1.1	387	1	US-08-333-977-17	Sequence 17, Appl
557	6	1.1	352	3	US-09-218-176-4	Sequence 4, Appl1	630	6	1.1	387	1	US-08-483-278-10	Sequence 10, Appl
558	6	1.1	352	4	US-08-981-490B-4	Sequence 4, Appl1	631	6	1.1	387	1	US-08-449-153-1	Sequence 1, Appl1
559	6	1.1	353	3	US-08-997-803-14	Sequence 14, Appl	632	6	1.1	387	1	US-08-434-877-3	Sequence 3, Appl1
560	6	1.1	353	4	US-09-731-030A-16	Sequence 16, Appl	633	6	1.1	387	1	US-08-449-651-1	Sequence 1, Appl1
561	6	1.1	354	2	US-08-512-955-2	Sequence 2, Appl1	634	6	1.1	387	1	US-08-470-299-4	Sequence 4, Appl1
562	6	1.1	354	3	US-09-325-897-2	Sequence 2, Appl1	635	6	1.1	387	2	US-08-884-072-5	Sequence 5, Appl1
563	6	1.1	354	4	US-09-837-726-2	Sequence 2, Appl1	636	6	1.1	387	2	US-08-487-811A-18	Sequence 18, Appl
564	6	1.1	357	4	US-09-252-991A-26979	Sequence 26979, A	637	6	1.1	387	2	US-08-833-963C-9	Sequence 9, Appl1
565	6	1.1	357	4	US-09-404-296B-10	Sequence 10, Appl	638	6	1.1	387	3	US-08-980-514-3	Sequence 3, Appl1
566	6	1.1	358	4	US-09-784-508-4	Sequence 4, Appl1	639	6	1.1	387	3	US-08-833-703-1	Sequence 1, Appl1
567	6	1.1	361	3	US-09-120-365-75	Sequence 75, Appl	640	6	1.1	387	3	US-08-475-742-4	Sequence 4, Appl1
568	6	1.1	361	3	US-09-515-039-75	Sequence 75, Appl	641	6	1.1	387	3	US-09-060-694-18	Sequence 18, Appl
569	6	1.1	361	4	US-09-339-159B-30	Sequence 30, Appl	642	6	1.1	387	4	US-09-212-168-5	Sequence 5, Appl1
570	6	1.1	362	4	US-09-252-991A-30517	Sequence 30517, A	643	6	1.1	387	4	US-09-378-074-18	Sequence 18, Appl
571	6	1.1	364	4	US-09-107-533A-4231	Sequence 4231, Ap	644	6	1.1	387	5	US-08-261-293-4	Sequence 4, Appl1
572	6	1.1	365	4	US-09-134-001C-5075	Sequence 5075, Ap	645	6	1.1	387	5	PCT-US93-07370-18	Sequence 18, Appl
573	6	1.1	366	4	US-09-328-352-7979	Sequence 7979, Ap	646	6	1.1	390	3	US-08-961-564A-2	Sequence 2, Appl1
574	6	1.1	369	4	US-09-252-991A-28650	Sequence 28650, A	647	6	1.1	390	4	US-09-050-861B-2	Sequence 2, Appl1
575	6	1.1	371	2	US-08-928-692-20	Sequence 20, Appl	648	6	1.1	390	4	US-09-198-452A-248	Sequence 248, App
576	6	1.1	371	4	US-09-339-972-20	Sequence 33, Appl	649	6	1.1	390	4	US-09-328-352-7880	Sequence 4891, Ap
577	6	1.1	372	1	US-08-278-729A-33	Sequence 33, Appl	650	6	1.1	390	4	US-09-328-352-7880	Sequence 7880, Ap
578	6	1.1	372	1	US-08-155-343A-33	Sequence 33, Appl	651	6	1.1	396	3	US-08-208-007A-13	Sequence 13, Appl
579	6	1.1	372	1	US-08-406-672-33	Sequence 33, Appl	652	6	1.1	396	3	US-08-032-533-9	Sequence 9, Appl1
580	6	1.1	372	1	US-08-643-563A-33	Sequence 33, Appl	653	6	1.1	396	4	US-08-915-095A-13	Sequence 13, Appl
581	6	1.1	372	1	US-08-643-763A-33	Sequence 33, Appl	654	6	1.1	396	4	US-08-798-096A-13	Sequence 13, Appl
582	6	1.1	372	1	US-08-462-623-33	Sequence 33, Appl	655	6	1.1	396	4	US-08-798-096A-13	Sequence 13, Appl
583	6	1.1	372	2	US-08-451-953A-33	Sequence 33, Appl	656	6	1.1	396	4	US-09-953-956-13	Sequence 13, Appl
584	6	1.1	372	2	US-08-459-346-15	Sequence 15, Appl	657	6	1.1	396	4	US-08-553-125A-13	Sequence 13, Appl
585	6	1.1	372	2	US-08-445-468A-33	Sequence 33, Appl	658	6	1.1	399	2	US-08-282-197C-54	Sequence 54, Appl
586	6	1.1	372	2	US-08-461-397A-33	Sequence 33, Appl	659	6	1.1	399	2	US-08-839-581A-2	Sequence 2, Appl1
587	6	1.1	372	2	US-08-912-088-33	Sequence 33, Appl	660	6	1.1	399	3	US-09-023-591A-2	Sequence 2, Appl1
588	6	1.1	372	3	US-08-278-730A-33	Sequence 33, Appl	661	6	1.1	400	4	US-09-252-991A-22821	Sequence 22821, A
589	6	1.1	372	3	US-08-889-419-15	Sequence 15, Appl	662	6	1.1	405	4	US-09-252-991A-31137	Sequence 31137, A
590	6	1.1	372	3	US-08-445-467-33	Sequence 33, Appl	663	6	1.1	406	4	US-09-252-991A-25824	Sequence 25824, A
591	6	1.1	372	3	US-08-480-515A-33	Sequence 33, Appl	664	6	1.1	407	4	US-09-489-847-80	Sequence 280, App
592	6	1.1	372	4	US-09-170-936-33	Sequence 33, Appl	665	6	1.1	409	4	US-09-569-804-21	Sequence 21, Appl
593	6	1.1	372	4	US-08-402-542-15	Sequence 15, Appl	666	6	1.1	411	4	US-09-015-188-2	Sequence 2, Appl1
594	6	1.1	372	4	US-08-461-113-33	Sequence 33, Appl	667	6	1.1	411	4	US-09-333-208-2	Sequence 2, Appl1
595	6	1.1	372	4	US-08-456-033-33	Sequence 33, Appl	668	6	1.1	416	3	US-09-183-254-2	Sequence 2, Appl1
596	6	1.1	372	4	US-08-643-321-31	Sequence 31, Appl	669	6	1.1	416	4	US-09-183-254-2	Sequence 2, Appl1
597	6	1.1	372	4	US-09-328-352-5436	Sequence 5436, Ap	670	6	1.1	416	4	US-09-252-991A-17015	Sequence 17015, A
598	6	1.1	372	5	PCT-US93-07189-15	Sequence 15, Appl	671	6	1.1	416	4	US-09-252-991A-28499	Sequence 28499, A
599	6	1.1	372	5	PCT-US93-07190-33	Sequence 33, Appl	672	6	1.1	417	4	US-09-252-991A-26638	Sequence 26638, A
600	6	1.1	372	5	PCT-US93-07231-33	Sequence 33, Appl	673	6	1.1	419	1	US-08-056-051-4	Sequence 4, Appl1
601	6	1.1	372	5	PCT-US93-08742-33	Sequence 33, Appl	674	6	1.1	419	1	US-07-928-611-20	Sequence 20, Appl
602	6	1.1	372	5	PCT-US93-08808-33	Sequence 33, Appl	675	6	1.1	419	1	US-08-335-186-2	Sequence 2, Appl1
603	6	1.1	372	5	PCT-US93-08885-33	Sequence 33, Appl	676	6	1.1	419	2	US-08-487-811A-20	Sequence 20, Appl
604	6	1.1	373	4	US-09-996-243-503	Sequence 503, App	677	6	1.1	419	3	US-09-060-694-20	Sequence 20, Appl
605	6	1.1	374	3	US-08-821-994-70	Sequence 70, Appl	678	6	1.1	419	3	US-08-974-691-3	Sequence 3, Appl1
606	6	1.1	376	4	US-09-252-991A-17262	Sequence 17262, A	679	6	1.1	419	4	US-09-630-155-2	Sequence 2, Appl1
607	6	1.1	376	4	US-09-252-991A-19927	Sequence 19927, A	680	6	1.1	419	4	US-09-705-448-10	Sequence 10, Appl
608	6	1.1	376	4	US-09-325-991A-20454	Sequence 20454, A	681	6	1.1	419	4	US-09-378-074-20	Sequence 20, Appl
609	6	1.1	378	4	US-09-325-991A-158	Sequence 158, App	682	6	1.1	419	5	PCT-US93-07370-20	Sequence 20, Appl
610	6	1.1	379	3	US-09-191-136-32	Sequence 32, Appl	683	6	1.1	420	4	US-09-328-352-7729	Sequence 4729, Ap
611	6	1.1	379	4	US-09-252-991A-31643	Sequence 31643, A	684	6	1.1	423	4	US-09-252-991A-29094	Sequence 29094, A

685	6	1.1	423	4	US-09-252-991A-32110	Sequence 32110, A	758	6	1.1	485	4	US-09-107-532A-4797	Sequence 4797, Ap
686	6	1.1	423	4	US-09-073-009-147	Sequence 142, App	759	6	1.1	486	3	US-08-348-518C-2	Sequence 2, Appl
687	6	1.1	424	4	US-09-252-991A-20642	Sequence 20642, A	760	6	1.1	487	4	US-09-252-991A-28079	Sequence 28079, A
688	6	1.1	426	4	US-09-107-532A-5246	Sequence 5246, Ap	761	6	1.1	487	4	US-09-107-532A-4946	Sequence 4946, Ap
689	6	1.1	428	4	US-09-252-991A-33081	Sequence 33081, A	762	6	1.1	488	4	US-08-311-731A-29	Sequence 29, Appl
690	6	1.1	429	4	US-09-461-325-366	Sequence 366, App	763	6	1.1	490	4	US-09-461-325-350	Sequence 250, App
691	6	1.1	431	3	US-09-381-681-3	Sequence 3, Appl	764	6	1.1	490	4	US-09-461-325-518	Sequence 518, App
692	6	1.1	433	2	US-08-919-624-1	Sequence 1, Appl	765	6	1.1	492	4	US-09-794-236-2	Sequence 2, Appl
693	6	1.1	433	2	US-08-941-532-6	Sequence 6, Appl	766	6	1.1	493	4	US-09-345-469-1	Sequence 1, Appl
694	6	1.1	433	4	US-09-051-239A-2	Sequence 2, Appl	767	6	1.1	495	4	US-09-252-991A-17194	Sequence 17194, A
695	6	1.1	433	4	US-09-170-496B-48	Sequence 48, Appl	768	6	1.1	496	4	US-09-252-991A-17605	Sequence 17605, A
696	6	1.1	433	4	US-09-170-496B-190	Sequence 190, App	769	6	1.1	497	2	US-09-047-125-3	Sequence 3, Appl
697	6	1.1	434	4	US-09-252-991A-28333	Sequence 28333, A	770	6	1.1	497	3	US-07-736-335E-3	Sequence 3, Appl
698	6	1.1	435	4	US-09-252-991A-18163	Sequence 18163, A	771	6	1.1	497	4	US-08-709-731A-29	Sequence 29, Appl
699	6	1.1	437	4	US-09-252-991A-25619	Sequence 25619, A	772	6	1.1	499	4	US-09-252-991A-32922	Sequence 32922, A
700	6	1.1	439	4	US-09-252-991A-20958	Sequence 20958, A	773	6	1.1	501	2	US-08-408-085-21	Sequence 31, Appl
701	6	1.1	439	4	US-09-328-352-7206	Sequence 7206, Ap	774	6	1.1	501	2	US-08-980-060-6	Sequence 6, Appl
702	6	1.1	441	3	US-09-191-136-31	Sequence 31, Appl	775	6	1.1	501	3	US-09-307-185-6	Sequence 6, Appl
703	6	1.1	444	4	US-09-252-991A-20496	Sequence 1, Appl	776	6	1.1	504	4	US-09-134-001C-4170	Sequence 4170, Ap
704	6	1.1	444	4	US-09-414-189-1	Sequence 1, Appl	777	6	1.1	505	1	US-08-149-105-16	Sequence 16, Appl
705	6	1.1	446	4	US-09-328-352-6076	Sequence 6076, Ap	778	6	1.1	505	1	US-08-317-847-16	Sequence 16, Appl
706	6	1.1	447	4	US-08-511-731A-246	Sequence 246, App	779	6	1.1	505	3	US-09-240-915-3	Sequence 3, Appl
707	6	1.1	448	3	US-08-476-509B-2	Sequence 2, Appl	780	6	1.1	505	3	US-09-591-435-3	Sequence 3, Appl
708	6	1.1	449	4	US-09-252-991A-18235	Sequence 18235, A	781	6	1.1	508	4	US-09-252-991A-24250	Sequence 24250, A
709	6	1.1	450	4	US-09-252-991A-17149	Sequence 17149, A	782	6	1.1	509	4	US-09-252-991A-30864	Sequence 30864, A
710	6	1.1	451	2	US-08-679-635A-2	Sequence 2, Appl	783	6	1.1	510	4	US-09-107-532A-5470	Sequence 5470, Ap
711	6	1.1	451	4	US-09-419-163-2	Sequence 2, Appl	784	6	1.1	510	3	US-08-246-489-2	Sequence 2, Appl
712	6	1.1	455	1	US-08-476-008-3	Sequence 3, Appl	785	6	1.1	513	4	US-09-595-857B-30	Sequence 30, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 3, Application US/09485549
; Patent No. 6361948
; GENERAL INFORMATION:
; APPLICANT: James Tricoli
; APPLICANT: Rachel Rhondine11
; APPLICANT: Fox Chase Cancer Center
; TITLE OF INVENTION: Prognostic Compositions for Prostate Cancer and Methods of Use
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; Sequence 2, Application US/09485549
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; GENERAL INFORMATION:
; APPLICANT: James Tricoli
; APPLICANT: Rachel Rhondine11
; APPLICANT: Fox Chase Cancer Center
; TITLE OF INVENTION: Prognostic Compositions for Prostate Cancer and Methods of Use
; TITLE OF INVENTION: thereof
```

```
FILE REFERENCE: FCCC 96-13
; CURRENT APPLICATION NUMBER: US/09/485,549
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/16768
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/055,285
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-485-549-2

Query Match 1.5%; Score 8; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 379 GSISETP 386
Db 174 GSISETP 181

RESULT 3
US-09-073-569-2
; Sequence 2, Application US/09073569
; Patent No. 6084088
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,569
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-073-569-2

Query Match 1.5%; Score 8; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 466 VLLALLLG 473
Db 4 VLLALLLG 11

RESULT 4
US-09-996-243-355
Sequence 355, Application US/09996243
Patent No. 6478825
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auecin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pao, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026

PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22

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; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

```

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Query Match      1.5%; Score 8; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      466 VLLALLG 473
      |||||
DB      4 VLLALLG 11

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RESULT 5

```

5486473-4
; Patent No. 5486473
; APPLICANT: FUKITA, HIROYUKI, YOSHIDA, IMAO, TAKAGI, MITSUO;
; MANABE, SADAJO, FUKAI, KONOSUKE
; TITLE OF INVENTION: A DNA CODING FOR A FLAVIVIRUS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,049
; FILING DATE: 09-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 809,255
; FILING DATE: 18-DEC-1991
; APPLICATION NUMBER: 279,685
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 932,419
; FILING DATE: 19-NOV-1986
; SEQ ID NO:4:
; LENGTH: 497
5486473-4

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Query Match      1.5%; Score 8; DB 6; Length 497;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      461 LAVGVLL 468
      |||||
DB      482 LAVGVLL 489

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RESULT 6
US-09-252-991A-18990
; Sequence 18990, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18990
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18990

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Query Match      1.5%; Score 8; DB 4; Length 689;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 GLVGVQL 9
      |||||
DB      587 GLVGVQL 594

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RESULT 7
US-08-332-562A-88
; Sequence 88, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, Ian F.C.
; APPLICANT: HOGARTH, Mark P.
; APPLICANT: HIBBS, Margaret L.
; APPLICANT: SCOTT, Bernadette M.
; APPLICANT: BONADONNA, Lisa
; APPLICANT: HULETT, Mark D.
; TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 136

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,562A
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,457
FILING DATE: 27-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 54270/119/GRHA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5339
TELEX: 904136
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-332-562A-88

Query Match 1.3%; Score 7; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
DB 42 GSLSEET 48

RESULT 8
US-09-205-258-1046
Sequence 1046, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1237
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1046
LENGTH: 100
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-1046

Query Match 1.3%; Score 7; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 LSAITSG 41
|||||
DB 48 LSAITSG 54

RESULT 9
US-09-904-615-163
Sequence 163, Application US/09904615

PATENT NO. 6566325
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: P2032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 163
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-615-163

Query Match 1.3%; Score 7; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 LLLALIG 473
|||||
DB 23 LLLALIG 29

RESULT 10
US-09-252-991A-21858
Sequence 21858, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 21858
LENGTH: 146
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: UNSURE
LOCATION: (145), (146)
OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-21858

Query Match 1.3%; Score 7; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 LLLALIG 474
|||||
DB 89 LLLALIG 95

RESULT 11
US-09-252-991A-31557
Sequence 31557, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 31557
LENGTH: 147
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31557

Query Match 1.3%; Score 7; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 LALLGGG 475
|||||
DB 93 LALLGGG 99

RESULT 12
US-08-756-387B-13
Sequence 13, Application US/08756387B

PATENT NO. 5945294
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wasson, Donald L.
TITLE OF INVENTION: Method to Detect IGE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for windows, version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B
FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-756-387B-13

Query Match 1.3%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
Db 43 GSLSEET 49

RESULT 13

US-09-285-873-13
Sequence 13, Application US/09285873
Patent No. 6309832
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rubiow, Keith E.
APPLICANT: Wassom, Donald L.
TITLE OF INVENTION: Method to Detect IGE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: No. 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-873-13

Query Match 1.3%; Score 7; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
Db 43 GSLSEET 49

RESULT 14
US-09-252-991A-26925
Sequence 26925, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26925
LENGTH: 176
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26925

Query Match 1.3%; Score 7; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 GLAVGV 466
Db 57 GLAVGV 63

RESULT 15
US-08-469-260A-52
Sequence 52, Application US/08469260A
Patent No. 6451578
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHRHOF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AB6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-469-260A-52

Query Match 1.3%; Score 7; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVVL 467
| | | | |
DB 30 LAVGVVL 36

RESULT 16
US-08-488-446-52

Sequence 52, Application US/08488446
Patent No. 6558898

GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMM J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE J. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAMMAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-446-52

Query Match 1.3%; Score 7; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVVL 467
| | | | |
DB 30 LAVGVVL 36

RESULT 17
US-08-467-344A-52

Sequence 52, Application US/08467344A
Patent No. 6586568

GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMM J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE J. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAMMAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-08-467-344A-52

Query Match 1.3%; Score 7; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVVL 467
| | | | |
DB 30 LAVGVVL 36

RESULT 18

US-09-252-991A-30129
Sequence 30129, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 30129
;; LENGTH: 191
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30129

Query Match 1.3%; Score 7; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALL 472
Db 53 VLLALL 59

RESULT 19
US-08-765-536-1
; Sequence 1, Application US/08765536
; Patent No. 5962634
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Sutton, Brian J. M.
; APPLICANT: McDonnell, James M.
; APPLICANT: Gould, Hannah J.
; APPLICANT: Korgold, Robert
; APPLICANT: Beavill, Andrew J.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5962634rls
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,536
; FILING DATE: April 30, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,943
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1619
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3439
; TELEFAX: 215-568-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-536-1

Query Match 1.3%; Score 7; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEET 385
Db 63 GSLSEET 69

RESULT 20
PCT-US95-08401-1
; Sequence 1, Application PC/TUS9508401
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Sutton, Brian J. M.
; APPLICANT: McDonnell, James M.
; APPLICANT: Gould, Hannah J.
; APPLICANT: Korgold, Robert
; APPLICANT: Beavill, Andrew J.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08401
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,943
; FILING DATE: 08-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1597
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08401-1

Query Match 1.3%; Score 7; DB 5; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEET 385
Db 63 GSLSEET 69

RESULT 21
US-08-756-387B-11
; Sequence 11, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B
FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-756-387B-11

Query Match 1.3%; Score 7; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSISET 385
DB 68 GSISET 74

RESULT 22
US-08-788-954-2
Sequence 2, Application US/08788954
Patent No. 6090384
GENERAL INFORMATION:
APPLICANT: RA, CHISEI
APPLICANT: NAITO, KOJI
APPLICANT: HIRAMA, MINORU
APPLICANT: OKUMURA, KO
TITLE OF INVENTION: ANTIALLERGIC COMPOSITION
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK, & SEAS
STREET: 2100 PENNSYLVANIA AVE., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,954
FILING DATE: 24-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/474,188
FILING DATE:
APPLICATION NUMBER: US 08/023,912

FILING DATE: 26-FEB-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-788-954-2

Query Match 1.3%; Score 7; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSISET 385
DB 68 GSISET 74

RESULT 23
US-09-285-873-11
Sequence 11, Application US/09285873
Patent No. 6309832
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Nassom, Donald L.
TITLE OF INVENTION: Method to Detect IGE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: No. 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-873-11

Query Match 1.3%; Score 7; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSISET 385

Db 68 GSLSEET 74

RESULT 24

US-09-252-991A-18239
; Sequence 18239, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18239
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18239

Query Match 1.3%; Score 7; DB 4; Length 205;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ASGLSSS 26
Db 84 ASGLSSS 90

RESULT 25

US-09-252-991A-32491
; Sequence 32491, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32491
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32491

Query Match 1.3%; Score 7; DB 4; Length 212;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 370 SAAVSYT 376
Db 101 SAAVSYT 107

RESULT 26

US-08-107-684B-9
; Sequence 9, Application US/08107684B
; Patent No. 5552273
; GENERAL INFORMATION:
; APPLICANT: CLEUZAT, Philippe L.
; APPLICANT: AMADE, Abalo

APPLICANT: ROBERT-BAUDOUY, Jeanine
; APPLICANT: GAYRAL, Jean-Pierre

TITLE OF INVENTION: POLYPEPTIDES CONTAINING SEQUENCES
; TITLE OF INVENTION: CHARACTERISTIC OF PYROLIDONE CARBOXYLYL PEPTIDASES.

TITLE OF INVENTION: POLYNUCLEOTIDES CONTAINING A SEQUENCE CODING FOR SUCH
; TITLE OF INVENTION: POLYPEPTIDES, AND THEIR USE, IN PARTICULAR FOR DIAGNOSTIC

NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIF & BERRIDGE

STREET: P.O. Box 19928
CITY: Alexandria

STATE: VA
COUNTRY: USA

ZIP: 22320
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,684B

FILING DATE: 17-AUG-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.

REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 26478

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400

TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-107-684B-9

Query Match 1.3%; Score 7; DB 1; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 371 AAVSYTA 377
Db 133 AAVSYTA 139

RESULT 27

US-08-107-684B-13
; Sequence 13, Application US/08107684B
; Patent No. 5552273
; GENERAL INFORMATION:
; APPLICANT: CLEUZAT, Philippe L.
; APPLICANT: AMADE, Abalo
; APPLICANT: ROBERT-BAUDOUY, Jeanine
; APPLICANT: GAYRAL, Jean-Pierre
; TITLE OF INVENTION: POLYPEPTIDES CONTAINING SEQUENCES
; TITLE OF INVENTION: CHARACTERISTIC OF PYROLIDONE CARBOXYLYL PEPTIDASES.
; TITLE OF INVENTION: POLYNUCLEOTIDES CONTAINING A SEQUENCE CODING FOR SUCH
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIF & BERRIDGE
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,684B
; FILING DATE: 17-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Beridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-107-684B-13

Query Match      1.3%; Score 7; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      371 AAVSYTA 377
DB      133 AAVSYTA 139

RESULT 28
US-09-205-258-1044
; Sequence 1044, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
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; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1044
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-1044

Query Match      1.3%; Score 7; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      35 LSASTSG 41
DB      96 LSASTSG 102

RESULT 29
US-09-252-991A-23837
; Sequence 23837, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
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PRIOR APPLICATION NUMBER: US 60/074,768
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23837
LENGTH: 228
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23837

Query Match 1.3%; Score 7; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 465 GVLALL 471
Db 213 GVLALL 219

RESULT 30
US-07-869-933-13
Sequence 13, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIND
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
STRAIN: FCRI alpha subunit
US-07-869-933-13

Query Match 1.3%; Score 7; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEET 385
Db 43 GSLSEET 49

RESULT 31
US-08-756-387B-6
Sequence 6, Application US/08756387B
Patent No. 5945294
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wasson, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B
FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-756-387B-6

Query Match 1.3%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEET 385
Db 43 GSLSEET 49

RESULT 32
US-09-103-663-13
Sequence 13, Application US/09103663D
Patent No. 6171803
GENERAL INFORMATION:
APPLICANT: Kinet et al.
TITLE OF INVENTION: Isolation, characterization, and use of the human beta
TITLE OF INVENTION: subunit of the high affinity receptor for
TITLE OF INVENTION: immunoglobulin E.
FILE REFERENCE: 50490
CURRENT APPLICATION NUMBER: US/09/103,663D
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 07/869,933
EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 232
TYPE: PRT
ORGANISM: Homo sapiens

US-09-103-663-13

Query Match 1.3%; Score 7; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
DB 43 GSLSEET 49

RESULT 33
US-09-285-873-6
Sequence 6, Application US/09285873
Patent No. 6309832

GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wasson, Donald L.
TITLE OF INVENTION: Method to Detect Igs
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: No. 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-873-6

Query Match 1.3%; Score 7; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
DB 43 GSLSEET 49

RESULT 34
US-09-364-230-10
Sequence 10, Application US/09364230
Patent No. 6348339
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.

APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 234
TYPE: PRT
ORGANISM: Glycine max
US-09-364-230-10

Query Match 1.3%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 YPLTQA 320
DB 194 YPLTQA 200

RESULT 35
US-07-869-933-11
Sequence 11, Application US/07869933
Patent No. 5770396

GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIND
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-869-933-11

Query Match 1.3%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
DB 43 GSLSEET 49

Db 68 GSLSEET 74

RESULT 36

US-08-756-387B-2
Sequence 2, Application US/08756387B

Patent No. 5943294

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

APPLICANT: Porter, James P.

APPLICANT: Rushlow, Keith E.

APPLICANT: Wassom, Donald L.

TITLE OF INVENTION: Method to Detect IGE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756,387B

FILING DATE: No. 5945294ember 26, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-756-387B-2

Query Match

Best Local Similarity 1.3%; Score 7; DB 2; Length 257;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEET 385

Db 68 GSLSEET 74

RESULT 37

US-09-103-663-11

Sequence 11, Application US/09103663D

Patent No. 6171803

GENERAL INFORMATION:

APPLICANT: Kinet et al.

TITLE OF INVENTION: Isolation, characterization, and use of the human beta

TITLE OF INVENTION: subunit of the high affinity receptor for

TITLE OF INVENTION: immunoglobulin E.

FILE REFERENCE: 50490

CURRENT APPLICATION NUMBER: US/09/103,663D

CURRENT FILING DATE: 1998-06-23

EARLIER APPLICATION NUMBER: 07/869,933

EARLIER FILING DATE: 1992-04-16

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 11

LENGTH: 257

TYPE: PRT

ORGANISM: Homo sapiens

US-09-103-663-11

Query Match

Best Local Similarity 1.3%; Score 7; DB 3; Length 257;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEET 385

Db 68 GSLSEET 74

RESULT 38

US-09-285-873-2

Sequence 2, Application US/09285873

Patent No. 6309832

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

APPLICANT: Porter, James P.

APPLICANT: Rushlow, Keith E.

APPLICANT: Wassom, Donald L.

TITLE OF INVENTION: Method to Detect IGE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/285,873

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/756,387

FILING DATE: No. 6309832ember 26, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-285-873-2

Query Match

Best Local Similarity 1.3%; Score 7; DB 4; Length 257;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEET 385

Db 68 GSLSEET 74

RESULT 39

US-08-897-956A-1

Sequence 1, Application US/08897956A

Patent No. 6423512

GENERAL INFORMATION:

APPLICANT: Kinet et al.

TITLE OF INVENTION: Isolation, characterization, and use of the human beta

TITLE OF INVENTION: subunit of the high affinity receptor for

TITLE OF INVENTION: immunoglobulin E.

FILE REFERENCE: 50490

CURRENT APPLICATION NUMBER: US/09/103,663D

CURRENT FILING DATE: 1998-06-23

EARLIER APPLICATION NUMBER: 07/869,933

EARLIER FILING DATE: 1992-04-16

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 11

LENGTH: 257


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; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-08-897-956A-1

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Query Match          1.3%: Score 7; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      68 GSI:SEET 74

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RESULT 40
US-09-252-991A-17952
; Sequence 17952, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17952
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-17952

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Query Match          1.3%: Score 7; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      124 GNP:PGG 130
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Db      242 GNP:PGG 248

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Search completed: October 2, 2003, 16:06:59
Job time : 43 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: October 2, 2003, 16:06:00 ; Search time 68 Seconds
(without alignments)
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Title: US-10-039-770a-1

Perfect score: 541

Sequence: 1 MGVLGVQLVLVADCTIFA.....EAEENIQDGETHWVEGDY 541

Scoring table: OLIGO

Searched: 587654 seqs, 158212981 residues

Word size : 0

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	9	1.7	280	US-10-156-424A-13	Sequence 13, App1
3	9	1.5	106	US-09-950-933A-70	Sequence 70, App1
4	8	1.5	200	US-10-080-170-438	Sequence 438, App1
5	8	1.5	238	US-10-102-806-499	Sequence 499, App
6	8	1.5	255	US-10-106-698-5043	Sequence 5043, App
7	8	1.5	437	US-09-989-722-355	Sequence 355, App
8	8	1.5	437	US-09-989-723-355	Sequence 355, App
9	8	1.5	437	US-09-989-279-355	Sequence 355, App
10	8	1.5	437	US-09-989-727-355	Sequence 355, App
11	8	1.5	437	US-09-989-731-355	Sequence 355, App
12	8	1.5	437	US-09-989-732-355	Sequence 355, App
13	8	1.5	437	US-09-991-073-355	Sequence 355, App
14	8	1.5	437	US-09-990-442-355	Sequence 355, App
15	8	1.5	437	US-09-991-163-355	Sequence 355, App

16	8	1.5	437	US-09-993-604-355	Sequence 355, App
17	8	1.5	437	US-09-990-456-355	Sequence 355, App
18	8	1.5	437	US-09-989-721-355	Sequence 355, App
19	8	1.5	437	US-09-992-598-355	Sequence 355, App
20	8	1.5	437	US-09-989-292A-355	Sequence 355, App
21	8	1.5	437	US-09-989-735-355	Sequence 355, App
22	8	1.5	437	US-09-990-444-355	Sequence 355, App
23	8	1.5	437	US-09-991-181-355	Sequence 355, App
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87	8	1.5	437	US-10-145-628-466	Sequence 466, App
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238	8	1.5	437	15	US-10-137-865-466	Sequence 466, App	311	8	1.5	437	15	US-10-125-930A-466	Sequence 466, App
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248	8	1.5	437	15	US-10-142-423-162	Sequence 466, App	321	8	1.5	437	15	US-10-127-850A-466	Sequence 466, App
249	8	1.5	437	15	US-10-230-414-162	Sequence 162, App	322	8	1.5	437	15	US-10-127-851A-466	Sequence 466, App
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271	8	1.5	437	15	US-10-127-829A-466	Sequence 466, App	344	8	1.5	437	15	US-10-123-907-466	Sequence 466, App
272	8	1.5	437	15	US-10-127-829A-466	Sequence 466, App	345	8	1.5	437	15	US-10-125-921A-466	Sequence 466, App
273	8	1.5	437	15	US-10-127-835A-466	Sequence 466, App	346	8	1.5	437	15	US-10-125-928A-466	Sequence 466, App
274	8	1.5	437	15	US-10-127-839A-466	Sequence 466, App	347	8	1.5	437	15	US-10-127-841A-466	Sequence 466, App
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276	8	1.5	437	15	US-10-131-813A-466	Sequence 466, App	349	8	1.5	437	15	US-10-127-843A-466	Sequence 466, App
277	8	1.5	437	15	US-10-131-813A-466	Sequence 466, App	350	8	1.5	437	15	US-10-127-844A-466	Sequence 466, App
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280	8	1.5	437	15	US-10-131-823A-466	Sequence 466, App	353	8	1.5	437	15	US-10-127-847A-466	Sequence 466, App
281	8	1.5	437	15	US-10-131-824A-466	Sequence 466, App	354	8	1.5	437	15	US-10-127-848A-466	Sequence 466, App
282	8	1.5	437	15	US-10-131-830A-466	Sequence 466, App	355	8	1.5	437	15	US-10-127-849A-466	Sequence 466, App
283	8	1.5	437	15	US-10-131-837A-466	Sequence 466, App	356	8	1.5	437	15	US-10-127-850A-466	Sequence 466, App
284	8	1.5	437	15	US-10-137-872A-466	Sequence 466, App	357	8	1.5	437	15	US-10-127-851A-466	Sequence 466, App
285	8	1.5	437	15	US-10-147-500-466	Sequence 466, App	358	8	1.5	437	15	US-10-127-852A-466	Sequence 466, App
286	8	1.5	437	15	US-10-147-502-466	Sequence 466, App	359	8	1.5	437	15	US-10-127-853A-466	Sequence 466, App
287	8	1.5	437	15	US-10-147-515-466	Sequence 466, App	360	8	1.5	437	15	US-10-127-854A-466	Sequence 466, App
288	8	1.5	437	15	US-10-147-517-466	Sequence 466, App	361	8	1.5	437	15	US-10-127-855A-466	Sequence 466, App
289	8	1.5	437	15	US-10-147-526-466	Sequence 466, App	362	8	1.5	437	15	US-10-128-687A-466	Sequence 466, App
290	8	1.5	437	15	US-10-147-527-466	Sequence 466, App	363	8	1.5	437	15	US-10-128-688A-466	Sequence 466, App
291	8	1.5	437	15	US-10-121-041-466	Sequence 466, App	364	8	1.5	437	15	US-10-128-689A-466	Sequence 466, App
292	8	1.5	437	15	US-10-121-043-466	Sequence 466, App	365	8	1.5	437	15	US-10-128-690A-466	Sequence 466, App
293	8	1.5	437	15	US-10-121-047-466	Sequence 466, App	366	8	1.5	437	15	US-10-131-825A-466	Sequence 466, App
294	8	1.5	437	15	US-10-123-915-466	Sequence 466, App	367	8	1.5	437	15	US-10-130-417-466	Sequence 466, App
295	8	1.5	437	15	US-10-123-902-466	Sequence 466, App	368	8	1.5	437	15	US-10-219-003-162	Sequence 162, App
296	8	1.5	437	15	US-10-123-908-466	Sequence 466, App	369	8	1.5	437	15	US-10-219-075-162	Sequence 162, App
297	8	1.5	437	15	US-10-123-909-466	Sequence 466, App	370	8	1.5	437	15	US-10-219-464-162	Sequence 162, App
298	8	1.5	437	15	US-10-123-908-466	Sequence 466, App	371	8	1.5	437	15	US-10-219-466-162	Sequence 162, App
299	8	1.5	437	15	US-10-124-813-466	Sequence 466, App	372	8	1.5	437	15	US-10-219-479-162	Sequence 162, App
300	8	1.5	437	15	US-10-124-817-466	Sequence 466, App	373	8	1.5	437	15	US-10-219-481-162	Sequence 162, App
301	8	1.5	437	15	US-10-125-922-466	Sequence 466, App	374	8	1.5	437	15	US-10-230-260-162	Sequence 162, App
302	8	1.5	437	15	US-10-125-924-466	Sequence 466, App	375	8	1.5	437	15	US-10-232-231-162	Sequence 162, App
303	8	1.5	437	15	US-10-140-860-466	Sequence 466, App	376	8	1.5	437	15	US-10-232-233-162	Sequence 162, App
304	8	1.5	437	15	US-10-142-417-466	Sequence 466, App	377	8	1.5	437	15	US-10-131-815A-466	Sequence 466, App
305	8	1.5	437	15	US-10-147-519-466	Sequence 466, App	378	8	1.5	437	15	US-10-131-817A-466	Sequence 466, App
306	8	1.5	437	15	US-10-157-782-466	Sequence 466, App	379	8	1.5	437	15	US-10-131-821A-466	Sequence 466, App
307	8	1.5	437	15	US-10-152-395-466	Sequence 466, App	380	8	1.5	437	15	US-10-131-822A-466	Sequence 466, App

381	8	1.5	437	15	US-10-131-828A-466	Sequence 466, App	454	8	1.5	437	16	US-10-146-727-466	Sequence 466, App
382	8	1.5	437	15	US-10-131-835A-466	Sequence 466, App	455	8	1.5	437	16	US-10-146-788-466	Sequence 466, App
383	8	1.5	437	15	US-10-137-864A-466	Sequence 466, App	456	8	1.5	437	16	US-10-152-380-466	Sequence 466, App
384	8	1.5	437	15	US-10-137-869A-466	Sequence 466, App	457	8	1.5	437	16	US-10-153-634-466	Sequence 466, App
385	8	1.5	437	15	US-10-147-523-466	Sequence 466, App	458	8	1.5	559	15	US-10-271-697-4	Sequence 24, App1
386	8	1.5	437	15	US-10-158-785-466	Sequence 466, App	459	8	1.5	616	11	US-09-946-574-24	Sequence 24, App1
387	8	1.5	437	15	US-10-121-051-466	Sequence 466, App	460	8	1.5	616	12	US-10-015-387-24	Sequence 24, App1
388	8	1.5	437	15	US-10-216-165-162	Sequence 162, App	461	8	1.5	616	12	US-10-006-130A-24	Sequence 24, App1
389	8	1.5	437	15	US-10-218-956-162	Sequence 162, App	462	8	1.5	616	12	US-10-199-672-158	Sequence 158, App
390	8	1.5	437	15	US-10-219-468-162	Sequence 162, App	463	8	1.5	616	12	US-10-006-172A-24	Sequence 24, App1
391	8	1.5	437	15	US-10-219-478-162	Sequence 162, App	464	8	1.5	616	12	US-10-187-749-158	Sequence 158, App
392	8	1.5	437	15	US-10-219-536-162	Sequence 162, App	465	8	1.5	616	12	US-10-184-657-158	Sequence 158, App
393	8	1.5	437	15	US-10-233-205-162	Sequence 162, App	466	8	1.5	616	12	US-10-194-452-158	Sequence 158, App
394	8	1.5	437	15	US-10-121-042-466	Sequence 466, App	467	8	1.5	616	12	US-10-196-747-158	Sequence 158, App
395	8	1.5	437	15	US-10-219-072-162	Sequence 162, App	468	8	1.5	616	12	US-10-015-392A-24	Sequence 24, App1
396	8	1.5	437	15	US-10-219-470-162	Sequence 162, App	469	8	1.5	616	12	US-10-017-253A-24	Sequence 24, App1
397	8	1.5	437	15	US-10-219-474-162	Sequence 162, App	470	8	1.5	616	12	US-10-173-689-158	Sequence 158, App
398	8	1.5	437	15	US-10-219-524-162	Sequence 162, App	471	8	1.5	616	12	US-10-173-690-158	Sequence 158, App
399	8	1.5	437	15	US-10-227-528-162	Sequence 162, App	472	8	1.5	616	12	US-10-173-691-158	Sequence 158, App
400	8	1.5	437	15	US-10-227-880-162	Sequence 162, App	473	8	1.5	616	12	US-10-173-692-158	Sequence 158, App
401	8	1.5	437	15	US-10-227-881-162	Sequence 162, App	474	8	1.5	616	12	US-10-173-694-158	Sequence 158, App
402	8	1.5	437	15	US-10-227-882-162	Sequence 162, App	475	8	1.5	616	12	US-10-173-698-158	Sequence 158, App
403	8	1.5	437	15	US-10-230-436-162	Sequence 162, App	476	8	1.5	616	12	US-10-173-699-158	Sequence 158, App
404	8	1.5	437	15	US-10-233-223-162	Sequence 162, App	477	8	1.5	616	12	US-10-173-707-158	Sequence 158, App
405	8	1.5	437	15	US-10-233-225-162	Sequence 162, App	478	8	1.5	616	12	US-10-174-569-158	Sequence 158, App
406	8	1.5	437	15	US-10-233-227-162	Sequence 162, App	479	8	1.5	616	12	US-10-174-583-158	Sequence 158, App
407	8	1.5	437	15	US-10-233-229-162	Sequence 162, App	480	8	1.5	616	12	US-10-174-587-158	Sequence 158, App
408	8	1.5	437	15	US-10-233-224-162	Sequence 162, App	481	8	1.5	616	12	US-10-174-589-158	Sequence 158, App
409	8	1.5	437	15	US-10-219-060-162	Sequence 162, App	482	8	1.5	616	12	US-10-175-591-158	Sequence 158, App
410	8	1.5	437	15	US-10-123-912-466	Sequence 466, App	483	8	1.5	616	12	US-10-175-736-158	Sequence 158, App
411	8	1.5	437	15	US-10-216-160-162	Sequence 162, App	484	8	1.5	616	12	US-10-175-742-158	Sequence 158, App
412	8	1.5	437	15	US-10-216-162-162	Sequence 162, App	485	8	1.5	616	12	US-10-175-744-158	Sequence 158, App
413	8	1.5	437	15	US-10-216-164-162	Sequence 162, App	486	8	1.5	616	12	US-10-175-745-158	Sequence 158, App
414	8	1.5	437	15	US-10-216-167-162	Sequence 162, App	487	8	1.5	616	12	US-10-175-748-158	Sequence 158, App
415	8	1.5	437	15	US-10-216-168-162	Sequence 162, App	488	8	1.5	616	12	US-10-175-751-158	Sequence 158, App
416	8	1.5	437	15	US-10-219-065-162	Sequence 162, App	489	8	1.5	616	12	US-10-175-754-158	Sequence 158, App
417	8	1.5	437	15	US-10-219-071-162	Sequence 162, App	490	8	1.5	616	12	US-10-176-480-158	Sequence 158, App
418	8	1.5	437	15	US-10-219-074-162	Sequence 162, App	491	8	1.5	616	12	US-10-176-489-158	Sequence 158, App
419	8	1.5	437	15	US-10-219-077-162	Sequence 162, App	492	8	1.5	616	12	US-10-176-754-158	Sequence 158, App
420	8	1.5	437	15	US-10-219-465-162	Sequence 162, App	493	8	1.5	616	12	US-10-176-755-158	Sequence 158, App
421	8	1.5	437	15	US-10-219-467-162	Sequence 162, App	494	8	1.5	616	12	US-10-176-759-158	Sequence 158, App
422	8	1.5	437	15	US-10-219-469-162	Sequence 162, App	495	8	1.5	616	12	US-10-176-920-158	Sequence 158, App
423	8	1.5	437	15	US-10-219-471-162	Sequence 162, App	496	8	1.5	616	12	US-10-176-922-158	Sequence 158, App
424	8	1.5	437	15	US-10-219-473-162	Sequence 162, App	497	8	1.5	616	12	US-10-176-924-158	Sequence 158, App
425	8	1.5	437	15	US-10-219-476-162	Sequence 162, App	498	8	1.5	616	12	US-10-176-984-158	Sequence 158, App
426	8	1.5	437	15	US-10-219-482-162	Sequence 162, App	499	8	1.5	616	12	US-10-179-508-158	Sequence 158, App
427	8	1.5	437	15	US-10-227-874-162	Sequence 162, App	500	8	1.5	616	12	US-10-179-512-158	Sequence 158, App
428	8	1.5	437	15	US-10-227-876-162	Sequence 162, App	501	8	1.5	616	12	US-10-179-515-158	Sequence 158, App
429	8	1.5	437	15	US-10-227-878-162	Sequence 162, App	502	8	1.5	616	12	US-10-017-306A-24	Sequence 24, App1
430	8	1.5	437	15	US-10-229-974-162	Sequence 162, App	503	8	1.5	616	12	US-10-173-702-158	Sequence 158, App
431	8	1.5	437	15	US-10-230-024-162	Sequence 162, App	504	8	1.5	616	12	US-10-173-703-158	Sequence 158, App
432	8	1.5	437	15	US-10-230-113-162	Sequence 162, App	505	8	1.5	616	12	US-10-173-704-158	Sequence 158, App
433	8	1.5	437	15	US-10-230-183-162	Sequence 162, App	506	8	1.5	616	12	US-10-174-574-158	Sequence 158, App
434	8	1.5	437	15	US-10-230-234-162	Sequence 162, App	507	8	1.5	616	12	US-10-176-486-158	Sequence 158, App
435	8	1.5	437	15	US-10-230-306-162	Sequence 162, App	508	8	1.5	616	12	US-10-176-490-158	Sequence 158, App
436	8	1.5	437	15	US-10-230-308-162	Sequence 162, App	509	8	1.5	616	12	US-10-176-752-158	Sequence 158, App
437	8	1.5	437	15	US-10-230-427-162	Sequence 162, App	510	8	1.5	616	12	US-10-176-981-158	Sequence 158, App
438	8	1.5	437	15	US-10-230-431-162	Sequence 162, App	511	8	1.5	616	12	US-10-176-983-158	Sequence 158, App
439	8	1.5	437	15	US-10-230-435-162	Sequence 162, App	512	8	1.5	616	12	US-10-176-988-158	Sequence 158, App
440	8	1.5	437	15	US-10-230-438-162	Sequence 162, App	513	8	1.5	616	12	US-10-179-517-158	Sequence 158, App
441	8	1.5	437	15	US-10-232-222-162	Sequence 162, App	514	8	1.5	616	12	US-10-179-521-158	Sequence 158, App
442	8	1.5	437	15	US-10-192-007-466	Sequence 466, App	515	8	1.5	616	12	US-10-012-064A-24	Sequence 24, App1
443	8	1.5	437	15	US-10-194-359-466	Sequence 466, App	516	8	1.5	616	12	US-10-017-667A-24	Sequence 24, App1
444	8	1.5	437	15	US-10-219-070-162	Sequence 162, App	517	8	1.5	616	12	US-10-202-475-158	Sequence 158, App
445	8	1.5	437	15	US-10-219-472-162	Sequence 162, App	518	8	1.5	616	14	US-10-032-586-158	Sequence 158, App
446	8	1.5	437	15	US-10-219-527-162	Sequence 162, App	519	8	1.5	616	15	US-10-174-590-158	Sequence 158, App
447	8	1.5	437	15	US-10-227-877-162	Sequence 162, App	520	8	1.5	616	15	US-10-176-758-158	Sequence 158, App
448	8	1.5	437	15	US-10-127-847A-466	Sequence 466, App	521	8	1.5	616	15	US-10-175-737-158	Sequence 158, App
449	8	1.5	437	15	US-10-216-166-162	Sequence 162, App	522	8	1.5	616	15	US-10-173-706-158	Sequence 158, App
450	8	1.5	437	15	US-10-218-612-162	Sequence 162, App	523	8	1.5	616	15	US-10-175-728-158	Sequence 158, App
451	8	1.5	437	15	US-10-175-590-466	Sequence 466, App	524	8	1.5	616	15	US-10-175-752-158	Sequence 158, App
452	8	1.5	437	16	US-10-137-866-466	Sequence 466, App	525	8	1.5	616	15	US-10-176-482-158	Sequence 158, App
453	8	1.5	437	16	US-10-146-726-466	Sequence 466, App	526	8	1.5	616	15	US-10-176-757-158	Sequence 158, App

527	8	1.5	616	15	US-10-176-913-158	Sequence 158, App	600	8	1.5	616	15	US-10-184-616-158	Sequence 158, App
528	8	1.5	616	15	US-10-180-552-158	Sequence 158, App	601	8	1.5	616	15	US-10-184-617-158	Sequence 158, App
529	8	1.5	616	15	US-10-180-557-158	Sequence 158, App	602	8	1.5	616	15	US-10-184-622-158	Sequence 158, App
530	8	1.5	616	15	US-10-173-700-158	Sequence 158, App	603	8	1.5	616	15	US-10-184-628-158	Sequence 158, App
531	8	1.5	616	15	US-10-174-572-158	Sequence 158, App	604	8	1.5	616	15	US-10-184-629-158	Sequence 158, App
532	8	1.5	616	15	US-10-174-579-158	Sequence 158, App	605	8	1.5	616	15	US-10-184-630-158	Sequence 158, App
533	8	1.5	616	15	US-10-174-582-158	Sequence 158, App	606	8	1.5	616	15	US-10-184-631-158	Sequence 158, App
534	8	1.5	616	15	US-10-174-588-158	Sequence 158, App	607	8	1.5	616	15	US-10-184-633-158	Sequence 158, App
535	8	1.5	616	15	US-10-175-739-158	Sequence 158, App	608	8	1.5	616	15	US-10-184-636-158	Sequence 158, App
536	8	1.5	616	15	US-10-175-740-158	Sequence 158, App	609	8	1.5	616	15	US-10-184-640-158	Sequence 158, App
537	8	1.5	616	15	US-10-175-743-158	Sequence 158, App	610	8	1.5	616	15	US-10-184-650-158	Sequence 158, App
538	8	1.5	616	15	US-10-176-488-158	Sequence 158, App	611	8	1.5	616	15	US-10-184-653-158	Sequence 158, App
539	8	1.5	616	15	US-10-176-492-158	Sequence 158, App	612	8	1.5	616	15	US-10-187-588-158	Sequence 158, App
540	8	1.5	616	15	US-10-176-747-158	Sequence 158, App	613	8	1.5	616	15	US-10-187-597-158	Sequence 158, App
541	8	1.5	616	15	US-10-176-750-158	Sequence 158, App	614	8	1.5	616	15	US-10-187-599-158	Sequence 158, App
542	8	1.5	616	15	US-10-176-985-158	Sequence 158, App	615	8	1.5	616	15	US-10-187-743-158	Sequence 158, App
543	8	1.5	616	15	US-10-176-987-158	Sequence 158, App	616	8	1.5	616	15	US-10-187-746-158	Sequence 158, App
544	8	1.5	616	15	US-10-176-992-158	Sequence 158, App	617	8	1.5	616	15	US-10-187-601-158	Sequence 158, App
545	8	1.5	616	15	US-10-176-993-158	Sequence 158, App	618	8	1.5	616	15	US-10-187-603-158	Sequence 158, App
546	8	1.5	616	15	US-10-184-658-158	Sequence 158, App	619	8	1.5	616	15	US-10-187-741-158	Sequence 158, App
547	8	1.5	616	15	US-10-176-991-158	Sequence 158, App	620	8	1.5	616	15	US-10-187-743-158	Sequence 158, App
548	8	1.5	616	15	US-10-173-695-158	Sequence 158, App	621	8	1.5	616	15	US-10-187-746-158	Sequence 158, App
549	8	1.5	616	15	US-10-173-697-158	Sequence 158, App	622	8	1.5	616	15	US-10-187-747-158	Sequence 158, App
550	8	1.5	616	15	US-10-173-705-158	Sequence 158, App	623	8	1.5	616	15	US-10-187-753-158	Sequence 158, App
551	8	1.5	616	15	US-10-174-576-158	Sequence 158, App	624	8	1.5	616	15	US-10-187-753-158	Sequence 158, App
552	8	1.5	616	15	US-10-174-585-158	Sequence 158, App	625	8	1.5	616	15	US-10-187-754-158	Sequence 158, App
553	8	1.5	616	15	US-10-174-586-158	Sequence 158, App	626	8	1.5	616	15	US-10-187-757-158	Sequence 158, App
554	8	1.5	616	15	US-10-175-747-158	Sequence 158, App	627	8	1.5	616	15	US-10-187-748-158	Sequence 158, App
555	8	1.5	616	15	US-10-176-481-158	Sequence 158, App	628	8	1.5	616	15	US-10-188-767-158	Sequence 158, App
556	8	1.5	616	15	US-10-176-485-158	Sequence 158, App	629	8	1.5	616	15	US-10-188-769-158	Sequence 158, App
557	8	1.5	616	15	US-10-176-487-158	Sequence 158, App	630	8	1.5	616	15	US-10-188-770-158	Sequence 158, App
558	8	1.5	616	15	US-10-176-493-158	Sequence 158, App	631	8	1.5	616	15	US-10-188-773-158	Sequence 158, App
559	8	1.5	616	15	US-10-176-756-158	Sequence 158, App	632	8	1.5	616	15	US-10-188-781-158	Sequence 158, App
560	8	1.5	616	15	US-10-176-911-158	Sequence 158, App	633	8	1.5	616	15	US-10-194-361-158	Sequence 158, App
561	8	1.5	616	15	US-10-176-919-158	Sequence 158, App	634	8	1.5	616	15	US-10-194-423-158	Sequence 158, App
562	8	1.5	616	15	US-10-176-925-158	Sequence 158, App	635	8	1.5	616	15	US-10-195-897-158	Sequence 158, App
563	8	1.5	616	15	US-10-176-978-158	Sequence 158, App	636	8	1.5	616	15	US-10-195-901-158	Sequence 158, App
564	8	1.5	616	15	US-10-179-510-158	Sequence 158, App	637	8	1.5	616	15	US-10-195-902-158	Sequence 158, App
565	8	1.5	616	15	US-10-180-543-158	Sequence 158, App	638	8	1.5	616	15	US-10-196-742-158	Sequence 158, App
566	8	1.5	616	15	US-10-180-544-158	Sequence 158, App	639	8	1.5	616	15	US-10-196-760-158	Sequence 158, App
567	8	1.5	616	15	US-10-180-546-158	Sequence 158, App	640	8	1.5	616	15	US-10-173-708-158	Sequence 158, App
568	8	1.5	616	15	US-10-180-547-158	Sequence 158, App	641	8	1.5	616	15	US-10-176-479-158	Sequence 158, App
569	8	1.5	616	15	US-10-180-549-158	Sequence 158, App	642	8	1.5	616	15	US-10-176-748-158	Sequence 158, App
570	8	1.5	616	15	US-10-180-555-158	Sequence 158, App	643	8	1.5	616	15	US-10-176-916-158	Sequence 158, App
571	8	1.5	616	15	US-10-180-559-158	Sequence 158, App	644	8	1.5	616	15	US-10-179-507-158	Sequence 158, App
572	8	1.5	616	15	US-10-181-000-158	Sequence 158, App	645	8	1.5	616	15	US-10-179-516-158	Sequence 158, App
573	8	1.5	616	15	US-10-183-010-158	Sequence 158, App	646	8	1.5	616	15	US-10-179-518-158	Sequence 158, App
574	8	1.5	616	15	US-10-183-012-158	Sequence 158, App	647	8	1.5	616	15	US-10-179-525-158	Sequence 158, App
575	8	1.5	616	15	US-10-184-614-158	Sequence 158, App	648	8	1.5	616	15	US-10-180-540-158	Sequence 158, App
576	8	1.5	616	15	US-10-184-623-158	Sequence 158, App	649	8	1.5	616	15	US-10-180-545-158	Sequence 158, App
577	8	1.5	616	15	US-10-184-635-158	Sequence 158, App	650	8	1.5	616	15	US-10-183-006-158	Sequence 158, App
578	8	1.5	616	15	US-10-184-637-158	Sequence 158, App	651	8	1.5	616	15	US-10-183-008-158	Sequence 158, App
579	8	1.5	616	15	US-10-184-646-158	Sequence 158, App	652	8	1.5	616	15	US-10-183-017-158	Sequence 158, App
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581	8	1.5	616	15	US-10-184-652-158	Sequence 158, App	654	8	1.5	616	15	US-10-184-628-158	Sequence 158, App
582	8	1.5	616	15	US-10-187-594-158	Sequence 158, App	655	8	1.5	616	15	US-10-184-628-158	Sequence 158, App
583	8	1.5	616	15	US-10-187-596-158	Sequence 158, App	656	8	1.5	616	15	US-10-184-628-158	Sequence 158, App
584	8	1.5	616	15	US-10-187-745-158	Sequence 158, App	657	8	1.5	616	15	US-10-184-627-158	Sequence 158, App
585	8	1.5	616	15	US-10-187-885-158	Sequence 158, App	658	8	1.5	616	15	US-10-184-644-158	Sequence 158, App
586	8	1.5	616	15	US-10-187-886-158	Sequence 158, App	659	8	1.5	616	15	US-10-184-654-158	Sequence 158, App
587	8	1.5	616	15	US-10-189-464-158	Sequence 158, App	660	8	1.5	616	15	US-10-184-655-158	Sequence 158, App
588	8	1.5	616	15	US-10-196-756-158	Sequence 158, App	661	8	1.5	616	15	US-10-188-774-158	Sequence 158, App
589	8	1.5	616	15	US-10-176-751-158	Sequence 158, App	662	8	1.5	616	15	US-10-188-775-158	Sequence 158, App
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591	8	1.5	616	15	US-10-176-990-158	Sequence 158, App	664	8	1.5	616	15	US-10-196-746-158	Sequence 158, App
592	8	1.5	616	15	US-10-180-541-158	Sequence 158, App	665	8	1.5	616	15	US-10-196-762-158	Sequence 158, App
593	8	1.5	616	15	US-10-180-542-158	Sequence 158, App	666	8	1.5	616	15	US-10-197-695-158	Sequence 158, App
594	8	1.5	616	15	US-10-180-548-158	Sequence 158, App	667	8	1.5	616	15	US-10-195-894-158	Sequence 158, App
595	8	1.5	616	15	US-10-180-551-158	Sequence 158, App	668	8	1.5	616	15	US-10-006-856A-24	Sequence 24, App1
596	8	1.5	616	15	US-10-180-551-158	Sequence 158, App	669	8	1.5	616	15	US-10-176-484-158	Sequence 158, App
597	8	1.5	616	15	US-10-180-998-158	Sequence 158, App	670	8	1.5	616	15	US-10-176-753-158	Sequence 158, App
598	8	1.5	616	15	US-10-183-013-158	Sequence 158, App	671	8	1.5	616	15	US-10-176-917-158	Sequence 158, App
599	8	1.5	616	15	US-10-184-612-158	Sequence 158, App	672	8	1.5	616	15	US-10-176-988-158	Sequence 158, App

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674	8	1.5	616	15	US-10-179-513-158	Sequence 158, App	747	8	1.5	616	15	US-10-139-313-158	Sequence 158, App
675	8	1.5	616	15	US-10-179-514-158	Sequence 158, App	748	8	1.5	616	15	US-10-139-458-158	Sequence 158, App
676	8	1.5	616	15	US-10-179-522-158	Sequence 158, App	749	8	1.5	616	15	US-10-139-462-158	Sequence 158, App
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681	8	1.5	616	15	US-10-184-620-158	Sequence 158, App	754	8	1.5	616	15	US-10-201-530-158	Sequence 158, App
682	8	1.5	616	15	US-10-184-643-158	Sequence 158, App	755	8	1.5	616	15	US-10-202-408-158	Sequence 158, App
683	8	1.5	616	15	US-10-184-656-158	Sequence 158, App	756	8	1.5	616	15	US-10-202-409-158	Sequence 158, App
684	8	1.5	616	15	US-10-192-010-158	Sequence 158, App	757	8	1.5	616	15	US-10-202-409-158	Sequence 158, App
685	8	1.5	616	15	US-10-205-908-158	Sequence 158, App	758	8	1.5	616	15	US-10-202-411-158	Sequence 158, App
686	8	1.5	616	15	US-10-186-855-158	Sequence 158, App	759	8	1.5	616	15	US-10-202-472-158	Sequence 158, App
687	8	1.5	616	15	US-10-184-619-158	Sequence 158, App	760	8	1.5	616	15	US-10-205-502-158	Sequence 158, App
688	8	1.5	616	15	US-10-187-599-158	Sequence 158, App	761	8	1.5	616	15	US-10-205-507-158	Sequence 158, App
689	8	1.5	616	15	US-10-187-750-158	Sequence 158, App	762	8	1.5	616	15	US-10-205-511-158	Sequence 158, App
690	8	1.5	616	15	US-10-188-780-158	Sequence 158, App	763	8	1.5	616	15	US-10-205-902-158	Sequence 158, App
691	8	1.5	616	15	US-10-192-015-158	Sequence 158, App	764	8	1.5	616	15	US-10-205-907-158	Sequence 158, App
692	8	1.5	616	15	US-10-194-394-158	Sequence 158, App	765	8	1.5	616	15	US-10-194-466-158	Sequence 158, App
693	8	1.5	616	15	US-10-194-425-158	Sequence 158, App	766	8	1.5	616	15	US-10-186-758-158	Sequence 158, App
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695	8	1.5	616	15	US-10-195-885-158	Sequence 158, App	768	8	1.5	616	15	US-10-199-308-158	Sequence 158, App
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697	8	1.5	616	15	US-10-196-748-158	Sequence 158, App	770	8	1.5	616	15	US-10-205-893-158	Sequence 158, App
698	8	1.5	616	15	US-10-196-750-158	Sequence 158, App	771	8	1.5	616	15	US-10-205-897-158	Sequence 158, App
699	8	1.5	616	15	US-10-197-699-158	Sequence 158, App	772	8	1.5	616	15	US-10-196-754-158	Sequence 158, App
700	8	1.5	616	15	US-10-197-700-158	Sequence 158, App	773	8	1.5	616	15	US-10-174-571-158	Sequence 158, App
701	8	1.5	616	15	US-10-197-705-158	Sequence 158, App	774	8	1.5	616	15	US-10-176-746-158	Sequence 158, App
702	8	1.5	616	15	US-10-197-708-158	Sequence 158, App	775	8	1.5	616	15	US-10-176-923-158	Sequence 158, App
703	8	1.5	616	15	US-10-198-764-158	Sequence 158, App	776	8	1.5	616	15	US-10-183-011-158	Sequence 158, App
704	8	1.5	616	15	US-10-198-764-158	Sequence 158, App	777	8	1.5	616	15	US-10-184-633-158	Sequence 158, App
705	8	1.5	616	15	US-10-198-765-158	Sequence 158, App	778	8	1.5	616	15	US-10-184-639-158	Sequence 158, App
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707	8	1.5	616	15	US-10-198-769-158	Sequence 158, App	780	8	1.5	616	15	US-10-187-748-158	Sequence 158, App
708	8	1.5	616	15	US-10-199-305-158	Sequence 158, App	781	8	1.5	616	15	US-10-188-766-158	Sequence 158, App
709	8	1.5	616	15	US-10-199-306-158	Sequence 158, App	782	8	1.5	616	15	US-10-188-771-158	Sequence 158, App
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711	8	1.5	616	15	US-10-199-311-158	Sequence 158, App	784	8	1.5	616	15	US-10-192-008-158	Sequence 158, App
712	8	1.5	616	15	US-10-199-317-158	Sequence 158, App	785	8	1.5	616	15	US-10-192-009-158	Sequence 158, App
713	8	1.5	616	15	US-10-199-665-158	Sequence 158, App	786	8	1.5	616	15	US-10-192-012-158	Sequence 158, App
714	8	1.5	616	15	US-10-199-666-158	Sequence 158, App	787	8	1.5	616	15	US-10-192-014-158	Sequence 158, App
715	8	1.5	616	15	US-10-199-669-158	Sequence 158, App	788	8	1.5	616	15	US-10-193-016-158	Sequence 158, App
716	8	1.5	616	15	US-10-201-534-158	Sequence 158, App	789	8	1.5	616	15	US-10-194-362-158	Sequence 158, App
717	8	1.5	616	15	US-10-201-770-158	Sequence 158, App	790	8	1.5	616	15	US-10-194-364-158	Sequence 158, App
718	8	1.5	616	15	US-10-201-855-158	Sequence 158, App	791	8	1.5	616	15	US-10-194-424-158	Sequence 158, App
719	8	1.5	616	15	US-10-201-856-158	Sequence 158, App	792	8	1.5	616	15	US-10-194-448-158	Sequence 158, App
720	8	1.5	616	15	US-10-202-469-158	Sequence 158, App	793	8	1.5	616	15	US-10-194-459-158	Sequence 158, App
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722	8	1.5	616	15	US-10-202-476-158	Sequence 158, App	795	8	1.5	616	15	US-10-194-486-158	Sequence 158, App
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724	8	1.5	616	15	US-10-202-935-158	Sequence 158, App	797	8	1.5	616	15	US-10-195-891-158	Sequence 158, App
725	8	1.5	616	15	US-10-202-936-158	Sequence 158, App	798	8	1.5	616	15	US-10-196-746-158	Sequence 158, App
726	8	1.5	616	15	US-10-202-939-158	Sequence 158, App	799	8	1.5	616	15	US-10-196-752-158	Sequence 158, App
727	8	1.5	616	15	US-10-205-504-158	Sequence 158, App	800	8	1.5	616	15	US-10-196-761-158	Sequence 158, App
728	8	1.5	616	15	US-10-205-509-158	Sequence 158, App	801	8	1.5	616	15	US-10-197-692-158	Sequence 158, App
729	8	1.5	616	15	US-10-205-895-158	Sequence 158, App	802	8	1.5	616	15	US-10-197-693-158	Sequence 158, App
730	8	1.5	616	15	US-10-205-899-158	Sequence 158, App	803	8	1.5	616	15	US-10-197-751-158	Sequence 158, App
731	8	1.5	616	15	US-10-205-900-158	Sequence 158, App	804	8	1.5	616	15	US-10-197-703-158	Sequence 158, App
732	8	1.5	616	15	US-10-205-909-158	Sequence 158, App	805	8	1.5	616	15	US-10-197-703-158	Sequence 158, App
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735	8	1.5	616	15	US-10-183-002-158	Sequence 158, App	808	8	1.5	616	15	US-10-198-751-158	Sequence 158, App
736	8	1.5	616	15	US-10-184-621-158	Sequence 158, App	809	8	1.5	616	15	US-10-198-762-158	Sequence 158, App
737	8	1.5	616	15	US-10-184-638-158	Sequence 158, App	810	8	1.5	616	15	US-10-198-763-158	Sequence 158, App
738	8	1.5	616	15	US-10-187-752-158	Sequence 158, App	811	8	1.5	616	15	US-10-198-763-158	Sequence 158, App
739	8	1.5	616	15	US-10-187-887-158	Sequence 158, App	812	8	1.5	616	15	US-10-198-767-158	Sequence 158, App
740	8	1.5	616	15	US-10-194-461-158	Sequence 158, App	813	8	1.5	616	15	US-10-199-301-158	Sequence 158, App
741	8	1.5	616	15	US-10-195-892-158	Sequence 158, App	814	8	1.5	616	15	US-10-199-307-158	Sequence 158, App
742	8	1.5	616	15	US-10-196-751-158	Sequence 158, App	815	8	1.5	616	15	US-10-199-312-158	Sequence 158, App
743	8	1.5	616	15	US-10-197-694-158	Sequence 158, App	816	8	1.5	616	15	US-10-199-315-158	Sequence 158, App
744	8	1.5	616	15	US-10-197-697-158	Sequence 158, App	817	8	1.5	616	15	US-10-199-316-158	Sequence 158, App
745	8	1.5	616	15	US-10-197-707-158	Sequence 158, App	818	8	1.5	616	15	US-10-199-457-158	Sequence 158, App

819	8	1.5	616	15	US-10-199-459-158	Sequence 158, App	892	8	1.5	616	15	US-10-205-904-158	Sequence 158, App
820	8	1.5	616	15	US-10-199-460-158	Sequence 158, App	893	8	1.5	616	15	US-10-175-553-158	Sequence 158, App
821	8	1.5	616	15	US-10-199-461-158	Sequence 158, App	894	8	1.5	616	15	US-10-180-553-158	Sequence 158, App
822	8	1.5	616	15	US-10-199-667-158	Sequence 158, App	895	8	1.5	616	15	US-10-201-327-158	Sequence 158, App
823	8	1.5	616	15	US-10-199-673-158	Sequence 158, App	896	8	1.5	616	15	US-10-121-062-158	Sequence 158, App
824	8	1.5	616	15	US-10-201-921-158	Sequence 158, App	897	8	1.5	616	15	US-10-006-116A-24	Sequence 24, App1
825	8	1.5	616	15	US-10-201-922-158	Sequence 158, App	898	8	1.5	616	15	US-10-017-527A-24	Sequence 24, App1
826	8	1.5	616	15	US-10-201-926-158	Sequence 158, App	899	8	1.5	616	15	US-10-183-003-158	Sequence 158, App
827	8	1.5	616	15	US-10-201-532-158	Sequence 158, App	900	8	1.5	616	15	US-10-183-006-158	Sequence 158, App
828	8	1.5	616	15	US-10-201-533-158	Sequence 158, App	901	8	1.5	616	15	US-10-173-696-158	Sequence 158, App
829	8	1.5	616	15	US-10-201-535-158	Sequence 158, App	902	8	1.5	616	15	US-10-125-923A-158	Sequence 158, App
830	8	1.5	616	15	US-10-201-769-158	Sequence 158, App	903	8	1.5	616	15	US-10-101-913A-24	Sequence 24, App1
831	8	1.5	616	15	US-10-201-771-158	Sequence 158, App	904	8	1.5	616	15	US-10-125-923A-158	Sequence 158, App
832	8	1.5	616	15	US-10-202-410-158	Sequence 158, App	905	8	1.5	616	15	US-10-176-491-158	Sequence 158, App
833	8	1.5	616	15	US-10-202-410-158	Sequence 158, App	906	8	1.5	616	15	US-10-176-491-158	Sequence 158, App
834	8	1.5	616	15	US-10-202-473-158	Sequence 158, App	907	8	1.5	616	15	US-10-187-592-158	Sequence 158, App
835	8	1.5	616	15	US-10-202-474-158	Sequence 158, App	908	8	1.5	616	15	US-10-107-194A-24	Sequence 24, App1
836	8	1.5	616	15	US-10-205-503-158	Sequence 158, App	909	8	1.5	616	15	US-10-197-691-158	Sequence 158, App
837	8	1.5	616	15	US-10-205-512-158	Sequence 158, App	910	8	1.5	616	15	US-10-198-771-158	Sequence 158, App
838	8	1.5	616	15	US-10-205-512-158	Sequence 158, App	911	8	1.5	616	15	US-10-013-430A-24	Sequence 24, App1
839	8	1.5	616	15	US-10-205-894-158	Sequence 158, App	912	8	1.5	616	15	US-10-174-575A-158	Sequence 158, App
840	8	1.5	616	15	US-10-205-896-158	Sequence 158, App	913	8	1.5	616	15	US-10-179-520-158	Sequence 158, App
841	8	1.5	616	15	US-10-205-898-158	Sequence 158, App	914	8	1.5	616	15	US-10-201-325-158	Sequence 158, App
842	8	1.5	616	15	US-10-205-901-158	Sequence 158, App	915	8	1.5	616	15	US-10-202-941-158	Sequence 158, App
843	8	1.5	616	15	US-10-205-903-158	Sequence 158, App	916	8	1.5	616	15	US-10-202-941-158	Sequence 158, App
844	8	1.5	616	15	US-10-206-909-158	Sequence 158, App	917	8	1.5	616	15	US-10-011-671A-24	Sequence 24, App1
845	8	1.5	616	15	US-10-206-910-158	Sequence 158, App	918	8	1.5	616	15	US-10-012-755A-24	Sequence 24, App1
846	8	1.5	616	15	US-10-206-911-158	Sequence 158, App	919	8	1.5	616	15	US-10-015-386A-24	Sequence 24, App1
847	8	1.5	616	15	US-10-206-912-158	Sequence 158, App	920	8	1.5	616	15	US-10-179-526-158	Sequence 158, App
848	8	1.5	616	15	US-10-206-913-158	Sequence 158, App	921	8	1.5	616	15	US-10-173-701-158	Sequence 158, App
849	8	1.5	616	15	US-10-206-914-158	Sequence 158, App	922	8	1.5	616	15	US-10-179-511-158	Sequence 158, App
850	8	1.5	616	15	US-10-206-920-158	Sequence 158, App	923	8	1.5	616	15	US-10-179-511-158	Sequence 158, App
851	8	1.5	616	15	US-10-206-921-158	Sequence 158, App	924	8	1.5	616	15	US-10-183-018-158	Sequence 158, App
852	8	1.5	616	15	US-10-206-923-158	Sequence 158, App	925	8	1.5	616	15	US-10-184-624-158	Sequence 158, App
853	8	1.5	616	15	US-10-206-925-158	Sequence 158, App	926	8	1.5	616	15	US-10-184-657-158	Sequence 158, App
854	8	1.5	616	15	US-10-206-926-158	Sequence 158, App	927	8	1.5	616	15	US-10-197-701-158	Sequence 158, App
855	8	1.5	616	15	US-10-206-927-158	Sequence 158, App	928	8	1.5	616	15	US-10-197-706-158	Sequence 158, App
856	8	1.5	616	15	US-10-207-916-158	Sequence 158, App	929	8	1.5	616	15	US-10-201-857-158	Sequence 158, App
857	8	1.5	616	15	US-10-207-917-158	Sequence 158, App	930	8	1.5	616	15	US-10-202-413-158	Sequence 158, App
858	8	1.5	616	15	US-10-207-918-158	Sequence 158, App	931	8	1.5	616	15	US-10-202-938-158	Sequence 158, App
859	8	1.5	616	15	US-10-207-919-158	Sequence 158, App	932	8	1.5	616	15	US-10-202-940-158	Sequence 158, App
860	8	1.5	616	15	US-10-207-920-158	Sequence 158, App	933	8	1.5	616	15	US-10-205-508-158	Sequence 158, App
861	8	1.5	616	15	US-10-207-925-158	Sequence 158, App	934	8	1.5	616	15	US-10-205-905-158	Sequence 158, App
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966 7 1.3 137 9 US-09-739-254-163 Sequence 163, App
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971 7 1.3 148 9 US-09-864-761-46739 Sequence 46739, A
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977 7 1.3 193 9 US-09-815-242-4983 Sequence 4983, Ap
978 7 1.3 197 9 US-09-944-277A-11 Sequence 11, Appl
979 7 1.3 216 12 US-09-933-767-1044 Sequence 1044, Ap
980 7 1.3 216 15 US-10-023-282-1044 Sequence 1044, Ap
981 7 1.3 221 15 US-10-156-761-13675 Sequence 13675, A
982 7 1.3 222 11 US-09-986-480-330 Sequence 330, App
983 7 1.3 232 9 US-09-944-277A-6 Sequence 6, Appl
984 7 1.3 240 15 US-10-156-761-9337 Sequence 9337, Ap
985 7 1.3 247 15 US-10-128-714-3316 Sequence 3316, Ap
986 7 1.3 256 10 US-09-738-626-6299 Sequence 6299, Ap
987 7 1.3 257 9 US-09-944-277A-2 Sequence 2, Appl
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989 7 1.3 257 12 US-10-384-850-45 Sequence 45, Appl
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991 7 1.3 271 10 US-09-479-040-2316 Sequence 23, Appl
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995 7 1.3 324 15 US-10-288-985-19 Sequence 19, Appl
996 7 1.3 324 15 US-10-289-980-19 Sequence 19, Appl
997 7 1.3 377 14 US-10-091-628-2 Sequence 2, Appl
998 7 1.3 424 15 US-10-127-032-94 Sequence 94, Appl
999 7 1.3 426 15 US-10-156-761-8581 Sequence 8581, Ap
1000 7 1.3 428 15 US-10-156-761-12746 Sequence 12746, A

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ALIGNMENTS

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RESULT 1
US-10-156-761-10882
; Sequence 10882, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10882
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10882

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RESULT 2
US-10-156-424A-13
; Sequence 13, Application US/10156424A
; Publication No. US20030039999A1
; GENERAL INFORMATION:
; APPLICANT: Yoshinaga, Steve Kiyoshi
; APPLICANT: Sun, Woong-Kyung
; APPLICANT: Mak, Tak W.
; TITLE OF INVENTION: B7 Related Protein-2 Molecules and Uses Thereof
; FILE REFERENCE: 01-384-A
; CURRENT APPLICATION NUMBER: US/10/156,424A
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,629
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Grus americana
US-10-156-424A-13

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RESULT 3
US-09-950-933A-70
; Sequence 70, Application US/09950933A
; Patent No. US20020166141A1
; GENERAL INFORMATION:
; APPLICANT: Simmonds, Carl R.
; APPLICANT: Navarro, Pedro
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/238472
; CURRENT APPLICATION NUMBER: US/09/950,933A
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Glycine max
US-09-950-933A-70

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Query Match 1.5%; Score 8; DB 10; Length 106;
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466 VLLVLLALL 473

9 VLLVLLALL 16

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RESULT 4
US-10-080-170-438
; Sequence 438, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

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;; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
;; FILE REFERENCE: TREATMENT OF MYCOBACTERIOSES
;; CURRENT APPLICATION NUMBER: US/10/080,170
;; PRIOR FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: 60/270,123
;; NUMBER OF SEQ ID NOS: 652
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 438
;; LENGTH: 200
;; TYPE: PRT
;; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-438

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Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 467 LLLALLGG 474
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Db 88 LLLALLGG 95

RESULT 5
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; Sequence 499, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.10
; SEQ ID NO 499
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-499

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Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEETP 386
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Db 136 GSLSEETP 143

RESULT 6
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; Sequence 5043, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03

;; NUMBER OF SEQ ID NOS: 8564
;; SOFTWARE: PatentIn Ver. 3.0
;; SEQ ID NO 5043
;; LENGTH: 255
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (242)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: MISC FEATURE
;; LOCATION: (249)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5043

Query Match 1.5%; Score 8; DB 15; Length 255;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLGG 473
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Db 6 VLLALLGG 13

RESULT 7
US-09-989-722-355
; Sequence 355, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bostein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottlieb, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavitt, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25

;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR APPLICATION NUMBER: 60/091978
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 VLLALLG 11

RESULT 8
US-09-989-723-355
; Sequence 355, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyere, Luc
; APPLICANT: Bacon, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730162
; CURRENT APPLICATION NUMBER: US/09/989, 723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-02-25
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; PRIOR FILING DATE: 1998-05-07
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;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLG 473
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RESULT 9
US-09-989-279-355
Sequence 355, Application US/09989279
Patent No. US20020072496A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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Query Match 1.5%; Score 8; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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Sequence 355, Application US/09989727
Patent No. US2002072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C65
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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Query Match 1.5%; Score 8; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11

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; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bostein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989, 731
; PRIOR FILING DATE: 2001-11-20
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLLG 473
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Db 4 VLLALLLG 11

RESULT 12
US-09-989-732-355
Sequence 355, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730FIC57
CURRENT FILING DATE: 2001-11-19
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
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Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      466 VLLALALG 473
DB      4 VLLALALG 11

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Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Godowski, Paul J.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC15
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PRIOR FILING DATE: 1998-07-09

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Query Match 1.5%; Score 8; DB 10; Length 437;
 Best Local Similarity 100.0%; Pred.No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLIG 473
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Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.

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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PICB
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALALG 473
Db 4 VLLALALG 11

RESULT 15

US-09-391-163-355
Sequence 355: Application US/09991163
Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC17
CURRENT APPLICATION NUMBER: us/09/991.163
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-09

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Qy 466 VLLALALG 473
Db 4 VLLALALG 11

RESULT 16
US-09-993-604-355
Sequence 355, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC25
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US/09/993,604
PRIOR FILING DATE: 1997-06-16

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PRIOR FILING DATE: 1998-07-09

Query Match      1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      466 VLLALLG 473
DB      4 VLLALLG 11

RESULT 17
US-09-990-456-355
Sequence 355, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaevin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C22
CURRENT APPLICATION NUMBER: US/09/990,456
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-09

Query March 1.5%; Score 8; DB 10; Length 437;
Best local similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4 VLLALLG 11

RESULT 18
US-09-989-721-355
Sequence 355, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auebin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C55
CURRENT APPLICATION NUMBER: US/09/989,721
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match .1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLG 473
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RESULT 19

US-09-992-598-355
Sequence 355, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eacon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C20
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CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 466 VLLIALLG 473
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RESULT 20
US-09-989-293A-355
Sequence 355, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Ealon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerder, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C6
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/09/989, 293A
PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLIALLG 473
DB 4 VLLIALLG 11

RESULT 21
US-09-989-735-355
Sequence 355, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Aekhenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 22
US-09-990-444-355
Sequence 355, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyere, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-06-24
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 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VILLALIG 473
 DB 4 VILLALLG 11

RESULT 23
 US-09-991-181-355
 ; Sequence 355, Application US/09991181
 ; Publication No. US20020197615A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC53
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR FILING DATE: 1998-07-09

Query Match      1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      466 VLLALLG 473
DB      4 VLLALLG 11

RESULT 24
US-09-989-730-355
; Sequence 355, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C69
; CURRENT APPLICATION NUMBER: US/09/989,730
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALALG 473
Db 4 VLLALALG 11

RESULT 25
US-09-990-436-355
;; Publication No. US20020198148A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnuyers, Luc
;; APPLICANT: Batou, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerlitsen, Mary E.
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;; APPLICANT: Pan, James
;; APPLICANT: Pao, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Matanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P.C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 26
US-09-993-687-355
Sequence 355, Application US/09993687
Publication No. US20020198149A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bockstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993,687

CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
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PRIOR APPLICATION NUMBER: 60/089653
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PRIOR APPLICATION NUMBER: 60/091360
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PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLG 473
DB 4 VLLALLG 11

RESULT 27
US-09-989-734-355
Sequence 355, Application US/09989734
Publication No. US20030003531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Boctstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC64
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,734
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12

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PRIOR APPLICATION NUMBER: 60/091478
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 28
US-09-997-653-355
Sequence 355, Application US/09997653
Publication No. US20030008297A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurley, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997, 653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626

PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALGL 473
Db 4 VLLALGL 11

RESULT 29
US-09-993-667-355
Sequence 355, Application US/09993667
Publication No. US2003002187A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730Pic4
CURRENT APPLICATION NUMBER: US/09/993.667
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28

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12	PRIOR FILING DATE: 1998-06-04
13	PRIOR APPLICATION NUMBER: 60/088026
14	PRIOR FILING DATE: 1998-06-04
15	PRIOR APPLICATION NUMBER: 60/088028
16	PRIOR FILING DATE: 1998-06-04
17	PRIOR APPLICATION NUMBER: 60/088029
18	PRIOR FILING DATE: 1998-06-04
19	PRIOR APPLICATION NUMBER: 60/088030
20	PRIOR FILING DATE: 1998-06-04
21	PRIOR APPLICATION NUMBER: 60/088033
22	PRIOR FILING DATE: 1998-06-04
23	PRIOR APPLICATION NUMBER: 60/088326
24	PRIOR FILING DATE: 1998-06-04
25	PRIOR APPLICATION NUMBER: 60/088167
26	PRIOR FILING DATE: 1998-06-05
27	PRIOR APPLICATION NUMBER: 60/088202
28	PRIOR FILING DATE: 1998-06-05
29	PRIOR APPLICATION NUMBER: 60/088212
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33	PRIOR APPLICATION NUMBER: 60/088655
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47	PRIOR APPLICATION NUMBER: 60/088858
48	PRIOR FILING DATE: 1998-06-11
49	PRIOR APPLICATION NUMBER: 60/088861
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51	PRIOR APPLICATION NUMBER: 60/088876
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63	PRIOR APPLICATION NUMBER: 60/089538
64	PRIOR FILING DATE: 1998-06-17
65	PRIOR APPLICATION NUMBER: 60/089598
66	PRIOR FILING DATE: 1998-06-17
67	PRIOR APPLICATION NUMBER: 60/089599
68	PRIOR FILING DATE: 1998-06-17
69	PRIOR APPLICATION NUMBER: 60/089600
70	PRIOR FILING DATE: 1998-06-17
71	PRIOR APPLICATION NUMBER: 60/089653
72	PRIOR FILING DATE: 1998-06-17
73	PRIOR APPLICATION NUMBER: 60/089801

1	PRIOR FILING DATE: 1998-06-18
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3	PRIOR FILING DATE: 1998-06-18
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5	PRIOR FILING DATE: 1998-06-18
6	PRIOR APPLICATION NUMBER: 60/089947
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12	PRIOR APPLICATION NUMBER: 60/090246
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25	PRIOR FILING DATE: 1998-06-24
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28	PRIOR APPLICATION NUMBER: 60/090444
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31	PRIOR FILING DATE: 1998-06-24
32	PRIOR APPLICATION NUMBER: 60/090472
33	PRIOR FILING DATE: 1998-06-24
34	PRIOR APPLICATION NUMBER: 60/090535
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52	PRIOR APPLICATION NUMBER: 60/090696
53	PRIOR FILING DATE: 1998-06-25
54	PRIOR APPLICATION NUMBER: 60/090682
55	PRIOR FILING DATE: 1998-06-26
56	PRIOR APPLICATION NUMBER: 60/090863
57	PRIOR FILING DATE: 1998-06-26
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61	PRIOR FILING DATE: 1998-07-02
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63	PRIOR FILING DATE: 1998-07-01
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66	PRIOR APPLICATION NUMBER: 60/091626
67	PRIOR FILING DATE: 1998-07-02
68	PRIOR APPLICATION NUMBER: 60/091633
69	PRIOR FILING DATE: 1998-07-02
70	PRIOR APPLICATION NUMBER: 60/091978
71	PRIOR FILING DATE: 1998-07-07
72	PRIOR APPLICATION NUMBER: 60/091982
73	PRIOR FILING DATE: 1998-07-07

;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLLG 473
Db 4 VLLALLLG 11

RESULT 30

US-09-997-428-355
;; Sequence 355, Application US/09997428
;; Publication No. US20030027162A1

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.

;; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David

;; APPLICANT: Desnoyers, Luc

;; APPLICANT: Eaton, Dan L.

;; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman

;; APPLICANT: Getber, Hanspeter

;; APPLICANT: Gerdsen, Mary E.

;; APPLICANT: Goddard, Audrey

;; APPLICANT: Grimaldi, Paul J.

;; APPLICANT: Gurney, Auerin L.

;; APPLICANT: Kljavin, Ivar J.

;; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James

;; APPLICANT: Paoni, Nicholas F.

;; APPLICANT: Roy, Margaret Ann

;; APPLICANT: Stewart, Timothy A.

;; APPLICANT: Tumas, Daniel

;; APPLICANT: Watanabe, Colin K.

;; APPLICANT: Williams, P. Mickey

;; APPLICANT: Wood, William I.

;; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; FILE REFERENCE: P2730PIC44

;; CURRENT APPLICATION NUMBER: US/09/997,428

;; PRIOR FILING DATE: 2001-11-15

;; PRIOR APPLICATION NUMBER: 60/049787

;; PRIOR FILING DATE: 1997-06-16

;; PRIOR APPLICATION NUMBER: 60/062250

;; PRIOR FILING DATE: 1997-10-17

;; PRIOR APPLICATION NUMBER: 60/065186

;; PRIOR FILING DATE: 1997-11-12

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;; PRIOR APPLICATION NUMBER: 60/066770

;; PRIOR FILING DATE: 1997-11-24

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;; PRIOR FILING DATE: 1998-02-25

;; PRIOR APPLICATION NUMBER: 60/078910

;; PRIOR FILING DATE: 1998-03-20

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;; PRIOR FILING DATE: 1998-05-28

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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLIG 473
DB 4 VLLALLIG 11
RESULT 31
US-09-997-666-355
Sequence 355, Application US/09997666
Publication No. US20030027163A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC42
CURRENT APPLICATION NUMBER: US/09/997,666
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLAG 473
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Db 4 VLLALLAG 11

RESULT 32
US-09-990-438-355

Sequence 355, Application US/09990438
Publication No. US20030027754A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guirney, Austin L.
APPLICANT: Kjaavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC3
CURRENT APPLICATION NUMBER: US/09/990,438
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-06-23

PRIOR APPLICATION NUMBER: 60/090429
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
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PRIOR APPLICATION NUMBER: 60/091633
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;

Best Local Similarity 100.0%; Pred. No. 41; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLG 473
|||||||
Db 4 VLLALLG 11

RESULT 33

US-09-990-562-355
Sequence 355, Application US/09990562
Publication No. US20030027985A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botschein, David
APPLICANT: Deemeyer, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C18
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US/09/990,562
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/088202
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PRIOR APPLICATION NUMBER: 60/088212
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PRIOR APPLICATION NUMBER: 60/088217
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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5% Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VILLALG 473
Db 4 VILLALG 11

RESULT 34
US-09-990-711-355
Sequence 355, Application US/09990711
Publication No. US20030032023A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auelin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C2
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-06-09
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090444
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090678
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PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
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PRIOR APPLICATION NUMBER: 60/090696
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PRIOR APPLICATION NUMBER: 60/090862
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VILLALLG 473
Db 4 VILLALLG 11

RESULT 35
US-09-989-726-355
Sequence 355, Application US/09989726
Publication No. US2003040473A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavyn, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
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PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676

PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLG 473
DB 4 VLLALLG 11

RESULT 36
US-09-998-156-355
Sequence 355, Application US/09998156
Publication No. US20030044806A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301PC28
CURRENT APPLICATION NUMBER: US/09/998,156
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
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PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25

Tue Oct 7 10:37:58 2003

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;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09
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Query Match 1.5%; Score 8; DB 11; Length 437;

Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 466 VLLALLG 473
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Db 4 VLLALLG 11
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RESULT 37

US-09-990-437-355
Sequence 355, Application US/09990437
Publication No. US20030045463A1

GENERAL INFORMATION:

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;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gottlieb, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Grimaldi, Paul J.
;; APPLICANT: Grimaldi, U. Christopher
;; APPLICANT: Gurney, Auelin L.
;; APPLICANT: Klavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumes, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C49
;; CURRENT APPLICATION NUMBER: US/09/990,437
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-06-11
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;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863

PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 38
US-09-991-157-355
Sequence 355, Application US/09991157
Publication No. US20030049638A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Aubelin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC51
CURRENT APPLICATION NUMBER: US/09/991,157
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/07594545	PRIOR FILING DATE: 1998-02-25	PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/087106	PRIOR FILING DATE: 1998-05-28	PRIOR APPLICATION NUMBER: 60/087607	PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087609	PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087759	PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087827	PRIOR FILING DATE: 1998-06-03	PRIOR APPLICATION NUMBER: 60/088021	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088025	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088026	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088030	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088033	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088326	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088157	PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088202	PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088212	PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088217	PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088655	PRIOR FILING DATE: 1998-06-09	PRIOR APPLICATION NUMBER: 60/088734	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088738	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088742	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088810	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088824	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088826	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088858	PRIOR FILING DATE: 1998-06-11	PRIOR APPLICATION NUMBER: 60/088861	PRIOR FILING DATE: 1998-06-11	PRIOR APPLICATION NUMBER: 60/088876	PRIOR FILING DATE: 1998-06-11	PRIOR APPLICATION NUMBER: 60/089105	PRIOR FILING DATE: 1998-06-12	PRIOR APPLICATION NUMBER: 60/089440	PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/089512	PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/089514	PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089538
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[illegible]


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; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      1.5%  Score 8;  DB 11;  Length 437;
Best Local Similarity 100.0%;  Fred. No. 41;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      466 VLLALLG 473
      |||||
Db      4 VLLALLG 11

RESULT 39
US-09-997-514-355
; Sequence 355, Application US/09997514
; Publication No. US20030049681A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, U. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P146
; CURRENT APPLICATION NUMBER: US/09/997,514
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR APPLICATION NUMBER: 60/087759
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; PRIOR APPLICATION NUMBER: 60/087827
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
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; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978

PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLIG 473
Db 4 VLLALLIG 11

RESULT 40
US-09-997-573-355
Sequence 355, Application US/09997573
Publication No. US20030049682A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C45
CURRENT APPLICATION NUMBER: US/09/997,573
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02

Query Match . 4.5%; Score 8; DB 11; Length 437;

Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLG 473
|||||
Db 4 VLLALLG 11

Search completed: October 2, 2003, 16:15:26
Job time : 80 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 2, 2003, 15:46:24 / Search time 104 Seconds
(without alignments)
1342.370 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 2922
Sequence: 1 MGLVGVQLLVLVADCTIFP.....EAEENIDQGETHWVEGDY 541

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacterioph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2922	100.0	541	5	015681 toxoplasma
2	434	14.9	622	5	094661 plasmodium
3	433	14.8	622	5	0967K3 plasmodium
4	432.5	14.8	592	5	025745 plasmodium
5	431	14.8	622	5	0967K2 plasmodium
6	431	14.8	622	5	096Z05 plasmodium
7	431	14.8	622	5	0967K1 plasmodium
8	426	14.6	622	5	0967J3 plasmodium
9	425	14.5	622	5	0967K0 plasmodium
10	422.5	14.4	558	5	025687 plasmodium
11	422	14.4	562	5	061130 plasmodium
12	420.5	14.4	555	5	026162 plasmodium
13	420.5	14.4	563	5	096413 plasmodium
14	419.5	14.4	604	5	025747 plasmodium
15	419	14.3	557	5	026225 plasmodium
16	419	14.3	622	5	096712 plasmodium

17	418	14.3	622	5	0967J4 plasmodium
18	416.5	14.3	555	5	026163 plasmodium
19	415.5	14.2	605	5	096F99 plasmodium
20	413	14.1	526	5	09N9C0 plasmodium
21	413	14.1	526	5	096738 plasmodium
22	413	14.1	622	5	096735 plasmodium
23	412.5	14.1	621	5	097Y48 plasmodium
24	412	14.1	557	5	026224 plasmodium
25	412	14.1	622	5	095N21 plasmodium
26	412	14.1	622	5	096739 plasmodium
27	410.5	14.0	620	5	000784 plasmodium
28	410	14.0	556	5	025657 plasmodium
29	410	14.0	622	5	095N02 plasmodium
30	410	14.0	622	5	096736 plasmodium
31	407	13.9	526	5	09N9E4 plasmodium
32	407	13.9	622	5	096737 plasmodium
33	406.5	13.9	605	5	096V27 plasmodium
34	406	13.9	622	5	096718 plasmodium
35	405	13.9	526	5	09N9E2 plasmodium
36	405	13.9	622	5	09N9E1 plasmodium
37	404	13.8	526	5	09N9F4 plasmodium
38	404	13.8	562	5	025667 plasmodium
39	404	13.8	622	5	096719 plasmodium
40	403	13.8	526	5	09N9E6 plasmodium
41	402	13.8	622	5	095N04 plasmodium
42	401	13.7	622	5	096732 plasmodium
43	400	13.7	526	5	09N9D9 plasmodium
44	398.5	13.6	592	5	025749 plasmodium
45	398.5	13.6	604	5	025746 plasmodium

ALIGNMENTS

RESULT 1

ID	015681	PRELIMINARY;	PRT;	541 AA.
AC	015681;			
DT	01-JAN-1998 (TREMUREL. 05, Created)			
DT	01-JAN-1998 (TREMUREL. 05, Last sequence update)			
DT	01-MAR-2003 (TREMUREL. 23, Last annotation update)			
DE	Apical membrane antigen 1 homolog.			
GN	AMA1G.			
OS	Toxoplasma gondii.			
OC	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;			
OC	Toxoplasma.			
OX	NCBI_TaxID=5811;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ME49;			
RX	MEDLINE=20516458; PubMed=11083833;			
RA	Hohl A.B., Lekutis C., Grigg M.E., Bradley P.J., Dubremetz J.F.,			
RA	Ortega-Barria E., Boothroyd J.C.,			
RT	"Toxoplasma gondii Homologue of Plasmodium Apical Membrane Antigen 1			
RT	is involved in invasion of Host Cells."			
RL	Infect. Immun. 68:7078-7086(2000).			
DR	EMBL; AF010264; AAB65410.1; -			
DR	InterPro; IPR003298; Apmem_Ag1.			
DR	Pfam; PF02430; AMA-1; 1.			
DR	PRINTS; PRO1361; MEROZOITESA.			
DR	SEQUENCE 541 AA; 59978 MW; DD38EF3A0F258E27 CRC64;			

Query Match 100.0%; Score 2922; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.2e-245; Indels 0; Gaps 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGLVGVQLLVLVADCTIFPAGLSSTRSRSQTLASSTGNPQAVNEMKTFERNLNT 60
Db	1	MGLVGVQLLVLVADCTIFPAGLSSTRSRSQTLASSTGNPQAVNEMKTFERNLNT 60
Qy	61	HHHOSGIYVDIGQKXVDGTLTYREPAGLCPIWGKHILOQPDRLPYRNNFLQEDVPTKEY 120
Db	61	HHHOSGIYVDIGQKXVDGTLTYREPAGLCPIWGKHILOQPDRLPYRNNFLQEDVPTKEY 120

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OY 121 KOSGNPLRGCFNLNFTVTSBGORISPPMELLEKNKNIKASTLDGRCAEFAFTVAMDKN 180
DB 121 KOSGNPLRGCFNLNFTVTSBGORISPPMELLEKNKNIKASTLDGRCAEFAFTVAMDKN 180
OY 181 KATKRRYPVYVSKKRLCHILLYVSMQLMGKKYCSVKGEPDPTWYCFKPKSTVENHNL 240
DB 181 KATKRRYPVYVSKKRLCHILLYVSMQLMGKKYCSVKGEPDPTWYCFKPKSTVENHNL 240
OY 241 IYGSAYVGENPDPAFISKCPNOLRGYRFGVWKKGRCCLDTYELTDVIERVESKACQWKT 300
DB 241 IYGSAYVGENPDPAFISKCPNOLRGYRFGVWKKGRCCLDTYELTDVIERVESKACQWKT 300
OY 301 FENDGVAASQPHPTPLTTSQASWMDWPHLQSDQPHSGGVRNYPFYVDTTGEKCALSD 360
DB 301 FENDGVAASQPHPTPLTTSQASWMDWPHLQSDQPHSGGVRNYPFYVDTTGEKCALSD 360
OY 361 QVPDCLVSDSAVSTYAGSLSEETPNFIIPSNPSVTPPTPTALQCTADKPPDSFGACD 420
DB 361 QVPDCLVSDSAVSTYAGSLSEETPNFIIPSNPSVTPPTPTALQCTADKPPDSFGACD 420
OY 421 VOACRROKTSVGVGOISTSVDTCTADBEQNECGSNTALLIAGLAVGVLLALLGGGCFYAK 480
DB 421 VOACRROKTSVGVGOISTSVDTCTADBEQNECGSNTALLIAGLAVGVLLALLGGGCFYAK 480
OY 481 RUDRKNQVAAHHEHFOSDRGAKRRKPSDLMQEAEPFWDDEAENIEDDGETHWVEGD 540
DB 481 RUDRKNQVAAHHEHFOSDRGAKRRKPSDLMQEAEPFWDDEAENIEDDGETHWVEGD 540
OY 541 Y 541
DB 541 Y 541

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RESULT 2

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OY 094661 PRELIMINARY; PRT; 622 AA.
AC 094661, Q25744;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Apical membrane antigen 1.
GN AMA-1 OR PPI1 0344.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_Taxid=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Tine J.A., Iannar D.E., Smith D.M., Wellde B.T., Schultzeis P.,
RA Ware L.A., Kaufman E.B., Wirtz R.A., de Taisne C., Hui G.S.N.,
RA Chang S.P., Church P., Hollingdale M.R., Kaslow D.C., Hoffman S.,
RA Guico K.P., Bailou W.R., Sadoff J.C., Paolletti E.;
RU Infect. Immun. 64:0-0(0).
RN [2]
RP SEQUENCE OF 9-604 FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=96379227; PubMed=8784778;
RA Marshall V.M., Zhang L.X., Anders R.F., Coppel R.L.;
RT "Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum";
RM Mol. Biochem. Parasitol. 77:109-113(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=2255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyse S.,
RA Chan M.-S., Nene V., Shallow S.J., Sun B., Peterson J., Angiuoli S.,
RA Pereira M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

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RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum";
RL Nature 419:498-511(2002).
DR EMBL; U65407; AAB36701.1;
DR EMBL; U33274; AAC47104.1;
DR EMBL; AE014841; AAN35928.1;
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1;
DR PRINTS; PRO1361; MERZOCTTESA.
SQ SEQUENCE 622 AA; 72041 MW; 60FE442074C38E94 CRC64;

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Query Match 14.9%; Score 434; DB 5; Length 622;
Best Local Similarity 26.4%; Pred. No. 6,6e-29;
Matches 150; Conservative 84; Mismatches 213; Indels 122; Gaps 24;

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OY 41 GNPFOANVEMKTFMERFNLTHHOSGIYVDIGQDEVDGTLYREBAGLCPTWKGHIELOQ 100
DB 107 GNPW-----TEYMAKYDIEEVHSGSIRVDIGDAEAVAGTQYRLPSGCKPFGKGIILEN 160
OY 101 PDRLPYRNPFLEDPTEKEYKQSGNPLRGCFNLNFTVTSBGORISPPME-----LLEKSN 156
DB 161 SN-----TTFLLTPVATGNQYLKD-----GGAF--PTEPLMBPMTLDENRHFYKDKY 207
OY 157 IKASTDLGRCAEFAFTVAMDKNNKATKRYRPFYVDSKKRLCHILLYVSMQLMGKKYCSV 216
DB 208 VKNDELFLCSRHAGNMT--PDNDKSNYKYPAYYDDKDKCHILLYIAQENNGRYCN- 264
OY 217 KGEPPDLTWYCFKPKKSTVENHNL IYGSAYVGEN- PDAFISKCPNOLRGYRFGVWKGR 275
DB 265 KDESERNMSFCFRPAKDISFONY-----TYLSKNVVDWMEKVCPRKNLQNNKAFGLMVDGN 319
OY 276 CLDTYELTD-VIERVESKACQWKT FENDGVAASQPHPTP--LTSQASWMDWMP----- 327
DB 320 CEDIPHNEFPALIDFE---CNKLVPFLS--ASDPQRYQOHLVDYKIEKGFNKRNAS 373
OY 328 -----LHSDQPHSGGVRNYPFYVDTTGEKCALSDQVPDCLVSDSAVSTYTA 377
DB 374 MKSAFELPTGAFCADRYSHGKYMGYNMETQ---KCELFNVKPTLLINSSVIATTA 430
OY 378 AGSLSEETPNFIIPSN-----PSYTPPTPTPTAL 405
DB 431 LSHPIEVENNPF--PCLYKDEIMKEIERESRKIKLNDNDGNNKIIAPRIFISDDKSL 488
OY 406 OCTAPKFPDSGACDVQACRQKTSVGVGOISTSVDTCTA-----DEQNECGS----- 454
DB 489 KCPCDPEWNSVSTCRFEVCK-----CVERRAVTSNNVNVVKEEYKXDYADIPHEKPTPD 543
OY 455 --TALIAGLAVGVLLALLGGGCFYAKRLDRNKGVAHHEHFOSDRGAKRRKPSDLM 512
DB 544 KKKIILIASAAYAVATILM---VLYYKR-----KONAKYDKMDPQDYGKSNR-NDEN 595
OY 513 CEAPSPFWDDEAENIEDDGETHWVEGDY 541
DB 596 LDPEASFWGEEK---RASHTTPVLMKPY 621

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RESULT 3

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OY 0967K3 PRELIMINARY; PRT; 622 AA.
AC 0967K3;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_Taxid=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VEN760;
RX MEDLINE=21192561; PubMed=11295182;

```

RA	Becsalan A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Blawas S.,
RB	Nahlen B.L., Lal A.A.;
RT	"Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
RL	1) of Plasmodium falciparum. X. Aeemo Bay Cohort Project.";
RM	Mol. Biochem. Parasitol. 113:279-287(2001).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN-VEN760;
RA	Ananiae E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Blawas S.,
RB	Nahlen B.L., Lal A.A.;
RL	Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR	EMBL; AY016412; AAC50119.1; -
DR	InterPro: IPR003298; Apmem_Ag1.
DR	Pfam: PF02430; AMA-1; 1
DR	PRINTS; PRO1361; MERZOITTESA.
FT	NON_TER 622
SQ	SEQUENCE 622 AA; 72016 MW; AFCA807826AF9CBA CRC64;
Query Match	14.8%; Score 433; DB 5; Length 622;
Best Local Similarity	25.9%; Pred. No. 86-29; Indels 120; Gaps 23
Matches 147; Conservative 86; Mismatches 215;	
OY	41 GNPFQANVEMKTFMERFNLTHHOSGIVYVDLGQDEVDGTLYREBAGLCPIWGHIELOQ 100 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	107 GNPW-----TEYMAKYDIEBHSGSIGIRVDLGEDAEVAGTQRLLSGSCPVGKKIILEN 160 : : : : : : : : : : : : : : : : : : : : : : : : :
OY	101 PDLRYNNPLEDVETEKEYKGNSPLPGCFNLNFVTDSGORISFPME---LLEKSN 156 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	161 SN-----TTFLTPVATGNQLKD-----GGFAF---PTEPHMSPTLDKMHFYKDNKY 207 : : : : : : : : : : : : : : : : : : : : : : : : :
OY	157 IKASDGLRCAEFAYAMDGNKATKRYRFYVDSKKRLCHILTVSNQLMEGKKYSV 216 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	208 VKNUDELTLCSHAAGNM--PUNDKSNXYKPAAVYDDDKCKCHILYIAOENNNGRYCN- 264 : : : : : : : : : : : : : : : : : : : : : : : : :
OY	217 KGEPPDLTWYCFKPKRSYTENHLITYSAAYVEN-PDAFISKCPNALRGYFGWKGR 275 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	265 KDQSIRSMFCRPAKDISFOY-----TYLSKNVYDWMEKCYCRKULENAKFGMLWDGN 319 : : : : : : : : : : : : : : : : : : : : : : : : :
OY	276 CLDYTELDTVLIERVESKAQCWVKTFENDGVASDPHTYP--LTSQAOWNDMWP----- 327 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	320 CEDIPDVNIET---SANDLFECHKLVFELS--ASDPKQYEQHLTIDYEKIKEGFKNKNASM 374 : : : : : : : : : : : : : : : : : : : : : : : : :
OY	328 -----LHSDDPHGSGVGNRNIGFYVDTGTGSKCALSDQVDCLVSDSAVSYNRA 378 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	375 IKSAPLPTGAFFADYYKSHGKGYNNGNNTET---HKCEIFNVKPTCLINNSSYATTAL 431 : : : : : : : : : : : : : : : : : : : : : : : : :
OY	379 GSLSEETENFIIPSN-----PSVTPPTDETALO 406 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	432 SHPEVENNF--PCSLYDEIMKELIERBSRKALKANDNDENKAKIIARIFISDDKSLK 489 : : : : : : : : : : : : : : : : : : : : : : : : :
OY	407 CTADKFPDSPGACDVQACKROKTS CVGQIOGSTVDTCTA-----DEONECGSN----- 454 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	490 CPCDPEWVSNSICRFVCVCK-----CVERRAEVTSNNEVVVKEEYDEYADI PEHNPYDX 544 : : : : : : : : : : : : : : : : : : : : : : : : :
OY	455 -TALIAGLA VGVLLALLGGGCYFAKILDRKKYQAAAHHEHFSPDSGARAKKRPSDLMO 513 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	545 MKIIIASAAVAVLTILM---VYLTKR---KGAERYDKXDPODYGKNSR-NDEWL 596 : : : : : : : : : : : : : : : : : : : : : : : : :
OY	514 EAEPSEFMDEAEENITEODGETHMVVEGDY 541 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	597 DPBASFWGEEK---RASHTTPVLMEXPY 621 : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 4	
ID O25745	PRELIMINARY; PRT: 592 AA.
AC O25745:	
DT 01-NOV-1996 (TREMBLrel. 01, Created)	
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE Apical membrane antigen-1 (Fragment).	
NC AMA-1.	
OS Plasmodium falciparum.	

Query Match	14.8%	Score 432.5	DB 5	Length 592
Best Local Similarity	26.7%	Pred. No. 8.3e-29		
Matches 147	Conservative 77	Mismatches 202	Indels 125	Gaps 23
OC Eukaryota: Alveolata: Agicomplexa; Haemosporida: Plasmodium.				
OX NCBI_TaxID=5833;				
RN (1)				
RP SEQUENCE FROM N.A.				
RC STRAIN=CMP1;				
RX MEDLINE=96147889; PubMed=8556798;				
RA Zhang L.X., Zhan B., Wang J., Feng X.;				
RT "Sequence analysis of apical membrane antigen 1 from a Plasmodium				
RT falciparum isolate collected from Mengpeng Township, Yunnan				
RT Province.";				
RL Chung Kuo Chi Sheng Chung Hsueh Yu Chi Sheng Chung 13:203-208(1995).				
RN (2)				
RP SEQUENCE FROM N.A.				
RC STRAIN=CMP1;				
RX MEDLINE=96379227; PubMed=8784778;				
RA Marshall V.M., Zhang L., Anders R.F., Coppel R.L.;				
RT "Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";				
RL Mol. Biochem. Parasitol. 77:109-113(1996).				
DR EMBL: U33275; AAC47105.1; -				
DR InterPro: IPR003298; Aqmem_Ag1.				
DR Pfam: PF02430; AMA-1; 1.				
DR PRINTS: PR01361; MERZOITESA.				
FT NON TER 1				
FT NON TER 1				
SEQ SEQUENCE 592 AA; 68412 MW; 5496A73680E7128C CRC64;				
QY 41 GNPFAVEMKTFMRPNLTHHSGIYVDLGDQKEVDTLYRPPGLCPINGKHLEQQ 100				
DB 95 GNPW-----TEYMAKYDIEEYHVGSGIRDLGDEADVAGTQYRLPBGKCPVFGKGIIEEN 148				
QY 101 PDRLEPRNNPFLQEDVTEK-EYKOSGNPLPGCFNLNFPVTSGORISPPME---LLEKNS 155				
DB 149 SN-----TFPLTPVATEKQDLKDGFAFP-----PTNPLMSMTLTDNRRLTKDNE 194				
QY 156 NIKASTDLGRCAEFAPKTVAMDKNNAKATRYRPFYDYSKKRLCHILVSMQMEGKKYCS 215				
DB 195 DVKNLDELTLGSRHAGNMII--PDNDKNSYKYPAVYDDKDKKCHILYIAAQENNGRYCN 252				
QY 216 VKGEPPDLTWICFKRKSVTEHHNLVYSAYGEN-PDAFISKCPQALRGYFGWYKKG 274				
DB 253 -KDQSKRSMFCFRPAKD---KLFOYTYLTKRVVDMEKVCPRKNLQNAKFGFLWVG 306				
QY 275 RCLDVTELTDTVIEVESKAOQCVWTFENDVVASDQPHYR--LTSQASMDMP----- 327				
DB 307 NCEDIPLVHNEF---SANDLFECKLVFELS--ASDQPKQYEGHLLDYEKIKGCFKKKNS 361				
QY 328 -----LHSDQPHSGGVGRNYGFYVDVTGEGKCALSDQVDDCLVSDAASVYTA 377				
DB 362 MIKSAFLPTGAFPKADRYKSHGKGYMWGVNTEF---HKEIENVKPTCLINNSSVYATTA 418				
QY 378 AGSLSEETPNFLIPSN-----PSVTPPTPETL 405				
DB 419 LSHPIEVENNF--PCSLYKDEIMKEIERESKRRIKLNDDNDEGNKKIIARIFISDKDSL 476				
QY 406 OCTADKFPDPSFGACVQVQCKRQTSVCGSGLQSTS-----VDCRAD--EQNEGCS 453				
DB 477 KCPCDPEWNSSTCFPVCK-----CVERRAEVTSNVEYVVKKEKYDEVDALPEHKPTD 531				
QY 454 NTALI---AGLAVGVLALLLGGCGCFYAKFLDRNKGVAQAHHEHFEFOSDRGARKRPS 509				
DB 532 NMKIIIASAVALVATILMV-----YLYKR-----KGAEKYDKMDQGDGKSNR-N 580				
QY 510 DLMQEAEPSPFW 520				
DB 581 DEMLDPEASFW 591				

ID 0967K2 PRELIMINARY; PRT; 622 AA.
 AC 0967K2;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_taxid=5833;
 RX STRAIN=08-0697;
 RP SEQUENCE FROM N.A.
 RC STRAIN=08-0697;
 RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY016413; AAG50120.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR NON TER 622
 FT SEQUENCE 622 AA; 72038 MW; 918543446A57E30 CRC64;
 SQ

Query Match 14.8%; Score 431; DB 5; Length 622;
 Best Local Similarity 25.9%; Pred. No. 1.2e-28;
 Matches 147; Conservative 85; Mismatches 216; Indels 120; Gaps 23;

QY 41 GNPFGAVEMKTFMERFNLTHHOSGIYVDGQKXVDGLTYRBPAGLCPFWGKHIELOQ 100
 DB 107 GNPW-----TEYMAKYDIEVHSGIRVDGEAEVAGTQYRLPSGKCPVFGKGIIEEN 160
 QY 101 PDRLPYRNFLFEDVPTFTEKEYKSGNPLPGGFNLNFTVPSGORISPFPMB-----LLEKSN 156
 DB 161 SN-----TTFLLPVAITGNQYLKD-----GGFAF-----PTEPHMSPTLDMKHFYKDNKY 207
 QY 157 IKASTDLGRCAEFKATYVAMDKNKAATKRRPYVYDSKRLCHILYVSKQMLEGKKYCSV 216
 DB 208 VGNLDELTLCSRHAGNMV--PDNDKNSNYKYPAYDDKDKCHILYIAOENNGPRYCN- 264
 QY 217 KGEPRDLTMVCFKPRKSVTEENHLLYGSAYVGEN--PDAFISCPNOALRGVFGVWKKGR 275
 DB 265 KDQGRNSMFCFRPAKDISFQNY-----TYSKNAVVDNWEKVCPRKULENAKFGGLWVDGN 319
 QY 276 CLDYLTELDTVIERVESKAQCWVKTENDGVASDOPHTYP--LTSQASWMDWP----- 327
 DB 320 CEDIDHVAE---SANDLFECNKLVFELS--ASDQKQYEQHLTDYEKIKEGFKKNKNSM 374
 QY 328 -----LHOSDQPHSGGVRNGFYVDTTGEGKALSQVDPCLVSDSAASYTA 378
 DB 375 IKSATFLPTGAFKADRYKSHGKGYNGWNTYET--HKCEIFVWKPTCLINNSYIATYAL 431
 QY 379 GSLSEETPFIIIPSN-----PSVTPTPTETA 406
 DB 432 SHPTVENNF--PCSLYKDEIKKEIERESKRITKLANDNDEGNKKTIAPIFISDDKDSLK 489
 QY 407 CTADKFPDSFGACDVQACRKQKTSVCGQIOSTSYDCTA-----DEONECGSN----- 454
 DB 490 CPCDEPMVNSNCRFPVCK-----CYERAEVTSNNEVVVKEBYDEVADIPEHKPTYDK 544
 QY 455 -TALLAGLAVGVLALLGGGCTYFAKRLDRNKGVOAAHNEHFQSDRARKKRPSDLMO 513
 DB 545 MKIIIASAANAVLATILM-----YLYKR-----KGNAEKYDKMDEPOHYGKNSNR-NDKWL 596
 QY 514 EAEPSPWDAEENIEDDGETHVVVBGDY 541

DB 597 DPEASFWGEEK---RASHTPVLMEKPY 621

RESULT 6

ID 09GZ05 PRELIMINARY; PRT; 622 AA.
 AC 09GZ05;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Apical membrane antigen 1.
 GN AMA-1.
 OS Plasmodium falciparum.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_taxid=5833;
 RX STRAIN=FCCL1/HN;
 RP SEQUENCE FROM N.A.
 RC STRAIN=FCCL1/HN;
 RA Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
 RL "Cloning and structure of apical membrane antigen 1 (AMA-1) gene of Plasmodium falciparum isolate FCCL1/HN";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF277003; AAG01325.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR NON TER 622
 FT SEQUENCE 622 AA; 72045 MW; 69045B6776C3BBB CRC64;
 SQ

Query Match 14.8%; Score 431; DB 5; Length 622;
 Best Local Similarity 26.4%; Pred. No. 1.2e-28;
 Matches 151; Conservative 83; Mismatches 209; Indels 130; Gaps 25;

QY 41 GNPFGAVEMKTFMERFNLTHHOSGIYVDGQKXVDGLTYRBPAGLCPFWGKHIELOQ 100
 DB 107 GNPW-----TEYMAKYDIEVHSGIRVDGEAEVAGTQYRLPSGKCPVFGKGIIEEN 160
 QY 101 PDRLPYRNFLFEDVPTFTEKEYKSGNPLPGGFNLNFTVPSGORISPFPMB-----EKNS 155
 DB 161 S-----KTFLLPVAITGNQYLKD-----GGFAF-----PTEPHMSPTLDMKHFYKDNKY 206
 QY 156 NIKASTDLGRCAEFKATYVAMDKNKAATKRRPYVYDSKRLCHILYVSKQMLEGKKYCS 215
 DB 207 YVKNLDELTLCSRHAGNMV--PDNDKNSNYKYPAYDDKDKCHILYIAOENNGPRYCN 264
 QY 216 VKGEPRDLTMVCFKPRKSVTEENHLLYGSAYVGEN--PDAFISCPNOALRGVFGVWKK 273
 DB 265 -KDSKNSMFCFRPAKDKLFENY-----TYSKNAVVDNWEVCPRKULENAKFGGLWVD 317
 QY 274 GRCLDYLTELDTVIERVESKAQCWVKTENDGVASDOPHTYP--LTSQASWMDWP----- 327
 DB 318 GNCEIDIPVAE---SANDLFECNKLVFELS--ASDQKQYEQHLTDYEKIKEGFKKNKNSA 372
 QY 328 -----LHOSDQPHSGGVRNGFYVDTTGEGKALSQVDPCLVSDSAASYT 376
 DB 373 SMISAFPLPTGAFKADRYKSHGKGYNGWNTYET--KCEIFVWKPTCLINNSYIATY 429
 QY 377 AAGSLSEETPFIIIPSN-----PSVTPTPTETA 404
 DB 430 ALSHNEVENNF--PCSLYKDEIKKEIERESKRITKLANDNDEGNKKTIAPIFISDDKDS 487
 QY 405 LQCTADKFPDSFGACDVQACRKQKTSVCGQIOSTSYDCTA-----VDCTAD--EONECG 452
 DB 488 LKCPDDEPVIANSNCRFPVCK-----CYERAEVTSNNEVVVKEBYDEVADIPEHKPTY 542
 QY 453 SNTALI---AGLAVGVLALLGGGCTYFAKRLDRNKGVOAAHNEHFQSDRARKKRPSDLMO 508
 DB 543 DNMKIIIASAANAVLATILM-----YLYKR-----KGNAEKYDKMDEPOHYGKNSNR- 591
 QY 509 SDLMQAEPSFWDAEENIEDDGETHVVVBGDY 541
 DB 592 NDEMIDPEASFWGEEK---RASHTPVLMEKPY 621

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RESULT 7
ID 0967K1 PRELIMINARY; PRT; 622 AA.
AC 0967K1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VEN766;
RX MEDLINE=2192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
RT 1) of Plasmodium falciparum. X. Asambo Bay Cohort Project."
RL Mol. Biochem. Parasitol. 113:279-287(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VEN766;
RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY016414; AAG50121.1;
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MERZOITESA.
FT NON TER 622
SQ SEQUENCE 622 AA; 7186 MW; 58A92EA691CD6F21 CRC64;

Query Match 14.8%; Score 431; DB 5; Length 622;
Best Local Similarity 26.2%; Pred. No. 1.2e-28;
Matches 149; Conservative 86; Mismatches 212; Indels 122; Gaps 24;

41 GNPFQAVNEMKTFMERENLTHHOSGIYDLGQKVEDGLTYRPAAGLCPIWGHILOQ 100
Db 107 GNPF-----TEYAKYDIEKHSGIRVDLGEDAEVAGTQYRLPSGKCPVFGKIIEN 160
Qy 101 PDLRYNNFLLEDVPTKEKYKQSGNPLPGGFNLNFTVPSGQRIAPPME-----LLEKNS 156
Db 161 SN-----TTLFLTPATNGQYKD-----GGRFAF--PPTBLSMSPMLDEKHHYKDKY 207
Qy 157 IKASTDLGRCAEFAPKTVAMDKNKATKYRYPFYVDSKRLCHILLYVSMQLMGKRYCSV 216
Db 208 VKNLDELTLCSRHAGNM1--PDNDKNSNYKYPAYVDDKKCHILLYIAQENNGPRYCN- 264
Qy 217 KGEPPDLTYTCFKRKRSVTENHLLIYGSAYYGEN-PDAFISKCPNOLRGIRFGYWK 275
Db 265 KDESKNMSMFCFRPAKDISFGNY-----TYSKNVNVNWEVCPRKNLQNAKFFGLMVDGN 319
Qy 276 CLDYTELTD-TVIRVESKAQCVKTFENDGVASDOPHTYR--LTQASNMNDMP----- 327
Db 320 CEDIPHNESALDLE-----CNKLVEFLS--ASDQPKQYEGHLLDYBKIKGFKNKAS 373
Qy 328 -----LHOSDPHSGGVGRNYGYVVDITGEGKALSDQVPCLVSDSAVSYTA 377
Db 374 MIKSAFLPTGAFKADRYKSHGKGYMGVNTETQ--KCEIFNVKPTCLINNSYIATTA 430
Qy 378 AGSLSETPFIITSN-----PSTPTPTETA 405
Db 431 LSHDIEVNNF--PCSLYKDEIKKEIERESKRIKLNNDDEGNKIIAPRIFISDDKSL 488
Qy 406 QCTADKPPDSFGACDVACKRKQTSVGGQISTSVDTA-----DEONEGCSN----- 454
Db 489 KCPCDPDEIVSNTGNCFFVCK-----CYEKRAEYVSNNEVVKERYKDEYADIPHKPT 543
Qy 455 --TALLGLAVGVLLALLGGGCGYFAKRLDRNKGVAAAHNEHFQSDRGARKKRPDDL 512

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Db 544 KMKIIASSAAVAVLATILM---VLYKR----KGNAEKTDKDEPOHYGKNSNR-NDEN 595
Qy 513 QEAPSPFWEAEENIEODGETHWVEGDY 541
Db 596 LDPEASFWESEK--RASHTTPVLMKEPY 621

RESULT 8
ID 0967I3 PRELIMINARY; PRT; 622 AA.
AC 0967I3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2180;
RX MEDLINE=2192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
RT 1) of Plasmodium falciparum. X. Asambo Bay Cohort Project."
RL Mol. Biochem. Parasitol. 113:279-287(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2180;
RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY016438; AAG50145.1;
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MERZOITESA.
FT NON TER 622
SQ SEQUENCE 622 AA; 71975 MW; 4B346552F3636455 CRC64;

Query Match 14.6%; Score 426; DB 5; Length 622;
Best Local Similarity 26.5%; Pred. No. 3.3e-28;
Matches 152; Conservative 81; Mismatches 210; Indels 130; Gaps 25;

41 GNPFQAVNEMKTFMERENLTHHOSGIYDLGQKVEDGLTYRPAAGLCPIWGHILOQ 100
Db 107 GNPF-----TEYAKYDIEKHSGIRVDLGEDAEVAGTQYRLPSGKCPVFGKIIEN 160
Qy 101 PDLRYNNFLLEDVPTKEXYKQSGNPLPGGFNLNFTVPSGQRIAPPME-----LLEKNS 155
Db 161 S-----KTLFLTPATNQLKDGGRFAF-----PTEPLISPTLQMRHLLYKNE 206
Qy 156 NIKASTDLGRCAEFAPKTVAMDKNKATKYRYPFYVDSKRLCHILLYVSMQLMGKRYCS 215
Db 207 YVKNLDELTLCSRHAGN--WNPNDKNSNYKYPAYVYEDKKCHILLYIAQENNGPRYCN 264
Qy 216 VKGEPDLTYTCFKRKRSVTENHLLIYGSAYYGEN-PDAFISKCPNOLRGIRFGYWK 273
Db 265 -KDESKNMSMFCFRPAKDKFFENY-----TYSKNVNVNWEVCPRKNLENAKFFGLMVD 317
Qy 274 GRCLDYTELTDYIERVESKAQCVKTFENDGVASDOPHTYR--PLTQASNMNDMP----- 327
Db 318 GNCEDIPHNVEF--SANDLFECKVLVEFLS--ASDQPKQYEGHLLDYBKIKGFKNKMA 372
Qy 328 -----LHOSDPHSGGVGRNYGYVVDITGEGKALSDQVPCLVSDSAVSYT 376
Db 373 SWIKSAFLPTGAFKADRYKSHGKGYMGVNTETQ--KCEIFNVKPTCLINNSYIATTA 429
Qy 377 AAGSLSETPNFIIITSN-----PSTPTPTETA 404
Db 430 ALSPHNEVENNF--PCSLYKDEIKKEIERESKRIKLNNDDEGNKIIAPRIFISDDKDS 487

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QY 405 LQCTADKPPDSFGACDVQACKROKTSVCGGQIOSTS-----VDCTAD--EQNECG 452
 DB 488 LKCCPDEIYVNSGTCNFFVCK-----CYEKRAEYTSNNEVVVKEEYKDEYADIEBHKEY 542
 QY 453 SNTALI-----AGLAVGVLLALLGGGCFPAKRLDRNKGVQAAHHEHFGSDRGARKRP 508
 DB 543 DNKKIITIASAAVAVLATILV-----YLYKR-----KG-NAEKYDKMDQPOHYGKSNSR 591
 QY 509 SDLMQEAEPFWDAAENIEDDGETHWVWEGDY 541
 DB 592 NDEMIDPEASFWGEBK---RASHHTPVLMEXY 621

RESULT 9

Q967KO PRELIMINARY; PRT; 622 AA.
 AC Q967KO;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (fragment).
 GN AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN761;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chaiyaroj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asembo Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN761;
 RA Ananias E.A., Grebert H.M., Chaiyaroj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY016415; AAG50122.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 FT NON_TER 622
 SQ SEQUENCE 622 AA; 71853 MW; F44453994D8013B9 CRC64;

Query Match 14.5%; Score 425; DB 5; Length 622;
 Best Local Similarity 26.0%; Pred. No. 4e-28;
 Matches 148; Conservative 86; Mismatches 213; Indels 122; Gaps 24;

QY 41 GNPQANVEMKTFMERFNLTHHOSGIYVDLQDKEVDGLYREPAGLCPIGKHIELOQ 100
 DB 107 GNPW-----TEYMAKYDIEVHGSGIRVLDGEDAEVAGTQYRLPSGKCPVFGKGIITEN 160
 QY 101 PDRLRYRNFLLEDVPTKEKYGKSNPLPGCFNLFPVTPSGQRISPPFM-----LLEKSN 156
 DB 161 SN-----TTFLLPVATGNOYLKD-----GGFAP---PTEPLMASPTLDEMHPFYDKNY 207
 QY 157 IKASTDLGCAEFAKTYAMDKNNKATKYRYPFYVDSKRLCHILYVSMOLMEGKKYCSV 216
 DB 208 VGNLDELTLCSRHAGMI--PNDKSNKYKAGYDDKDKKCHILYIAQENNGRPTCN- 264
 QY 217 KGEPPDLTWYCFKPKRSTENHLLYGSAYVGEN-PDAFISKCPNOLRGYFGWKKGR 275
 DB 265 KQESKNSWFCRPAKDISFQNY-----TYSKTVVDNWEKVCPRKILQNAKFGJLWVNGN 319
 QY 276 CLDYELTD-TYIERESKAQCVKTFENDGVAADOPHTYP--LTSQASMNWMP----- 327
 DB 330 CBDIPIVNEFSAIDFE---CNKLVEELS--ASDOPKOYEHHLLTDYEKIKGFGKKNAS 373
 QY 328 -----LHSDQPHSGGVGRNYGYVVDTTGEGCALSDOVPDCLVSDAANSYTA 377

DB 374 MISAFLPTGAFKADRYKSHGKGYMGNVNTETO---KCEIFNVKPTCLINNSSYIATTA 430
 QY 378 AGLSSEETPPIIPSN-----PSVTPTPETAL 405
 DB 431 LSHPIEVENN--PCSLYKQEIKEIRESEBRIKLNNDDEGNKIIAPRIFISDDDSL 488
 QY 406 QCTADKPPDSFGACDVQACKROKTSVCGGQIOSTVDTA-----DEONECGSN----- 454
 DB 489 KCPCDPEIYVNSGTCNFFVCK-----CYEKRAEYTSNNEVVVKEEYKDEYADIEBHKEY 543
 QY 455 -TALLGLAVGVLLALLGGGCFPAKRLDRNKGVQAAHHEHFGSDRGARKRPDLM 512
 DB 544 KMKIITIASAAVAVLATILM---YLYKR-----KGNAEKYDKMDQPOHYGKSNSR-NDEN 595
 QY 513 QEAEPFWDAAENIEDDGETHWVWEGDY 541
 DB 596 LDPEASFWGEBK---RASHHTPVLMEXY 621

RESULT 10

Q25687 PRELIMINARY; PRT; 558 AA.
 AC Q25687;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE Apical membrane antigen 1.
 GN AMA-1.
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DS;
 RX MEDLINE=96333375; PubMed=8757869;
 RA Crewther P.E., Matthew M.L., Flegg R.H., Anders R.F.;
 RT "Protective immune responses to apical membrane antigen 1 of Plasmodium chabaudi involve recognition of strain-specific epitopes.";
 RL Infect. Immun. 64:3310-3317(1996).
 DR EMBL; U49743; AAB36509.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 SQ SEQUENCE 558 AA; 63996 MW; 1DB43DF0E268DE63 CRC64;

Query Match 14.5%; Score 422.5; DB 5; Length 558;
 Best Local Similarity 26.3%; Pred. No. 5.6e-28;
 Matches 150; Conservative 94; Mismatches 191; Indels 135; Gaps 24;

QY 42 NPOANVEMKTFMERFNLTHHOSGIYVDLQDKEVDGLYREPAGLCPIGKHIELOQ 101
 DB 53 NPWE-----KFMEXYDIEKHGSGIRVLDGEDAEVAGTQYRLPSGKCPVFGKGIITKS 106
 QY 102 DRLPYRNFLLEDVPT-KEKYGKSNPLPGCFNLFPVTPSGQRISPPFM-----ELLEKSN 156
 DB 107 TK-----SFLDPVATGDKVREGGLAPF-----KADNISFVLLONLRWKKHPE 152
 QY 157 IKASTDLGCAEFAKTYAMDKNNKATKYRYPFYVDSKRLCHILYVSMOLMEGKKYCSV 216
 DB 153 ITALNDSMLCAKHA--SFVPGNNANSAVRHAYVDKNNKCTYILYVAAQENMGFRYCS- 209
 QY 217 KGEPPDLTWYCFKPKRSTENHLLYGSAYVGENPDAFISKCPNOLRGYFGWKKGR 276
 DB 210 NEENNENPFCFTTPK-K-DEYKNLSYLKQNRD---METSCPNNSIGNAKGVVVDGYC 265
 QY 277 LDY--TELTDYIERESKAQCVKTFENDGVAADOPHTY----- 314
 DB 266 SEYCKKEVHDS-----KSLSECNRIVF--DSASDOPKOYEHHLLTDYEKIKGFGKKNAS 318
 QY 315 -----PLTQASNDWMPHLSQPHSGGVGRNYGYVVDTTGEGCALSDOVPDCLV 367
 DB 319 LIGALLPTGS-----YRADOVKSKGKGYMGNVNTETO---DKKEKCYIFNKKPTCL 365

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Qy 368 SDSAAVSTTAAGSLSEETPNFIPSN-----PSVTPPT 400
Db 366 NDKRFVATTALSSL-EAPOSEFPDIIYKKIAEIKVMNVNRNNGNDITKPRIFISD 424
Qy 401 PETALQCADKFPDSFGACDVQAC---KROKTSVGOIOISTSDCTADEONEGSGS--- 453
Db 425 DKESLKCEPCEPTQLTQSSCNFPVCNCEVKRQFIS-----ENNEVEIIDEFESEYESPIN 478
Qy 454 -NTALAGLAVGVLLALIGGCYFAKRLDRNKGVQAAHHEHFQSDRGARKRPSDL 511
Db 479 QRMIIITLITAGLALSLT---FYFK---SNK--PGDDYDKKGQADYTKGAKSRDE 530
Qy 512 MQEAEPSPWDEAENIEQDGETHWVWEGDY 541
Db 531 MLDEPVSFWGEDK---RASHTTPVLMKRPY 557

RESULT 11
ID 061130' PRELIMINARY; PRT; 562 AA.
AC 061130:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Apical merozoite antigen 1.
GN AMA1.
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5655;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sal I;
RX MEDLINE=99389346; PubMed=10462250;
RA Rogers W.O., Gowda K., Hoffman S.L.;
RT "Construction and immunogenicity of DNA vaccine plasmids encoding four
RT Plasmodium vivax candidate vaccine antigens.";
RL Vaccine 17:3136-3144(1999).
DR EMBL; AF063138; AAC16731.1; -
DR InterPro; IPRO03298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
KW Merozoite.
SQ SEQUENCE 562 AA; 64477 MW; 51B441344AD807FD CRC64;

Query Match 14.4%; Score 422; DB 5; Length 562;
Best Local Similarity 25.5%; Pred. No. 6.3e-28;
Matches 157; Conservative 90; Mismatches 232; Indels 136; Gaps 28;

Qy 6 VQVLLVAVDCTIFASGL-----SSSTRS-----RESQTLASLT-SGNPFOANVEKMT 52
Db 4 IYIIFLSAQLVHIGKGRNQKPSRLTRSANNVLEKGPVTERSTRNSNP-----KA 57
Qy 53 FMERFNLTHHOSGIYVDLGDQKEVDGTLYPEPAGLCPIWGKHIELQOPDRLLPYRNFL 112
Db 58 FMEKVIDIRTHSSSGVRVDLGEDAVENAKYRIPARCEVFGKGIYENS-----VSFLR 112
Qy 113 DVPT-EKEYKOSGNPLPGFNLNFTPSGORISPPM-----ELLEKSNIKASTDLGRCA 167
Db 113 PVAAGDQGLKQGGFAFP-----ANDHISPTTLANKERYKDNVEMKLANDIALCR 163
Qy 168 EFAFKTV-AMDKNKATKYRYPFYDYSKKRLCHILYVSMQMEGKKYCSVKGEPDRLTWY 226
Db 164 THAASFVWAGDQ---SSYRHPAVYDEKCKTCHMLYLSAQMNGRYSQPDQNDAY-F 219
Qy 227 CFKPKKSVT-ENHHLIYGSAYGENPDPAFISKCPNOLRGYRFGVWKKGRCLDYTELDT 285
Db 220 CFKPKKSNSEFN--LVYLSKVRNDW---KKCPKKNLGNKAFGLMVDGNCEIEIYVYEV 274
Qy 286 VIERVESAAQCQVVKTFENDGVASDOPHTYPLTSQASWMDWPLHQ----- 330
Db 275 ---EAEDRECKRIYF--GASASDOPYOT---EEMTDYQKIQGGFPQNNEMIKSAFL 325
Qy 331 -----SDPHSGGVGRNYGYVDTTGEGKALSDQVDCIIVSDAAVSTTAAGSLSE- 383

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Db 326 PVGAFNSNINFKSKRGFWANF---DSVKKCYIFNFKPTLINDKFIATLASHPOEV 382
Qy 384 -ETPNFIPSN-----PSVTPPTPETALQCADKFPDSFG 417
Db 383 DLEFPCSIYKDEIEREIKOSRNANLYSVDERIVLPPIFISNDKESIKCCCEPERINS 442
Qy 418 ACDVQACRKQKTSVCV--GGQIOSTSDCTADEONEGSGN-----TALAGLAVGV 466
Db 443 TGNFYVC-----NCVEKRAELKENNOVYIKEPRDYENGSEKSNKQMLIITIGI-TGCV 496
Qy 467 LLLALLGGCCYFAKRLDRNKGVQAAHHEHFQSDRGARKRPSDLMQEAEPSPWDEAEN 526
Db 497 CVVA-LASMAFYRRKKANNDK-----YDKMQDAGSGYKPTRKDEMLDPEASFWEDEK-- 547
Qy 527 IEQDGETHWVWEGDY 541
Db 548 -RASHTTPVLMKRPY 561

RESULT 12
ID 026162 PRELIMINARY; PRT; 555 AA.
AC 026162:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apical membrane antigen 1 (Fragment).
GN AMA-1.
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5655;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH-84;
RX MEDLINE=95021524; PubMed=7935625;
RA Cheng Q., Saul A.J.;
RT "Sequence analysis of the apical membrane antigen 1 (ama-1) of
RT Plasmodium vivax.";
RL Mol. Biochem. Parasitol. 65:183-187(1994).
DR EMBL; L27503; AAA29479.1; -
DR InterPro; IPRO03298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
DR NON TER 555
SQ SEQUENCE 555 AA; 63420 MW; 432DFC8FB82D9CDS CRC64;

Query Match 14.4%; Score 420.5; DB 5; Length 555;
Best Local Similarity 25.7%; Pred. No. 8.4e-28;
Matches 154; Conservative 87; Mismatches 218; Indels 141; Gaps 28;

Qy 6 VQVLLVAVDCTIFASGL-----SSSTRS-----RESQTLASLT-SGNPFOANVEKMT 52
Db 4 IYIIFLSAQLVHIGKGRNQKPSRLTRSANNVLEKGPVTERSTRNSNP-----KA 57
Qy 53 FMERFNLTHHOSGIYVDLGDQKEVDGTLYPEPAGLCPIWGKHIELQOPDRLLPYRNFL 112
Db 58 FMEKVIDIRTHSSSGVRVDLGEDAVENAKYRIPARCEVFGKGIYENS-----AVSFLT 112
Qy 113 DVPT-EKEYKOSGNPLPGFNLNFTPSGORISPPM-----ELLEKSNIKASTDLGRCA 167
Db 113 PVAAGDQGLKQGGFAFP-----KADHISPTTLANKERYKDNVEMKLANDIALCR 163
Qy 168 EFAFKTV-AMDKNKATKYRYPFYDYSKKRLCHILYVSMQMEGKKYCSVKGEPDRLTWY 226
Db 164 THAASFVWAGDQ---SSYRHPAVYDEKCKTCHMLYLSAQMNGRYSQPDQNDAY-F 219
Qy 227 CFKPKKSVT-ENHHLIYGSAYGENPDPAFISKCPNOLRGYRFGVWKKGRCLDYTELDT 285
Db 220 CFKPKKSNSEFN--LVYLSKVRNDW---KKCPKKNLGNKAFGLMVDGNCEIEIYVYEV 274
Qy 286 VIERVESK--AQCQVVKTFENDGVASDOPHTYPLTSQASWMDWPLHQ----- 330

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Db 270 YVKEVEAKDLRECNRIVF--GASASDQPTQY-----EEMTDYQKIQGFRQNNREMIKSA 323
Qy 331 -----SDQPHSGGVRNGFYVYDTTGCKALSDQVDCIVSDASVYTPAGSL 382
Db 324 PLVGAFAFSDNFKSGKGFNMANF---DSVKNKCIYFNTKPTCLINDKNFATATLSPQ 380
Qy 383 EETNFIIIPSN-----PSVTPPTETALQCTADKFP 413
Db 381 EVDFEF--PCSIYDEIEREIKKOSRNNMLYSVDGERIVLPRIPTSDNESIKCPCEPEH 438
Qy 414 DSFGACDVQACROKTSVCV--GGQIOSTSVDTCTADEQNECGSN-----TALLIAGLA 462
Db 439 ISNTGCTNFYVC-----NCEVKRAEIKENNQVVIKEEFEDYENGEBEKNQMLIIIGI- 492
Qy 463 VGVLLALLGCGCYFAKRLDRNKGVQAAHHEHFOSGRGARKRPSDLMOEAEPSFDE 522
Db 493 TGVGVVA--LASMAYFRKKANNDK-----YDKMDQAEAGYKPTTRKDEMLDPEASFWGE 545

RESULT 13
Q96413 PRELIMINARY; PRT; 563 AA.
AC Q96413;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Apical merozoite antigen 1.
GN AMA1.
OS Plasmodium knowlesi (strain H).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5851;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H;
RX MEDLINE=21391817; PubMed=11500430;
RA Rogers W.O., Baird J.K., Kumar A., Tine J.A., Weiss W., Aguilar J.C.,
Gowda K., Gwadz R., Kumar S., Gold M., Hoffman S.L.;
RT "Multistage Multiantigen Heterologous Prime Boost Vaccine for
Plasmodium knowlesi Malaria Provides Partial Protection in Rhesus
Macaques.";
RL Infect. Immun. 69:5565-5572(2001).
DR EMBL; AF298218; AAC24614.1; -
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1
DR PRINTS; PRO1361; MEROZOITESA.
KW Merozoite.
SQ SEQUENCE 563 AA; 64694 MW; 9CD4A3C1F019CA2B CRC64;

Query Match 14.4%; Score 420.5; DB 5; Length 563;
Beet Local Similarity 24.6%; Pred. No. 8.5e-28;
Matches 148; Conservative 95; Mismatches 251; Indels 107; Gaps 24;

Qy 6 VQVLLVLVADCTIPASGL---SSSTRSRESQTLASSTGSGNPQANVM---KTFMEREN 58
Db 4 IYIILFLSQCLVHNGKRCRNQKTRTLRSANNASLEKPIIERSIRMSNPWKAEKXD 63
Qy 59 LTHHOSGIYVDLGDQKVEDGTLTYREBAGLCPIWKGHIELQDPDLRYANNLVEDVPT-E 117
Db 64 LERAHNSGRIIDLGEDAEVNSKRYRIPAKCPVFGGIVTENS-----VSFLTPVATGA 118
Qy 118 KEYKSGNPRLPGGFNLFTPSGGRISPEPM---ELEKNSINIKASTDLGRCAEPAFKT 173
Db 119 ORLKSGGFAFVN-----ADHISPTITIANLERYKENDLKMKDIALCKTHAASF 169
Qy 174 VAMDKNKATKRYRPFVYDSKRLCHILYVSMQLMGKCYCSVKGEPPDLTWYCFKPKS 233
Db 170 VIAEON--TSYRHAIVYDEKNTKTMVLISAQENMGPRYCSPPDSQNKD-AAFCFKPDKN 226
Qy 224 VTENHHLIYGSAVYGENPDATISKCPNOLRGYRGVWKKGKCLDYTELDTLVIERVESK 293
Db 227 -EKFNILVYLSIKVNSD--WENKCPKRIKGNKFGELWVNGCEEI-----PYVNEVEAR 277
Qy 294 A--QCMVTKFENDGVASDQPHY--PLTSGQASNMWMLPHQSDQPHSG----- 337

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Db 278 SLRECNRIVE--ASASDQPTQYEEELTDYEKIQGFRQNNRDMIKSAFLPVGAFAFNSDNF 335
Qy 338 -GVARNYGFYVDTTGCKALSDQVDCIVSDASVYTPAG---SLSEETPFIIIPSN 393
Db 336 KSKGRGYMANPDSV--NNKCYIFNTKPTCLINDKNFATATLSPQEVNDPEPSIKDE 394
Qy 394 -----PSVTPPTETALQCTADKFPDSFGACDVQACROKT 429
Db 395 IEREIKKOSRNNMLYSVDKERIVLPRIPTSDNESIKCPCEPEHISNTGCTNFYVC----- 449
Qy 430 SCV--GGQIOSTSV---VDCTADEQNECGSN--TALLIAGLVGVLALLGCGCYFAK 480
Db 450 NCEVKRAEIKENNQVVIKEEFKEDYENPDGKHKKMLIIIGYGAVCVAVASLFFYFRK 509
Qy 481 RLDNKNQVQAAHHEHFOSGRGARKRPSDLMOEAEPSFDEAEENIEQOGETHYVMEGD 540
Db 510 KAQDDK-----YDKMDQAEAGYKPTTRKDEMLDPEASFWGEDK--RASHTTVLMEKP 561

Qy 541 Y 541
Db 562 Y 562

RESULT 14
Q25747 PRELIMINARY; PRT; 604 AA.
AC Q25747;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB3;
RX MEDLINE=96379227; PubMed=8784778;
RA Marshall V.M., Zhang L., Anders R.F., Coppel R.L.;
RT "Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 77:109-113(1996).
DR EMBL; U33277; AAC47107.1; -
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1
DR PRINTS; PRO1361; MEROZOITESA.
DR NON_TER 604
FT SEQUENCE 604 AA; 69886 MW; 791620C3B2AD342B CRC64;

Query Match 14.4%; Score 419.5; DB 5; Length 604;
Beet Local Similarity 26.6%; Pred. No. 1.2e-27;
Matches 147; Conservative 78; Mismatches 200; Indels 127; Gaps 24;

Qy 41 GNPFOANVEMKTFMERFNLTHHOSGIYVDLGDQKVEDGTLTYREBAGLCPIWKGHIELQ 100
Db 107 GNPW-----TEYAKVVIDEKVHSGIRVLDGEDAEVAGTGYRLPSGKCPVFGKIIEN 160
Qy 101 PDRLPYRNNLEVDVTE-KEYKSGNPRLPGGFNLFTPSGGRISPEPM-----LLEKNS 155
Db 161 S-----KTFPLTPVATENQDLKDGFAFP-----PTBPLISPMFLDQMRHLKYKNE 206
Qy 156 NIKASTDLGRCAEPAFKTVANDKNKATKRYRPFVYDSKRLCHILYVSMQLMGKCYCS 215
Db 207 YVKNIDELTLLCSRHAGN--KNPDDNKSNTKTPAVYDYEKKCHILYIAQENMGPRYCN 264
Qy 216 VKGEPPDLTWYCFKPKR--SVTENHHLIYGSAVYGEN--PDATISKCPNOLRGYRGVWKK 273
Db 265 -KDESKRSMCFRRAKOKLFENT-----TYSKNVVDNMBEYVCPRIKULENAKFGELWVD 317
Qy 274 GRCGLDYTELDTLVIERVESKAQCVVTKTENDGVASDQPHY--LTSQASNMWMLP----- 327
Db 318 GNCEIDIPHVNEF---SANDLFECKNLVPELS--ASDQKQYEOHLTDYEKIQGFRQNNR 372

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OY 328 -----LHSGDQPHSGGVGRNYGYVDTTGECKALSDQVPCLVSDSAVSYT 376
Db 373 SMKSAFLPTGAFKADRYKSRGKYNMGVNTETO---KCEIFNVKPTCLINNSYIAT 429
OY 377 AAGSISEETPNFIISN-----PSTPTPTETA 404
Db 430 ALSHNEVENNF--PCSLDYKEIKKEIERESKRKILNDNDGKNKIAPRIFISDDKDS 487
OY 405 LQCTADKPPDSFGACDVQACKRQKTSVGGQIOSTS-----VPCDAD--EONECG 452
Db 488 LKCPDDEPVLVSSTCNFFVCK-----CCEKRAEVTISNNEVVKERYKDEYADIPEHKPT 542
OY 453 SNTALI---AGLAVGVLLALLGGGCVFAKRLDRNKGVOAHHEHFEQSDRGARKKRP 508
Db 543 DNMKIILIASAAVAVIATILMV-----LYYKR---KG-NAEKTDKMDQPHGKSNR 591
OY 509 SDLMQAEAPSF 520
Db 592 NDEMLDPEASF 603

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RESULT 15

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Q26225 PRELIMINARY; PRT; 557 AA.
ID Q26225 AC Q26225;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Apical membrane antigen-1.
OS Plasmodium yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5861;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17X;
RX MEDLINE=96408692; PubMed=8813699;
RA Kappe S.H., Adams J.H.;
RT "Sequence analysis of the apical membrane antigen-1 genes (ama-1) of
RL MoI. Biochem. Parasitol. 78:279-283 (1996).
DR EMBL, U45971; AAC47194.1;
DR InterPro, IPR003298; Apmem_Agt1.
DR Pfam, PF02430; AMA-1; 1.
DR PRINTS, PRO1361; MEROZOITESA.
SQ SEQUENCE 557 AA; 6351 MW; 34D4EDBCA42903F2 CRC64;

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Query Match 14.3%; Score 419; DB 5; Length 557;
Best Local Similarity 25.3%; Pred. No. 1.1e-27;
Matches 155; Conservative 91; Mismatches 214; Indels 152; Gaps 27;

OY 16 CTIFASGSSSTRSRESQTLASSTSGNPFQANVEM-----KTFMERNL 59
Db 11 CSIIYINISYCS--EGPNQVSDGDN--INVELIPKENTERSIKLINPMDKMEKDI 64
OY 60 THNHOSGIYVDLGQDEYDGLTYREPAGLCPIWGHIELOQPDRLPYRNNEFLQVPTKE 119
Db 65 EKVHSGSIRVDLGEARVENDRIRPSGKCPVIGGIIQNS-----VSLFKPATGNE 119
OY 120 YKSGCN-DLPGGFNLNFTPSGORISPPMELLE---KNSNIKASTDLGRCAEPAFTV 174
Db 120 SVRSGLPFP-----DTDVHISPKSIANLKIWSEHPEILKLNDSICAKHTSPYV 170
OY 175 AMDKNKATKRYRPVYDSKRLCHILYVSMQMGKTKCS---VKSEPDLTITGCKP 230
Db 171 P-GXDAKST-YRHPVAVDKSDSTCYMLYVAQENMGPRYCSNDANNENQP-----FCPTP 223
OY 231 RKSVTENHLIYSAVGEN-PDAFISKCPNOLRGVYVKKGRCLDYTELDTVIER 289
Db 224 EK-IEKYNL-----SYLTKNLRDDWETSCPKNSINAFGIWVDGYCTIDYQ---HYVHE 275
OY 290 VESIAQCVKTFPNDGVASDOPHTY-----PLTSQASW 322

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Db 276 SESILACNOIIFNES--ASDQPKOYERHLEDATKIROGIVERNGKLGEBALLPICS----- 329
OY 323 NDMMPLHOSDQPHSGGVGRNYGYVDTTGECKALSDQVPCLVSDSAVSYTAAAGSLS 382
Db 330 -----YISGQIKSHGKYNMGNT---DSKNNKCIIFETKPTCLINDKNFIATTLSSSTE 380
OY 383 EETPNF-----IIPSN-----PSVPTPTETAQCTADKPPDSF 416
Db 381 EPEENFPCEIYKKNKILAEIKVLINQNTSGNNSIKFPRIFLISDKNSLNCPEPTKISE 440
OY 417 GACDVQACKRQKTSVGGQ---IOSTSV-----DCTADQNECGSNTALIALAGVGVLL 469
Db 441 STCPFYVC-----SCVEQROYIAENNDVILKEEFIGDYENPOKLVIIILIGIITVI 495
OY 470 ALLGGGCVFAKRLDRNKGVOAHHEHFEQSDRGARKKRPSPILMOEAPSFDEAEENIEQ 529
Db 496 LIV--AYYRK-----SGKGENYIDRMQADLDYGSKSRKMDPEVSPMGEDK---RA 544
OY 530 DGETHVAVEGDY 541
Db 545 SHTPVVLMEKPY 556

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RESULT 16

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Q96712 PRELIMINARY; PRT; 622 AA.
ID Q96712 AC Q96712;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum,
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FDL NG;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asemo Bay Cohort Project."
RL MoI. Biochem. Parasitol. 113:279-287 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FDL NG;
RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL, AY016439; AAGS0146.1;
DR InterPro, IPR003298; Apmem_Agt1.
DR Pfam, PF02430; AMA-1; 1.
DR PRINTS, PRO1361; MEROZOITESA.
FT NON TER 622
SQ SEQUENCE 622 AA; 71959 MW; CCD62FCC45228065 CRC64;

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Query Match 14.3%; Score 419; DB 5; Length 622;
Best Local Similarity 26.0%; Pred. No. 1.3e-27;
Matches 148; Conservative 83; Mismatches 215; Indels 124; Gaps 24;

OY 41 GNPQOAVNEMKTFERNLTHNHOSGIYVDLGQDEYDGLTYREPAGLCPIWGHIELOQ 100
Db 107 GNPW-----TEYNAKTIDIEVHSGIRVDLGEBAEVAAGTIRLPSGKCPVFGKGIITEN 160
OY 101 PDRLPYRNNEFLQVPT-EKEYKSGNPLPGGFNLNFTPSGORISPPM-----ELERKNS 155
Db 161 SN-----TTFLKPVATNGQDLKOGFAFP-----PTEPLISPTLDMRDPFYKNE 206
OY 156 NIKASTDLGRCAEPAFTVAMDKNKATKRYRPVYDSKRLCHILYVSMQMGKTKCS 215
Db 207 YVKNLDELITCSRAAGNMI--PDNDKNSNYKYPVAVDDKKCKCHILYIAQENNGPRYCN 264

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0Y      113 DVPT--EKEKXGSGNPLPGGFENINFTVPSQGRISPPMELL-----EKXNSIN KASTDILGRCA 167
Db      113 PVATPDQRKDGSGFAP-----KADHDHISPMTEMLUKARYKONVEMKMLNDALCR 163
0Y      168 EFAFTV--AMDKNKATKRYRPFVYDSKRLCHILVYSQMLEGKRYCSYKVEPDLTWY 226
Db      164 THAASFVMAQDN-----SSYRHFAVYDEKKECTCYMLTISAQENMGPRYCSPPDAQNRAV--F 219
0Y      227 CFKPKRSVT--ENHHLIYGSAVYGENDAITSCPNALGCRGVAKKGRCLDYTELDT 285
Db      220 CFKPKRNSFEF--LVYLSKNVRMDM---KCPKRNKLINAKGVLWVDCBEI-----P 269
0Y      286 VIERVESK--AOCWVYTFENDGVASDQPHPTPLTSGASNMNMWPLHQ----- 330
Db      270 YKVEYEAQDLRECNRIVF--GASASQPIQY-----BEEMTDYQXIQOGRONNREMIKSA 323
0Y      331 -----SDPHSGGVGNRYGFEYYDDTTGEGKALSDVDPCLVSDAASVYTAAGSIS 382
Db      324 FLPVGAFNSDNKFSKGRGFNMWNF---DSVKKKCYIFNKPTCLINDKPIATTAALSHPO 380
0Y      383 EETPFIITPSN-----PSVTPTPETALCTADKPE 413
Db      381 EVDTRF--PCSIYKDEIEREIKKGSNNMMLYSVDSGRYLPRLFISNDKESITCPEPEH 438
0Y      414 DSFGACDVOACRKRKTSYV--GGQIOSTSVDTADBONEGSGN-----TALLAGLA 462
Db      439 ISNSTCNFVYC-----NCVEKRAEIKENNQVAVKEEFRDYUEGGEKSNKOMLIIIGI-- 492
0Y      463 VGVVLLLLLGSGCYFARKLDRNKGQVAAHNEHPEPSDDGARAKKRSDLMOAEPSPFMB 522
Db      493 TGVGVVVA--LASMAYFRKANNDK-----YDMMDAEGYGTTKKDEMLDEASFWGE 545

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RESULT 19			
Q9NFW9		PRELIMINARY;	PRT; 605 AA.
AC	Q9NFW9;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-DEC-2000 (TREMBLrel. 19, Last annotation update)		
DE	Apical membrane antigen 1 (fragment). 83/AWA-1.		
OS	Plasmodium reichenowi.		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
CX	NCBI_taxid=5854;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20416492; PubMed=10960173;		
RA	Kocken C.H.M., Natum D.L., Masegoudji A., Ayi'a B., Dubeld M.A., van der Wel A., Conway D.J., Sanni A., Thomas A.W.;		
RT	"Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AWA-1), comparison with P. falciparum AWA-1, and antibody- mediated inhibition of red cell invasion.";		
RL	Mol. Biochem. Parasitol. 109:147-156(2000).		
DR	EMBL, AJ252087; CAB6387.1; -;		
DR	InterPro, IPR003298; Apmem_Agl.		
DR	Pfam, PF02430; AWA-1. 1.		
DR	PRINTS; PRO1361; MERZOITESA.		
FT	NON_TER 1 605		
FT	NON_TER 1 605		
SO	SEQUENCE 605 AA; 70072 MW; E4959A99D5C880C6 CRC64;		

	Query Match	14.2%	Score 415.5;	DB 5;	Length 605;
	Best local similarity	25.1%	Pred. No. 2,66-27;		
	Matches 143;	Conservative	80;	Mismatches 219;	Indels 127; Gaps 21.
Qy	30 RESQTLSASTS-----GNPFQCNVEMKTYEMERFNLTHHQSGLYVDLGCKEVEDLT_81				
Dd	80 RHEQLPFSNNEIERSVNMYNGNPW-----TEWMARYDDEBYAGSGIRVDLGDADVAAGTQ_133				
Qy	82 YRPRLGCLPIWKSHIELQQPDRLLPYRNNFLIEDVPL-EKEYSKGSNPLLPGCFNLNFVTPTSG_140				

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Db 134 YRVEBGKCPVFGKGIIEINSN-----TTFELFVATGNQDLKDGGFAPF-----PTN 179
Qy 141 ORISFPFME-----LLEKSNITKASTDLGRCAEFATKYAMDNKNKATKRYGPFVYDSKR 196
Db 180 PLMSWMSJDDMRNFYKDNENIKNDELTLCSHAANMV--PNDKSNKSNKYPAVYDEQNK 237
Qy 197 LCHILYVSMQLMEGKKYCSVKGEPPDLTWYCEPKRKYTENHLLIYSAUYEEN--PDAET 255
Db 238 KCHILYIAAGENNNGRYCN-KDQSKRSMFCRPLTKDMSFOUY-----TYSKNVYDNNE 291
Qy 256 SKCPNOALRGYRFGYWKGRCLDYTELDTYIYERESKAQCVKTFENDVASDOPHTYP 315
Db 292 KVCPRKNQNNKFFGLMVGDNCENIPHVNPF---SANDLFECKRLVFEIS--ASDQKQYE 346
Qy 316 --LTSQASWMDWPF-----LHSDOPHSGGVGRNRYGFYVDTTGECKAL 358
Db 347 QHLDYQKIKRGFKNNNAKSMIKSALPLPGAFPAADRYKSHGKYNMGNTVTOQ--KCEI 403
Qy 359 SDQVPECLVSDSAVSYTAAGSLSEETPNFIIPSN-----393
Db 404 FNVKPTCLINNSYIATLALSHPIVEHNPF--PCLSLYKDEIMKEIERESKRITKANDDD 461
Qy 394 -----PSVTPRPETALOCYADKPFDPFSGADQVQACRQKTSYCGGLOSTSVCTA- 445
Db 462 GNKKIIVRIFISDDKESLCEPCDEBMSVNSNCHFFVC-----CVERTEVTSNNEVV 516
Qy 446 -----DEQNEGCSNTALITAGLAVGVLLALLLGGGCTYFAKRLDRNKGYOAAHH 493
Db 517 KEERYKDEYADIPDHKPAVDKMKIITIASAAIILATILM---VYLK-----KTVAEKY 568
Qy 494 EHEFQSDRGARKKRPSDLMOAEKPEFME 522
Db 569 DKMDOPQHGYGSKSRIDEMLPDEASFWBG 597

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SEQUENCE	526 AA	60799 MW	5654E6461BACF5ED CRC64
SO	NON TER	1	1
FT	NON TER	1	1
DR	PRINTS: PR01361; MEROZOITESA.		
DR	Pfam: PF02430; AMA-1; 1.		
DR	InterPro: IPR003298; Apmem_Ag1.		
DR	EMBL: AJ271169; CAB97181.1; -		
RL	Mol. Biochem. Parasitol. 109:147-156(2000).		
RT	mediated inhibition of red cell invasion."		
RT	antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-		
RA	van der Weij A., Conway D.J., Sanni A., Thomas A.W.;		
RA	Kocken C.H.M., Narum D.L., Massouhbodji A., Ayivi B., Dubbeld M.A.,		
RA	MedLine=20416492; PubMed=10960173;		
RC	STRAIN=C9-6.1;		
RP	SEQUENCE FROM N.A.		
RM	[1]		
OC	NCBI_TaxId=55833;		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
GN	83/AMA-1.		
OS	Plasmodium falciparum.		
DE	Apical membrane antigen 1 (Fragment).		
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)		
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)		
DT	01-DEC-2001 (TREMblrel. 19, Last annotation update)		
ID	C9N9G0; PRELIMINARY; PRT; 526 AA.		
AC	C9N9G0;		
AC	01-OCT-2000 (TREMblrel. 15, Created)		
AC	01-OCT-2000 (TREMblrel. 15, Last sequence update)		
AC	01-DEC-2001 (TREMblrel. 19, Last annotation update)		

Query Match 14.1%, Score 41.3, DB 5, length 526;
Best Local Similarity 27.3%, Pred. NO. 3.5e-27;
Matches 124; Conservative 72; Mismatches 161; Indels 98; Gaps 18;

QY 101 PDRLEPNNPLEDYPTKEKYGKSGNPLPGGFNLNVPSPGGRISPFME-----LLEKSN 156
 DB 153 S-----KTTFLTPATENQYIKD-----GFAF--PPTPLMSMTLIDENRHFYKDKY 199
 QY 157 IKASTDLCRCLEFAFKTVAMDKNKATKRYRYPVYDSKKRLCHILYVSMQLEMGKYYCSV 216
 DB 200 VKNDLDELTCGRHAGNM--PDNDKSNYKPAYVDDKDKCHILYIAAGNNGPRYCN- 256
 QY 217 KGEPPDLTWYCFKPKSVTEHHLLYGSAYGEN-PDAFISKCPNALRGYRFGVWKKGR 275
 DB 257 KDESKNMSFCRRPAKDISFONY-----TYSKNVVDNMERYCPRKNLQNNKFGGLWVDGN 311
 QY 276 CLDYTELTD-TVIERVESKACQWKTENDGVASDQHTYP--LTSQASNDMP----- 327
 DB 312 CEDIPHNEFSAIDLEF--CNKLVFELS--ASDQKQYOHULTDYEKIKEGFNKNAS 365
 QY 328 -----LHSDQPHSGVGNVGYVYDTTGECALSDQVPCIVSDSAVSYTA 377
 DB 366 MIKSAFLPTGAFKADRYKSHKGVMGNVNETQ--KCEIFNVKPTCLINSSYIATTA 422
 QY 378 AGSLSEETPNFIIIPSN-----PSVTPPTPETAL 405
 DB 423 LSHPEVHNPF--PCSLYKOEIKKEIERESKRILKNDNDGKKIAPRIFISDDIDSL 480
 QY 406 OCTADKFPDSFGACDVQACRQKTSVGGQIOSTS 440
 DB 481 KCPDPEIVSNSTCNFVCK-----CVERKAXVTS 510

RESULT 21

ID 096738 PRELIMINARY; PRT: 622 AA.
 AC 096738;

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN764;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asembo Bay Cohort Project."
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN764;
 RA Anantia E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY016419; AAG50126.1; -
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 FT NON TER 622
 SQ SEQUENCE 622 AA; 71943 MW; CB26061BCB14E82 CRC64;

Query Match 14.1%; Score 413; DB 5; Length 622;
 Best Local Similarity 25.8%; Pred. No. 4.4e-27;

Matches 147; Conservative 82; Mismatches 218; Indels 122; Gaps 23;

QY 41 GNPFOANVEMKTFMERFNLTTHHQSITYDLGDKKVDGTLREPAGLCPINGKIHLEQQ 100
 DB 107 GNPW-----TEMACYDIEVHSGIRVLDGEDAVAGTQYRLPSGKCPVFGKGIITN 160
 QY 101 PDRLEPNNPLEDYPTKEKYGKSGNPLPGGFNLNVPSPGGRISPFME-----LLEKSN 155

DB 161 SN-----TSFLKPVATGNQDLKDGIAFP-----PTNPILSPMTLDMRDYKQNE 206
 QY 156 NIKASTDLGCAEFAFKTVAMDKNKATKRYRYPVYDSKKRLCHILYVSMQLEMGKYYCS 215
 DB 207 YVKNLDELTCGRHAGN--MPPDDKSNYKPAYVDDKDKCHILYIAAGNNGPRYCN 264
 QY 216 VKGEPPDLTWYCFKPKSVTEHHLLYGSAYGEN-PDAFISKCPNALRGYRFGVWKKGR 274
 DB 265 -KDESKNMSFCRRPAKDISFONY-----TYSKNVVDNMERYCPRKNLEAKGGLWVDG 318
 QY 275 RCLDYTELTD-TVIERVESKACQWKTENDGVASDQHTYP--LTSQASNDMP----- 327
 DB 319 NCEDIPIHNEF--SANDLFCNKLVEELS--ASDQKQYOHULTDYEKIKEGFNKNAS 373
 QY 328 -----LHSDQPHSGVGNVGYVYDTTGECALSDQVPCIVSDSAVSYTA 377
 DB 374 MIKSAFLPTGAFKADRYKSHKGVMGNVNETQ--KCEIFNVKPTCLINSSYIATTA 430
 QY 378 AGSLSEETPNFIIIPSN-----PSVTPPTPETAL 405
 DB 431 LSHPEVHNPF--PCSLYKOEIKKEIERESKRILKNDNDGKKIAPRIFISDDIDSL 488
 QY 406 OCTADKFPDSFGACDVQACRQKTSVGGQIOSTSUDCTA-----DEONECGSN----- 454
 DB 489 KCPDPEIVSNSTCNFVCK-----CVERKAXVTSNNEVVKERYKDEYADIPHKPTTD 543
 QY 455 --TLINGLAVGVLLALLGCGCYFAKRLDRNKGVQAAHHEHFGSDRGARKKRPDLM 512
 DB 544 KMKIILIASAVALATILM--VLYKR--KGNAEKYDKDPODYKGSNR-NDEN 595
 QY 513 QEAEPFWEAEENIEDGETHVAVEGDY 541
 DB 596 LDPASFGEEK---RASHTPVMEKPY 621

RESULT 22

ID 096735 PRELIMINARY; PRT: 622 AA.
 AC 096735;

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN759;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asembo Bay Cohort Project."
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN759;
 RA Anantia E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY016422; AAG50129.1; -
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 FT NON TER 622
 SQ SEQUENCE 622 AA; 72010 MW; F4E1A1E610F4786B CRC64;

Query Match 14.1%; Score 413; DB 5; Length 622;
 Best Local Similarity 26.1%; Pred. No. 4.4e-27;
 Matches 150; Conservative 80; Mismatches 212; Indels 132; Gaps 24;

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OY 41 GNPFOANEMKTFMERFNLTHHNGSIVYDLDQDEKOVSTLYREARGCLPIKMKHLEQO 100
Db 107 GNPW-----TEYMAKYDIEEYVSGSIRDLDEADAEVATQYRLPBGKCPVFGKGIIEH 160
OY 101 PDLRYRNFFLEDVPT-EKEYKOSGNPLPGGGEFLNFTVPSGORISBPFM-----ELLEKNS 155
Db 161 SN-----TFLKRPVATGNODLKDGGFAF-----PTNPLISPTLDMHDFPKKNE 206
OY 156 NIKASTDLGRCAEFAFKTVAMDKNNKATKYRYPVYDSKKRLCHILLYVSMQMEGKKYCS 215
Db 207 YVKNDELTLTGRHAGN--MNPNDKNSNYKKPAAVYDYNDDKKCHILLYIAAENNGGRYCN 264
OY 216 VKGEPPDLWTYFFKPKRKSTENTHHLYLSAYLGEN-PDAFISCKPMQALRGYFPGWKKG 274
Db 265 -KDESKRNSMFCFRPAKDKSFQNY-----TYSKNVYDMWEKVCPRKKNLENAFGLMVDG 318
OY 275 RCLDYTELTDTYIERVESKA-----QCWVKTEPNDGASDOPHTY--LTSQASNDMPW 327
Db 319 NCED-----IPRVNESANDLPECNLTAVELS--ASDOPQYQCHLTVDYEKIEGKR 368
OY 328 -----LHOSDOPHSGGVRNRYGYVDTTGEKCALSDVPCVLVSDAA 372
Db 369 NKNASMIKSAFLPTGAFKADRYKSGKGVNMGVYNRKTO--KCELFVNVKPTCLINNSY 425
OY 373 VSYTAGSISETPNFIIPSN-----PSTVPT 400
Db 426 IATYTLSPHNEVENHF--PCSLYDKEIKEIERESKRILKLNNDDEGNKKIYAFRIFSD 483
OY 401 PETALQCNADKRPDSFGACDVQACKRQKTSYVGGOQSTSVQCTA-----DEQNGCSN 454
Db 484 DIDLCKPCDDPEIVSNSTCNFVCK-----CYEKRAEVTSSNNEVVYKKEYKDYAIPEH 538
OY 455 -----TALNGLAVGVLLTALLLGGGCFYAKRLDRNKGVAALHNHEHFOSDRGARKR 507
Db 539 KPTYDKMKIIIASAVALATILM--YLYLKR-----KGNMEKYDMDEPDQYGSNSR 591
OY 508 PSDLMQBAEPFWMDEABENIEDGGETHWVVEGDY 541
Db 592 -NDEMLDPEASFWGEEK--RASHTTPYLMEMKRY 621

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RESULT 23
09TY48
ID 09TY48 PRELIMINARY; PRT, 621 AA.
AC 09TY48;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Apical membrane antigen-1 (fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_taxid=5833;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=FVO;
RA Aguilar J.C., Hoffman S.L.;
RT "The immunogenicity and protective efficacy of Plasmodium falciparum AMA-1 DNA vaccines."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBD databases.
DR EMBL; U84348; AF003790.1; -
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1, 1.
DR PRINTS; PR01361; MEROZOITESA.
DR NON TER 621
FT SEQUENCE 621 AA; 71921 MW; 6EA2A8C512DBA7D CRC64;
SQ
Query Match 14.1%; Score 412.5; DB 5; Length 621;
Best Local Similarity 26.1%; Pred. No. 4,9e-27;
Matches 149; Conservative 80; Mismatches 216; Indels 125; Gaps 25
41 GNPFGANVEMKTFMERFNLTHHGSGIYVDLQDKEVDDTLVREPAGLCPINGKHILQQ

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Db 107 GNPW-----TEYMAKVDIEVHSGIGIVDLSEDAEVAQTQRLRBSGCKPVEFGKIIEN 160
QY 101 PDRLREYNNFLEVDPT-EKEYKQSGNPLRGFGNLFVTPESGORISBPM---ELLEKUS 155
Db 161 SN-----TTFLKRPVATGNQDLKDGGFAFP-----PTNPLISMTLNGMDPYKUNE 206
QY 156 NIKASTDGRCAEPFKTVAMDKNKATKTRRPFYDSSKKRLCHILYVSNQMLEGGKTCY 215
Db 207 YVKNLDELTLTCSRHAGN--MNPNDKNNSYKYPAYVDYNDKCHILYIAOENNGERYCN 264
QY 216 VKGEPPDLTWCKCFKARK-SYVENHHLIYSAAVGN-PDAFISCKNOALRGYRFGYWK 273
Db 265 -KDOGKNSMFCFRAKDKLPENT-----TLYSKVVDNMBEVCCRKLLENAKFGIAMD 317
QY 274 GRCLDYTELTDVIERVESKAQWVKTENDVASDQPHTPP--LTSQASWMDWP----- 327
Db 318 GNCEDIPIHVNPE---SANDLFECKNLTVFLFS--ASDQRPQYQHLLTDEKIKGFGFNKNA 372
QY 328 -----LHOSDDPHSGSGVGKNYGFYYDTTGEGKALSDDVFDCLVSDSAVSYT 376
Db 373 SMKSAFLPTGAFKADRYKSHGKGWGNVNETQ---KCELFNVKFPCLINNSXYIATT 429
QY 377 AAGSLSEETPNPLI-----PSNPVYPP---TPEHALQC 407
Db 430 ALSHPIEVEHNPPCSLYKDEIKGIERESKRKIKLNDNDEGKEKIIAPRIFLSDKSLKC 489
QY 408 TADKFPDPSFACDVACAKROKTSYVCGOIQST-----VDCTAD--EONECGSNT 455
Db 490 PCDEPMVNSNCRFPVCK-----CYERRAEVTSNNBEVVUKEVEKDEYALIIPEIKRPFYDNN 544
QY 456 ALI---AGLAVGVLLIALLGGGCFYAKRLDRNKGVOAAHHEHFEQSDRGARKRPSDL 511
Db 545 KIILASSAAVAVLTIILMV-----YLYKR---KG-NAEKYDKMDQPOHYGKSTSRNDE 593
QY 512 MOEAEPSPFMDAEENIEDQETHVNVVEDY 541
Db 594 MLDPASFWGEEK--RASHTTPVLMEXPY 620

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[illegible]

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DB 67 VHGSGIRVDLGDADARVENDYRIPSGKCVITSEGITIQNSE-----VSLTKVAHAGDKRV 121
QY 121 KOSGNPLPGGFMNFVTPSGORISPPPM-----ELIEKNSNIKASTDLGRCFAFRTVAM 176
DB 122 RSGGLAFLP-----ETDVHISPTITNLTKWYKHODIYNLNDMSICAHGT--SLVY 170
QY 177 DKNKATKTRYPYVDSKRLCHILYVSOQLMEGKYCS-----VKGEPTDLTWYCKPRK 232
DB 171 PKKDATSARHRYVVDKSNSTCYMLVYAAQEMNGPRYCSNDANNENQP-----FCTPERK 225
QY 223 STENHHLIYGSAYGEN--PDAFISKCPQALRGYFVGWKKGRCLDTYELDTYERIE 291
DB 226 --TENYKDI--SYLTKNLRDWERTSCPKSIKNAKFGIWDGYCTDYK--HVHDS 277
QY 292 SKAQCVKTFENDGVAADQPHTY-----PLTSQASWMD 324
DB 278 SLKKNQIIFNES--ASDQPKQYERHLEDATKIAQIVERNKLGIEALLPIS----- 329
QY 325 WMPFHOSDOPHSGGVRNGYFYVDITGEGKCALSDQVDCLVSDSAVSYTAAGLSRE 384
DB 330 ---YKSGQIKSHGKGYMNGY---DSKNNKCYIFETKPTCLINDKNFIATLALSTEEF 382
QY 385 TENF-----IIPSN-----PSVTPPTETALQCTADKFPDSFGA 418
DB 383 EENFCEIYKAKIAEIKYLNQNTSNGNSIKFRIFISTDKSLNCPDPTKLTST 442
QY 419 CDVQACKROKTSQVCGQ---IOSTSV---DCTADQNECGSNTALIAVLAVGVLLAL 471
DB 443 CEFYVC-----SCVEQROYIAENNDYIIEKEFIGDYENPKOKLLIIVIGIILVILL 497
QY 472 LGGGCFARLDRNKVQAHHHEFOSDRGARKRPSDLMQAEESFDEAEENIEQOG 531
DB 498 V---AYYFK-----SGKGENYDRMGQADYGKSKRDEMIDPEVSFWGDK--RASH 546
QY 532 ETHVWVEGDY 541
DB 547 TTPVLMEXKY 556

RESULT 25
Q95NZ1 PRELIMINARY; PRT; 622 AA.
AC 095NZ1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=5833;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VEN767, and VEN762;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
RT 1) of Plasmodium falciparum. X. Asemo Bay Cohort Project.";
RL Mol. Biochem. Parasitol. 113:279-287 (2001).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=VEN767, and VEN762;
RA Anandas E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY016416; AAC50123.1;
DR EMBL; AY016418; AAC50125.1;
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MEROZOITESA.
FT NON_TER 622 622

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SQ SEQUENCE 622 AA; 71991 MW; 129C8715D8E29243 CRC64;
Query Match 14.1%; Score 412; DB 5; Length 622;
Beet Local Similarity 25.8%; Pred. No. 5.4e-27;
Matches 147; Conservative 81; Mismatches 219; Indels 122; Gaps 23;

QY 41 GNPEQANVEMKTFMERFNLTHHOSGIYVDIGODKEVGTLYREBAGLCPIWGIHEDQ 100
DB 107 GNPM-----TEYMAKVIIEVHSGIRVDLGEDAEVAGTQYRLPSGCGPVGKIIEN 160
QY 101 PDRLPYRNNPLEDVPJ--EKYKQSGNPLPGGFMNFVTPSGORISPPM---ELLEKNS 155
DB 161 SN-----TTFILKPVATGNQDLKDGGFAP-----PTWPLSLPMLDHRDYPKNE 206
QY 166 NIKASTDGRCAEPFAFKVADKNNKATKRYRPFYVDSKRLCHILYVSOQLMEGKYCS 215
DB 207 YKKNLDELTLCSRAHGN--MNPDDKSNYKPAYDYNDKKCHILYTAAGDNNGPRICN 264
QY 216 VKGEPPDLTWYCFKPKSVTENHHLIYGSAYGEN--PDAFISKCPQALRGYFVGWKKG 274
DB 265 -KDESKRSMCFRPAKOKSFQNY-----TSLKVVVDNWEKVCPRKXLENKAPGLWVDG 318
QY 275 RCLDYTELDTYVIERVESKAQCWKTENDGVAADQPHTYP--LTSQASWMDWP----- 327
DB 319 NCEDIPHYNEF---SANDLFECNKLVEFELS--ASDQPKQYERHLEDATYERIKEGFNKQAS 373
QY 328 -----LHQSOPHSGGVRNGYFYVDITGEGKCALSDQVDCLVSDSAVSYTA 377
DB 374 MIKSAFLPTGAFKADRYKSRGKYNWGNRYNRKIQ--KCEIFNVKPTCLINNSIATTA 430
QY 378 AGSLSEETPNFIIPSN-----PSVTPPTETAL 405
DB 431 LSHPNVEVHNF--PCLYKDEIKKEIERESKRILKNDNDEGNKKIIPRIISDIDBL 488
QY 406 OCTADKFPDSFGACDVQACKROKTSQVCGQIOSTVDCIA-----DEONECGSN----- 454
DB 489 KCPDCEPIVSNSTCNPFVCK---CVKRAEVTSNNNEVWKEBYKDEVADIPKPKPTVD 543
QY 455 --TALIAVLAVGVLLALLGGGCFARLDRNKVQAHHHEFOSDRGARKRPSDLM 512
DB 544 KKKIITIASAAYAVLATITM--VLYLR---KQNAEKYDKMDPEODYGSNSR--NDEM 595

RESULT 26
Q967J9 PRELIMINARY; PRT; 622 AA.
AC 0967J9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=5833;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VEN765;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
RT 1) of Plasmodium falciparum. X. Asemo Bay Cohort Project.";
RL Mol. Biochem. Parasitol. 113:279-287 (2001).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=VEN765;
RA Anandas E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;

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RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY016417; AAC50124.1; -

DR InterPro; IPR003298; Apmem_Agl.

DR Pfam; PF02430; AMA-1; 1.

DR PRINTS; PR01361; MEROZOITESA.

FT NON TER 622 622

SQ SEQUENCE 622 AA; 71965 MW; C913CDB2C92A330 CRC64;

Query Match 14.1%; Score 412; DB 5; Length 622;

Best Local Similarity 25.6%; Pred. No. 5.4e-27;

Matches 147; Conservative 84; Mismatches 210; Indels 134; Gaps 24;

41 GNPPQAVNEMKTFERNLTHHOSGIYVDLGDKEVDGLYRBPAGLCPWKGHLEQ 100

107 GNPP-----TEYAKVDIEVHSGIRVDGEBAEVAAGTQYRLPSGCPVFGGIIEN 160

101 PDRLPYNNFLSDVPT-EKEYKQSGNPLPGGFNLFTVPSGORISPPFM---ELLEKNS 155

161 SN-----TFLKPVATGNQDLKDGFAFP-----PTNPILSPMTLDHMRDFFYKNE 206

156 NIKASTDLGRCAEFAFTVANDKNNKATKYRPPVYDSKRLCHILVYSMQLMEGKYCS 215

207 YVKRLDELTLCSRHAGN--NRPDNDKSNVYCPAYVDYNDKKCHILYIAQENNGPRYCN 264

216 VKGEPDLYWCYCFKPKSVTENHHLIYSAVYGEN-PDAFISKCPNQLRGYRFGWKKG 274

265 -KDSKSNMCFRPAKDKSFQNY-----TYSKNVVDWMEKVCPRKULENAKGLWVDG 318

275 RCLDYELTDTVIERVESKACQWKTPENDVASDOPHTYP--LTSQASNDWMP----- 327

319 NCEDIPIHNEF---SANDLFECKNLVFEIS--ASDOPQYEQHITDYEKIKEGKNKAS 373

328 -----LHOSDQPHSGGVGNVGYVYDTTGEGKCALSDQVPCLVSDSAVSYTA 377

374 MIKSAFLPTGAFKADRYKSGKGYMGNVNRKQ---KCEIFNVKPTCLINSSYIATTA 430

378 AGSLSEETPFIIPSN-----PSVTPPTPETAL 405

431 LSHNEVEHNF--PCLSYKDEIKKEIERESKRILKLNDDGNNKIIFRISDDDSL 488

406 QCTADKPPDFGACDVQACRKQKTS CVGGQIQSTG-----VDC-----TAD 446

489 KCPEDPEIVSNSTCNFVCK-----CYEKRAEVTSNSEVVVKEEYKDEYADIPHKPTVD 543

447 EQNCGSNTALLIAGLVGVLALLLGGCGYFAKRLDRNKGVAAHNEHFGSDRGARKK 506

544 KMKIIIISSAAVAVLAT--ILMV-----YLTKR---KGAERKXDKMDPRDQYKSN 590

507 RPSDLMOEAPSFWDSEENIEODETHVWEGDY 541

591 R-NDEMLDPEASFWEK---RASHTTPVLMEXKY 621

RESULT 27

000784 PRELIMINARY; PRT; 620 AA.

AC 000784; PRELIMINARY; PRT; 620 AA.

DT 01-JUL-1997 (TREMblrel. 04, Created)

DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)

DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)

DE Apical membrane antigen-1 (Fragment).

GN AMA-1.

OS Plasmodium falciparum (isolate Kf1916).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=51269;

RN NCBI_TaxID=51269;

RP SEQUENCE FROM N.A.

RC STRAIN=Kf1916;

RA Eileen D., Marshall J.M., Billman-Jacobe H., Coppel R.L.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

RN [12]

RT SEQUENCE FROM N.A.

RC STRAIN=Kf1916;

RA Eileen D.P., Marshall J.M., Billman-Jacobe H., Coppel R.L.;

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; U90276; AAB50405.1; -

DR InterPro; IPR003298; Apmem_Agl.

DR Pfam; PF02430; AMA-1; 1.

DR PRINTS; PR01361; MEROZOITESA.

FT NON TER 620 620

SQ SEQUENCE 620 AA; 71721 MW; 9194F06A0D138677 CRC64;

Query Match 14.0%; Score 410.5; DB 5; Length 620;

Best Local Similarity 26.4%; Pred. No. 7.3e-27;

Matches 146; Conservative 76; Mismatches 206; Indels 125; Gaps 24;

41 GNPPQAVNEMKTFERNLTHHOSGIYVDLGDKEVDGLYRBPAGLCPWKGHLEQ 100

107 GNPP-----TEYAKVDIEVHSGIRVDGEBAEVAAGTQYRLPSGCPVFGGIIEN 160

101 PDRLPYNNFLSDVPT-EKEYKQSGNPLPGGFNLFTVPSGORISPPFM---ELLEKNS 156

161 SN-----TFLKPVATGNQDLKDGFAFP-----PTNPILSPMTLDHMRDFFYKNE 207

157 IKASTDLGRCAEFAFTVANDKNNKATKYRPPVYDSKRLCHILVYSMQLMEGKYCSV 216

208 YVKRLDELTLCSRHAGN--NRPDNDKSNVYCPAYVDYNDKKCHILYIAQENNGPRYCN 264

217 KGEPPDLYWCYCFKPKSVTENHHLIYSAVYGEN-PDAFISKCPNQLRGYRFGWKKG 274

265 KDSKSNMCFRPAKDKLFENY-----TYSKNVVDWMEKVCPRKULENAKGLWVDG 318

275 RCLDYELTDTVIERVESKACQWKTPENDVASDOPHTYP--LTSQASNDWMP----- 327

319 NCEDIPIHNEF---SANDLFECKNLVFEIS--ASDOPQYEQHITDYEKIKEGKNKAS 373

328 -----LHOSDQPHSGGVGNVGYVYDTTGEGKCALSDQVPCLVSDSAVSYTA 377

374 MIKSAFLPTGAFKADRYKSGKGYMGNVNRKQ---KCEIFNVKPTCLINSSYIATTA 430

378 AGSLSEETPFIIPSN-----PSVTPPTPETAL 405

431 LSHNEVEHNF--PCLSYKDEIKKEIERESKRILKLNDDGNNKIIFRISDDDSL 488

406 QCTADKPPDFGACDVQACRKQKTS CVGGQIQSTG-----VDC-----EQNEGS 453

489 KCPEDPEIVSNSTCNFVCK-----CYEKRAEVTSNSEVVVKEEYKDEYADIPHKPTVD 543

454 NTALI-----AGLVGVLALLLGGCGYFAKRLDRNKGVAAHNEHFGSDRGARKKPS 509

544 NMKIIIISSAAVAVLATILMV-----YLTKR---KG-NAEKYDKMDOPQHYKSTSRN 592

510 DLMOEAPSFWDSE 522

593 DEMLDPEASFWE 605

RESULT 28

025657 PRELIMINARY; PRT; 556 AA.

AC 025657; PRELIMINARY; PRT; 556 AA.

DT 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Apical membrane antigen-1.

OS Plasmodium berghei (strain Anka).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=5823;

RN NCBI_TaxID=5823;

RP SEQUENCE FROM N.A.

RC STRAIN=ANKA;

RA Kappe S.H., Adams J.H.;

RL MEDLINE=96408692; PubMed=8013699;

RT "Sequence analysis of the apical membrane antigen-1 genes (ama-1) of Plasmodium yoelii yoelii and Plasmodium berghei."

RL Mol. Biochem. Parasitol. 78:279-283 (1996).
 DR EMBL; U45969; AAC47192.1; -;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR SEQUENCE 556 AA; 63660 MW; DB6FCE5E0FPE26 CRC64;

Query Match 14.0%; Score 410; DB 5; Length 556;
 Best Local Similarity 23.9%; Pred. No. 6.9e-27;
 Matches 148; Conservative 110; Mismatches 212; Indels 148; Gaps 27;

6 VQVLLVADCTPAGSGSSSTRS-----RESQTLASTSGNPROAWE 49
 4 IYVLLI--CSYVILNLSNCSGEGNNVISENGHINIMQKENTERSTKILNPE---- 56
 DB 50 MKTWERENLTHHOSGIYVDLGQDKEVDGTLREPAGLCPHWGHIHQDRLPYENN 109
 57 --KTEKVDIERMOSGIRVDGEDARVENRDYRIPSKCPVIGKITLQNSE-----VS 109
 DB 110 FLEDPVT-EKEYKOSGNPLPGGFNLNFTVTPSGQRISPPME---LLEKSNITKASTDLG 164
 110 FLTPATGDSVRSGLALP-----KTDVHLSPITIDILKTMKEHEIYVLNMS 160
 DB 165 RCAFAPFTVAMDKNKATKYRPPYVDSKKRLCHILYVSMQMEGKXYCSVKGEPPDLT 224
 161 LCAKRT--SFYVPGNANSAYRHPAVYDKNSTCYMLYVAQENNGPRYCS--NNANDNQ 217
 DB 225 WYCFKPKSVTENHLLIYGSAYVGEN-PDAFISKCPNOLRGYRPGVWKRCGLDYELT 283
 218 PFCFPER-IEKYKOL-----SYLTGNLRDMDMETSCPNISIKNAKGIWVDGCKYQKHT 272
 DB 284 DTVIERVESKAOQWVKTEPNDGVASDQHTY-----PL 316
 273 ---VHDSLSLKCNQIIFNES--ASDQKQYEHLEDTTKFRQVGAERNGKLIGALLPI 327
 DB 317 TSQAAMNWMWPLHOSDOPHSGGVGRNYGYVDTTGEKCALSDQVPCLVSDSAVSYT 376
 328 GS-----YKSDQIKSHGRGYNWNY--DSQNK-KCYIFETKPTCLINDRFIATY 374
 DB 377 AAGLSSEETPNF-----IIPSNPSVTPP-----TPETALQCTADKF 412
 375 ALSSTIEPEPEQPCDIYKKNKINEIKVLKNKISNGNSIEPRIFISTDKSLNCPCEPT 434
 DB 413 PDSFACDVQAC---KROKTCVGGQISTSYDCTAD-----EQNEGCSNALLAGLAY 463
 435 QLTBSSCNFYVCNVCYKQYIA-----ENNDEVEIKELLEVAMKHAQREVIIVIIIFCV 488
 DB 464 GGVLILLALIGGCYFAKRLDRNKGVQAANHEHFOSDRGARKKPSDLMOEAPSFWDPA 523
 469 GILLVILLVG---YFPK--SNK--KGENYDMGQADYIGKANSRKDGLDEVSFWGSD 540
 DB 524 BENIBODEGTHVWEGDY 541
 541 K---RASHTTPVLMKERY 555

RESULT 29

095NJ2 PRELIMINARY; PRT; 622 AA.
 ID 095NJ2
 AC 095NJ2
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SL81, and T422;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,

RA Nahlen B.L., Lai A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asambo Bay Cohort Project."
 RL Mol. Biochem. Parasitol. 113:279-287 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SL81, and T422;
 RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S., Nahlen B.L., Lai A.A.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY016429; AAG50136.1; -;
 DR EMBL; AY016430; AAG50137.1; -;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR NON TER 622 622
 FT SEQUENCE 622 AA; 72025 MW; C28A612D8F2A80 CRC64;

Query Match 14.0%; Score 410; DB 5; Length 622;
 Best Local Similarity 26.0%; Pred. No. 8.1e-27;
 Matches 149; Conservative 80; Mismatches 214; Indels 130; Gaps 25;

41 GNPPQAVNEMKTFMERENLTHHOSGIYVDLGQDKEVDGTLREPAGLCPHWGHIHQ 100
 107 GNPP-----TEYAKVDIEVHSGSIRVDGEDAEVAGTQYRLPSGKCPVFGKIIEN 160
 DB 101 PDRLPYRNNFLIEDPVT-EKEYKOSGNPLPGGFNLNFTVTPSGQRISPPME---ELLEKNS 155
 161 SN-----TTFKAPATGNGQDKDGFAP-----PTNPLISPMTLNGMRDPYKNE 206
 DB 156 NIKASTDGRCAFAPFTVAMDKNKATKYRPPYVDSKKRLCHILYVSMQMEGKXYCS 215
 207 YVKNLDELITLCSRAAGN--NMPDNDKSNYKYPAYVOYNDKKCHILYVAQENNGPRYCN 264
 DB 216 VKGEPPDLTWYCFKPKR-SYTENHLLIYGSAYVGEN-PDAFISKCPNOLRGYRPGVWK 273
 265 -KDSKRSNMFCEFRPAKDKLPENY-----YLSKNVVDNMEVCPRKLNNAKFGWLVD 317
 DB 274 GRCLDYELDTVIERVESKAOQWVKTEPNDGVASDQHTY--LTSQANNDWMP----- 327
 318 GNCEIDIPHNVEF---SANDLEFCNKLVFELS--ASDQKQYEHLEDTTKFRQVGAERNGKLIGALLPI 372
 DB 328 -----LHOSDOPHSGGVGRNYGYVDTTGEKCALSDQVPCLVSDSAVSYT 376
 373 SMKSAFLPTGAFADRYKSHGKYNWNYRERQ--KCEIFNVKPTCLINNSYIATY 429
 DB 377 AAGLSSEETPNFIIPSN-----PSVTPTPTETA 404
 430 ALSHPIEVENHF--FCSLYKDEIKKEIERESKRILKLANDDEGNKKIAPRIFISDDKDS 487
 DB 405 LQCTDKRPDSFGACDVQACKROKTSVGGQISTSYDCTAD--EQNECG 452
 488 LKPCDPPEMVSNSGTRFVCK-----CVERBAEVLSNNEVVYKERYKDEYADIPHKRTY 542
 DB 453 SNTALI-----AGLAVGVALLALIGGCYFAKRLDRNKGVQAANHEHFOSDRGARKKRP 508
 543 DNKKIILISSAANAVLATILNV-----YLYKR-----KG-NAEKYDKKDQPHYKSTSR 591
 DB 509 SDLMQABSPFWEDEAENIBODEGTHVWEGDY 541
 592 NDEMIDPEASFWEGER---RASHTTPVLMKERY 621

RESULT 30

0967J6 PRELIMINARY; PRT; 622 AA.
 ID 0967J6
 AC 0967J6
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN768;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
 RT 1) of Plasmodium falciparum. X. Asembo Bay Cohort Project."
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN768;
 RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AY016421, AAG50128.1, -
 DR InterPro, IPR003298; Apmem_Ag1.
 DR Pfam, PF02430; AMA-1, 1.
 DR PRINTS, PRO1361; MEROZOITESA.
 DR NON_TER 622
 FT SEQUENCE 622 AA; 71992 MW; F6D2CC94F7CDF041 CRC64;

Query Match 14.0%; Score 410; DB 5; Length 622;
 Best Local Similarity 25.8%; Pred. No. 8.1e-27;
 Matches 147; Conservative 80; Mismatches 220; Indels 122; Gaps 23;

OY 41 GNPFQAVNEMKTFMERFNLTHHOSGIYVDLGDKENVDTLYRPAAGLCPTWGHIELOQ 100
 DB 107 GNPF-----TEYAKKDIEVHSGIRVDLGDAEVAAGTQYRLPSGCPVFGKGIILEN 160
 OY 101 PDRLPYRNNFLEDPVT-EKEYKOSGNPLPGGFNLFTVPSGORISPPME---ELLEKNS 155
 DB 161 SN-----TTFKAPVATGNODLKOGFAFP-----PTNPILSPMTLDHMRDPTKANE 206
 OY 156 NIKASTDLGRCABFAFTVAMDKNKATKYRPPVYDSKKRLCHILYVSMQMEGKKYCS 215
 DB 207 YVKMLDELTLCSRHAGNNPPDDKN--SNYKYPAYVDYNDKKCHILYIAQENNGPRYCN 264
 OY 216 VKGPPDLTYCFPRKRSVTENHILYGSAYVGEN-PAFISKCPNOLRGYRGVWKKG 274
 DB 265 -KDSKSNMFCFRPADKSFQNY-----TYSKVVNDNMKVCPRKULENAKFGWLVDG 318
 OY 275 RCLDYTELDTVIRVESKAOQCVKTFENDGVAADQPTYP--LTSQASWMDWP----- 327
 DB 319 NCEDIPIVNEF---SANDLFECKNLVFEIS--ASDQPKQYEQHLTDYEKIKEGFKKNKAS 373
 OY 328 -----LHOSDQPHSGGVGRNYGFYVDTTGEGKCALSDQVDDCLVSDSAVSYTA 377
 DB 374 MIKSAFLPTGAFAADRYKSRGKYNMGVNNKTKQ---KCEIFNVKPTCLINSSYIATTA 430
 OY 378 AGSLSEETNFIISN-----PSVTPTPTPTAL 405
 DB 431 LSHNEVEHNF--PCSLYKDEIKKEIERESKRIKLNDDNDEGNKKIIARIFISDDIDSL 488
 OY 406 OCTADKFPDPSGACDVQACKROKTSYVGGQIOSTSVDTA-----DEQNSCGSN----- 454
 DB 489 KCPDDEPVSNSSTCNFVCK-----CCEKRAEVTSSNNEVVYKEKYKDEYADIPHKPTPD 543
 OY 455 --TALLAGLAVGVLLALLGGGCFPAKRLDRNKGVQAAHNEHFOSDGRARKRPSDLM 512
 DB 544 KMKIIIISSAAVAVLATILM---VLYKR-----KGNMEKDYKMBPDQYGSNSR-NDEN 595
 OY 513 QEAPPSFWDEAENIEDDGETHVAVEGDY 541
 DB 596 LDPEASFWGEEK---RASHTTPTVLMEXKY 621

RESULT 31
 ID O9N9B4 PRELIMINARY; PRT; 526 AA.
 AC O9N9B4;

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Apical membrane antigen 1 (Fragment).
 GN 83/AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=7-9-1.
 RX MEDLINE=20416492; PubMed=10960173;
 RA Kocken C.H.M., Narm D.L., Massouhoudji A., Ayivi B., Dubbeld M.A.,
 RA van der Wel A., Conway D.J., Sanni A., Thomas A.W.;
 RT "Molecular characterisation of Plasmodium reichenowi apical membrane
 RT antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-
 RT mediated inhibition of red cell invasion."
 RL Mol. Biochem. Parasitol. 109:147-156(2000).
 DR EMBL, AJ271185; CAB97197.1, -
 DR InterPro, IPR003298; Apmem_Ag1.
 DR Pfam, PF02430; AMA-1, 1.
 DR PRINTS, PRO1361; MEROZOITESA.
 DR NON_TER 1
 FT SEQUENCE 526 AA; 60917 MW; C6522FB072078D2D CRC64;

Query Match 13.9%; Score 407; DB 5; Length 526;
 Best Local Similarity 27.0%; Pred. No. 1.2e-26;
 Matches 123; Conservative 72; Mismatches 161; Indels 100; Gaps 18;

OY 41 GNPFQAVNEMKTFMERFNLTHHOSGIYVDLGDKENVDTLYRPAAGLCPTWGHIELOQ 100
 DB 99 GNPF-----TEYAKKDIEVHSGIRVDLGDAEVAAGTQYRLPSGCPVFGKGIILEN 152
 OY 101 PDRLPYRNNFLEDPVT-EKEYKOSGNPLPGGFNLFTVPSGORISPPME---ELLEKNS 155
 DB 153 S-----KTFELTPVATENODLKOGFAFP-----PTNPILSPMTLDHMRDPTKANE 198
 OY 156 NIKASTDLGRCABFAFTVAMDKNKATKYRPPVYDSKKRLCHILYVSMQMEGKKYCS 215
 DB 199 YVKMLDELTLCSRHAGNMT--PDNDKSNYKYPVYDQKCKCHILYIAQENNGPRYCN 256
 OY 216 VKGPPDLTYCFPRKRSVTENHILYGSAYVGEN-PAFISKCPNOLRGYRGVWKKG 274
 DB 257 -KDSKSNMFCFRPADKSFQNY-----TYSKVVNDNMKVCPRKULENAKFGWLVDG 310
 OY 275 RCLDYTELDTVIRVESKAOQCVKTFENDGVAADQPTYP--LTSQASWMDWP----- 327
 DB 311 NCEDIPIVNEFSAIDLE---CNKLVEFELS--ASDQPKQYEQHLTDYEKIKEGFKKNKNA 364
 OY 328 -----LHOSDQPHSGGVGRNYGFYVDTTGEGKCALSDQVDDCLVSDSAVSYT 376
 DB 365 SMIKSAFLPTGAFAADRYKSHGKYNMGVNNYNTETQ---KCEIFNVKPTCLINSSYIATTA 421
 OY 377 AAGSLSEETNFIISN-----PSVTPTPTPTAL 404
 DB 422 ALSHPIVENNF--PCSLYKDEIMKETERESKRIKLNDDNDEGNKKIIARIFISDDKDS 479
 OY 405 LQCTADKFPDPSGACDVQACKROKTSYVGGQIOSTS 440
 DB 480 LKCPXDPEVNSNSTCRFFVCK-----CVERRAEVTSS 510

RESULT 32
 ID O967J7 PRELIMINARY; PRT; 622 AA.
 AC O967J7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VEN763;
RX MEDLINE=21195561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaroj S.C., Magris M., Biewas S.,
Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asemo Bay Cohort Project.";
RL Mol. Biochem. Parasitol. 113:279-287(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VEN763;
RA Ananias E.A., Grebert H.M., Chaiyaroj S.C., Magris M., Biewas S.,
Nahlen B.L., Lal A.A.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY016420; AAG50127.1;
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
DR NON_TER 622
FT 622
SQ SEQUENCE 622 AA; 71989 MW; 468816B752CA30D4 CRC64;

Query Match 13.9%; Score 407; DB 5; Length 622;
Best Local Similarity 25.7%; Pred. No. 1.5e-26;
Matches 146; Conservative 81; Mismatches 220; Indels 122; Gaps 23;

QY 41 GNPFOANVEMKTEFRNLTTHHOSGIYVDIGDKVEDGTLYRPAAGLCPTWGHIELOQ 100
DB 107 GNPW-----TEYMAKYDIEVHSGIRVLDGEDAEVAGTQYRLPSGKCVFGGIIEN 160
QY 101 PDRLEPRNNFLEDPVT-EKEYKOSGNPLPGGFNLVFTPSGORISPPM-----ELLEKNS 155
DB 161 SN-----TTFLEKPVATGNQDLKDGFAFP-----PTNPLISPMTLNMRPFYKNE 206
QY 156 NIKASTDLCRCAEFAFTVAMDKNKATKRYRPFYVDSKKRLCHILYVSMQMECKKYCS 215
DB 207 YKNDDELTLCSRHGN--MNPNDKNSNYKYPAYVDYNDKCKCHILYIAQENNGPRYCN 264
QY 216 VGEPRDILTWYCFKPKRKSTENHLLYGSAYYGEN-PDAFISKCPNALRGYRGVWKKG 274
DB 265 -KDESKNSMFCFRPAKDKSPFY-----TYSKVVVDNWEKVCPRKULENAKFGELWVD 318
QY 275 RCLDYTELDTLYIERVESKAQCWKTENDGVASDOPHTP--LTSQASNDWMP----- 327
DB 319 NCEBDFPHVNEF--SANDLFECNKLVFELS--ASDQPKQYEQHILTDYEKIKEGFKKNAS 373
QY 328 -----LHOSDPHSGGVGNRYGFYVDTTGGKCALSDQVPDCLVSDSAVSYTA 377
DB 374 MIKSAFLPTGAFAKADRYKRGKGYMGNVNRQTQ--KCEIFNVKPTCLINNSSYIATTA 430
QY 378 AGSLSEETPNFIIPSN-----PSVTPPTPEETA 405
DB 431 LSHPNVENHF--PCSLYKDEIKKEIERESKRIKLANDNDGKNKIIPRIETSDIDBL 488
QY 406 OCTADKRPDSFGADVQACKRQKTSYVGQ--IGTSYDCTADEONECG----- 452
DB 489 KCPCEDEIYSNCSNCFVCK-----CYEKRAEYISNNEVVVKEEYKDEYADIPENKPTYD 543
QY 453 SNTALILAGLAVGVLLALLGGCCYFAKRLDRNKGYQAANHEHPEPSDRGARKRPSDL 512
DB 544 KMKIILIASAANVAVLATILM-----VLYYKR--KGNAEKYDKNDPODYGKNSR-NDEN 595
QY 513 QEAEPSEFMDAENIEODGETHYMVEDGY 541
DB 596 LDPEASFWGEEK--RASHTTPVLMCKPY 621

RESULT 33
ID 096VB7
AC 096VB7;
PRELIMINARY; PRT; 605 AA.

DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Apical membrane antigen 1 (fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVO;
RA Kocken C.H.M., Dubbeld M.A., Herrera S., Thomas A.W.;
RT "Diversity of Apical Membrane Antigen 1 sequence in Plasmodium falciparum FVO strain."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277646; CAC05390.1;
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
DR NON_TER 1
FT 1
FT NON_TER 605
SQ SEQUENCE 605 AA; 69897 MW; FED89F02F7690C19 CRC64;

Query Match 13.9%; Score 406.5; DB 5; Length 605;
Best Local Similarity 26.2%; Pred. No. 1.6e-26;
Matches 145; Conservative 77; Mismatches 205; Indels 127; Gaps 24;

QY 41 GNPFOANVEMKTEFRNLTTHHOSGIYVDIGDKVEDGTLYRPAAGLCPTWGHIELOQ 100
DB 99 GNPW-----TEYMAKYDIEVHSGIRVLDGEDAEVAGTQYRLPSGKCVFGGIIEN 152
QY 101 PDRLEPRNNFLEDPVT-EKEYKOSGNPLPGGFNLVFTPSGORISPPM-----ELLEKNS 155
DB 153 SN-----TTFLEKPVATGNQDLKDGFAFP-----PTNPLISPMTLNMRPFYKNE 198
QY 156 NIKASTDLCRCAEFAFTVAMDKNKATKRYRPFYVDSKKRLCHILYVSMQMECKKYCS 215
DB 199 YKNDDELTLCSRHGN--MNPNDKNSNYKYPAYVDYNDKCKCHILYIAQENNGPRYCN 256
QY 216 VGEPRDILTWYCFKPKRKSTENHLLYGSAYYGEN-PDAFISKCPNALRGYRGVWKKG 273
DB 257 -KDESKNSMFCFRPAKDKLPENY-----TYSKVVVDNWEKVCPRKULENAKFGELWVD 309
QY 274 RCLDYTELDTLYIERVESKAQCWKTENDGVASDOPHTP--LTSQASNDWMP----- 327
DB 310 NCEBDFPHVNEF--SANDLFECNKLVFELS--ASDQPKQYEQHILTDYEKIKEGFKKNAS 364
QY 328 -----LHOSDPHSGGVGNRYGFYVDTTGGKCALSDQVPDCLVSDSAVSYT 376
DB 365 MIKSAFLPTGAFAKADRYKSHGKGYMGNVNRQTQ--KCEIFNVKPTCLINNSSYIATTA 421
QY 377 AGSLSEETPNFIIPSN-----PSVTPPTPEETA 404
DB 422 ALSHPIEVENHF--PCSLYKDEIKKEIERESKRIKLANDNDGKNKIIPRIETSDIDBL 479
QY 405 OCTADKRPDSFGADVQACKRQKTSYVGQIOTS-----VDCTAD--EONECG 452
DB 480 LKCPCEDEIYSNCSNCFVCK-----CYEKRAEYISNNEVVVKEEYKDEYADIPENKPTYD 534
QY 453 SNTALILAGLAVGVLLALLGGCCYFAKRLDRNKGYQAANHEHPEPSDRGARKRPSDL 508
DB 535 DMKIIILIASAANVAVLATILM-----VLYYKR--KGNAEKYDKNDPODYGKNSR 583
QY 509 SLMQEAEPSEFYDE 522
DB 584 NDEMILPEASFWGE 597

RESULT 34
ID 096718
AC 096718;
PRELIMINARY; PRT; 622 AA.
DT 01-DEC-2001 (Tremblrel. 19, Created)


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0Y 41 GNPFQANVEMKTEMERFNLTHHNSGIVYDLCQDEVDGTLRYEPAGLCPINGKHIELQ 100
Db 107 GNPM-----TEYMAKYDIEEHVHSGIRVDLGEDEAVGTOYRLSGKPFVEGKGIEN 160
0Y 101 PDRLEPRNNPLEDVTE--KEYWQSONPLPGGNNLAFVMPSGORISPEPM-----ELLEKS 155
Db 161 S-----KTFPLPVTATENODLKDGGAPF-----PTKPLMSBMTLDHMRDPRKDE 206
0Y 156 NIKASTDGRCAEFAPKTVAMDKNKNAKATYRYPFYDSKKRLCHLILYVSMQMBEGKKYCS 215
Db 207 YVKNLDELTLCSRHAGN--MNPNDNKSXKYPAYVDYDKKCHILYIAAGENNBRVCN 264
0Y 216 VKGEPPDLTWYCFKPKRSVTENHHLLYGSAYGEN-PDAFIKCPNOALRGYRFGYKWKG 274
Db 265 -KDESKRNSMFCFRPAKOKSPONY-----TYLSKVYVDMEKVCYCRKLNENKFGILWVDG 318
0Y 275 RCLDYTELDTYIERVESKACQCMVKTFFENDVGASDOPTHYP--LTSQASBMMWP----- 327
Db 319 NCEDLPVHNEF---SANDLFECKNLVFELS--ASDPKQYEOGHLTDYEKIKGFFKRXKNS 373
0Y 328 -----LHQSODPHSGVGRNYGFYYVDTTGBEGCALSDQVDCLVSDSAVSYTA 377
Db 374 MIKSAFLPTGAFKADRYKSHGKYWMGNYNRKTO--KCEIFNVKPTCLINNSYIATTA 430
0Y 378 AGLSLEEPNFIIPSN-----PSVPRPPEPTEL 405
Db 431 LSHPIEVENHF--PESLYKDEIKKEIERESKRIKLANDNDEGNKKIARIIRFISDDIDL 488
0Y 406 OCTADKFPDSFACDVQACKROKTSVCGQIOSTS-----VDCTAD--EQNEGCS 453
Db 469 KCPCAPEIVSNSTCHPFVCK-----CVERARVETSNNEVVAVEEYKDEYADAPIENHPYTD 543
0Y 454 NTALI---AGLAVGVLILLALLGGCCYFRAKRLDRNKGYOAAHNEHEFOSDRGAKRKPS 509
Db 544 NMKIIIASAAVAVALATIMV-----YYKR--KGANEYKDYKMDQPODYGKSKSR-N 592
0Y 510 DIMQABPSPFMEAEENINEOGDETHMYVEGDY 541
Db 593 DEMUDPEASFWGEEK--RASHTTVPVLMKPY 621

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[illegible]

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DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DN AMA-1.
OS Plasmodium cynomolgi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5827;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96123401; PubMed=8577338;
RA Dutta S., Mahotra P., Chahan S.;
RT "Sequence analysis of apical membrane antigen 1 (AMA-1) of Plasmodium
RT cynomolgi baetiellii."
RL Mol. Biochem. Parasitol. 73:267-270(1995).
DR EMBL; X86099; CA60053.1;
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1; 1
DR PRINTS; PRO1361; MEROZOITESA.
KW Signal.
FT SIGNAL.
FT NON_TER
SQ SEQUENCE 562 AA; 64606 MW; 84E78359AB49B42 CRC64;

Query Match 13.8%; Score 404; DB 5; Length 562;
Best Local Similarity 24.6%; Pred. No. 2.3e-26;
Matches 150; Conservative 97; Mismatches 238; Indels 124; Gaps 26;

OY 6 VQVLTVADCTIFASGL-----SSSTRRESQTL-----ASTSGNPFQANVEKTI 52
DB 4 IYIYLFSAOCLVHIGKCGRDEKPSRLTRSKNVLEKGPVSTRNSTNFW-----KA 57
OY 53 FMERFNLTHHOSGIYVDLGDKEVDGTLVREPAGLCPIMGKHIELQPDRLPYRNPLE 112
DB 58 FMEKYDVERTHSSGIRVDLGDALVENSKYRIPOGKCVFPGKGIENSN-----VSFLK 112
OY 113 DVPT-EKEYKOSGNPLPGGFNLNFTVPSGQRIISPPM-----ELLEKSNITASTDLGRCA 167
DB 113 PVATGDOCLKDGGFAFP-----ADHISPTIINLKERYSVEYEMKLNIDIALCR 163
OY 168 EFARFVY-AMDKNNKATKYRPFYVYDSKKRLCHILYVSMOLMEGKYSVSGEPDRLTWY 226
DB 164 THAASFMAQDON--SYRHPAVYDEKCKTCHMLYSAQENNGRYSRDAENRD-AMF 219
OY 227 CFKPRKSVTEHHILYGSAYVGENPDAFISCPNOALRGYRFGWKGRCLDYTELDTV 286
DB 220 CFNVDK-IIDPENLVYLSKVNRD--WEKCPKRLGNNAFGILWVGNCEIEIYVKEV- 274
OY 287 IERVESKAQCQVKTFFENDGVASDQPHY--DLTSQASWMDW-----PLHQ5 331
DB 275 --EAEDLRKCRIVFE--ASASDQPTQYEELTDYOKIQEGYRQNNRSMIKSAFLPVGA 330
OY 332 DQPHSGGVGRNYGYVDVTGEGKALSDQVPCLVSAASVSTAAG--SLSEETPNF 388
DB 331 NSDHFSGKRGFNANFDSVKN-RCYIINSKPTCLINDKNFVATALLSHPOEVNEPFC5 389
OY 389 IIPSN-----PSVTPPTPETALQCTADKPPDSFGACDVQAC 424
DB 390 IYKOEIEREIKOSRNNQLVNDKARIVLPRIIFISNDKIDMKCEPHEINSNCFNYVC 449
OY 425 KRQKTSYV--GGQIGSTG---VDCTADEQNECG--SNYALLAGLAVGVLLALLGGG 475
DB 450 -----NCVEKRAEIKENNEVVIKEEFKEDYQNEDEKSNKMLIIGVTVGCVVALASL 504
OY 476 CYFAKRLDRNKGVAAHHEHFFQSDRGARKRPS---DLMOEAPSPFDEAEENIEDGE 532
DB 505 FYFQKK-----EHNKDYKMDQAEQYKGPARTARDEMIDPEASFGEDEK---RASHT 552
OY 533 THVAVEGDY 541
DB 553 TPVLMKRY 561

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O96719
ID ID O96719 PRELIMINARY; PRT; 622 AA.
AC O96718;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=395-94; PubMed=11295182;
RC MEDLINE=21192561;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
RT 1) of Plasmodium falciparum. X. Asambo Bay Cohort Project."
RL Mol. Biochem. Parasitol. 113:279-287(2001).
DR EMBL; AY016432; AGS50139.1;
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MEROZOITESA.
FT NON_TER
SQ SEQUENCE 622 AA; 71954 MW; 6A6A2FD2525F6E59 CRC64;

Query Match 13.8%; Score 404; DB 5; Length 622;
Best Local Similarity 25.5%; Pred. No. 2.7e-26;
Matches 145; Conservative 85; Mismatches 217; Indels 122; Gaps 23;

OY 41 GNPFQANVEKTFMERFNLTHHOSGIYVDLGDKEVDGTLVREPAGLCPIMGKHIELQ 100
DB 107 GNPF-----TEYAKYDIEVHOSGIYVDLGDALVAGTOYRLPSKCPFGGIIEN 160
OY 101 PDRLPYRNPLEDYPT-EKEYKOSGNPLPGGFNLNFTVPSGQRIISPPMELL-----EKNS 155
DB 161 SN-----TTELPVATENQCLKDGGFAFP-----PKRLISPTLTLDQMRDFYKNE 206
OY 156 NIKASTDLGCAEAFATVAMDKNKATKYRPFYVYDSKKRLCHILYVSMOLMEGKYS 215
DB 207 YVKNLDELTLCSRAAGN--MNPNDENSNYKYPAVVDYKDKKCHILYIAQENNGPREYCN 264
OY 216 VKGEPDLYVYCFKPRKSVTEHHILYGSAYVGEN--PDATISCPNOALRGYRFGWK 274
DB 265 -KDSKNSWFCFRPAKDKSFQNT-----TYSKVVNDNMEKCPKRLONAKFGLWVDG 318
OY 275 RCLDYTELDTVIERVESKAQCQVKTFFENDGVASDQPHY--DLTSQASWMDW----- 327
DB 319 NCEDIPIVNF-----SANDLPECNKLVPFLS--ASDQKQYEQHLTDYEXIKEGKKNAS 373
OY 328 -----LHSGDQHSQGVGRNYGYVDVTGEGKALSDQVPCLVSAASVSTAAG 377
DB 374 MIKSAFLPTGAFKADRYKSHGKGMGNVYTERO--KCEIFVNYKPTCLINNSSYIAVTTA 430
OY 378 AGSLSEETPNFIIPSN-----PSVTPPTPETAL 405
DB 431 LSHPNVEYEHNF--PCSYIKOEIEREIKERESKRITKANDNDEGNKKTIAPRIIFISDDISL 488
OY 406 QCTADKPPDSFGACDVQACRKQKTSYV--GGQIGSTG---VDCTADEQNECGN----- 454
DB 489 KCPCAPEIVNSNCFNYVC-----CYEKRAVTSNNEVVVKEEYKEDYADIPENKPTVD 543
OY 455 --TALLAGLAVGVLLALLGGGCTPAKRLDRNKGVAAHHEHFFQSDRGARKRPS---DL 512
DB 544 KMKTIIASAVALATILM--VLYLKR-----KGAUEKYDKMDEPHQYKSNR-NDEN 595

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513 QEAEPSPFWDEAEENIEQDGETHVMVEGDY 541

Db 596 LDPEASFWGEEK--RASHTPVLMEKPY 621

Job time : 110 secs

RESULT 40

ID	Q9N9E6:		PRELIMINARY;	PRT;	526 AA.
AC	Q9N9E6:				
DT	01-OCT-2000	(TREMBLrel. 15,	Created)		
DT	01-OCT-2000	(TREMBLrel. 15,	Last sequence update)		
DT	01-JUN-2001	(TREMBLrel. 17,	Last annotation update)		
DE	Apical membrane antigen 1 (Fragment).				
GN	83/AWA-1.				
OS	Plasmodium falciparum.				
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
OX	NCBI_TaxId=51853;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-C1-4-1:				
RX	MEDLINE=20416492; PubMed=10960173;				
RA	Kocken C.H.M., Natum D.L., Massoungboji A., Ayivi B., Dubeld M.A., van der Weij A., Conway D.J., Sanni A., Thomas A.W.;				
RT	"Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-				
RT	mediated inhibition of red cell invasion."				
RL	Mol. Biochem. Parasitol. 109:147-156(2000).				
DR	EMBL; AJ271183; CAB97195.1; -				
DR	InterPro; IPR003298; Apmem_Ag1.				
DR	Pfam; PF02430; AMA-1; 1.				
DR	PRINTS; PR01361; MERZOITPESA.				
FT	NON_TER	1			
FT	NON_TER	526	526		
SQ	SEQUENCE	526 AA;	60834 MW;	FB9F562E4DBE8DD1 CRCE4;	